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## SEQUENCE LISTING

<110> Pompejus, Markus  
 Kroger, Burkhard  
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 Zelder, Oskar  
 Haberhauer, Gregor

<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
 INVOLVED IN GENETIC STABILITY, GENE EXPRESSION,  
 AND PROTEIN SECRETION AND FOLDING

<130> BGI-127CP

<140> 09/602,839

<141> 2000-06-23

<150> 60/141031

<151> 1999-06-25

<150> 60/143752

<151> 1999-07-14

<150> 60/151671

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<223> RXA01278

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 Val Ala Gln Glu Val  
 1 5

ctt aag gat cta aac aag gtc cgc aac atc ggc atc atg gcg cac atc 163  
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gat gct ggt aag acc acg acc acc gaa cgc atc ctc ttc tac acc ggc 211  
 Asp Ala Gly Lys Thr Thr Thr Thr Glu Arg Ile Leu Phe Tyr Thr Gly  
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atc aac cgt aag gtc ggt gag acc cac gac ggt ggc gca acc acc gac 259  
 Ile Asn Arg Lys Val Gly Glu Thr His Asp Gly Gly Ala Thr Thr Asp

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ggt acc tgt ttc tgg gat aac aac cag gtc aac atc att gac acc cct Val Thr Cys Phe Trp Asp Asn Asn Gln Val Asn Ile Ile Asp Thr Pro 70 75 80 85			355
ggc cac gtt gac ttc acc gtt gag gtt gag cgt tcc ctc cgc gtg ctt Gly His Val Asp Phe Thr Val Glu Val Glu Arg Ser Leu Arg Val Leu 90 95 100			403
gac ggc gca gtt gct gtg ttc gac ggc aag gaa ggc gtt gag cca cag Asp Gly Ala Val Ala Val Phe Asp Gly Lys Glu Gly Val Glu Pro Gln 105 110 115			451
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ctc cca atc ggt gct gag gac aac ttc gac ggc gtc atc gac ctt ctt Leu Pro Ile Gly Ala Glu Asp Asn Phe Asp Gly Val Ile Asp Leu Leu 170 175 180			643
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atg gag aag tac ttc ggt ggc gaa gag ctc agc atc gct gag atc aag Met Glu Lys Tyr Phe Gly Gly Glu Glu Leu Ser Ile Ala Glu Ile Lys 230 235 240 245			835
gca gct atc cgt aag atg gtt gtt aac tct gag atc tac cct gtt tac Ala Ala Ile Arg Lys Met Val Val Asn Ser Glu Ile Tyr Pro Val Tyr 250 255 260			883
tgt ggc acc gcc tac aag aac aag ggc atc cag cca ctg ctc gac gca Cys Gly Thr Ala Tyr Lys Asn Lys Gly Ile Gln Pro Leu Leu Asp Ala 265 270 275			931
gtc gtt gac ttc ctg cct tcc cca ctg gat ctc ggc gag acc aag ggc Val Val Asp Phe Leu Pro Ser Pro Leu Asp Leu Gly Glu Thr Lys Gly 280 285 290			979

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Thr Asp Val Lys Asp Pro Glu Lys Val Leu Thr Arg Lys Pro Ser Asp	
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Glu Glu Pro Leu Ser Ala Leu Ala Phe Lys Ile Ala Ala His Pro Phe	
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Phe Gly Lys Leu Thr Phe Val Arg Leu Tyr Ser Gly Lys Val Glu Pro	
330 335 340	
ggc gag cag gtt ctt aac tcc acc aag aac aag aag gaa cgc att ggt	1171
Gly Glu Gln Val Leu Asn Ser Thr Lys Asn Lys Lys Glu Arg Ile Gly	
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aag ctg ttc cag atg cac gcc aac aag gaa aac cct gtt gag gtt gca	1219
Lys Leu Phe Gln Met His Ala Asn Lys Glu Asn Pro Val Glu Val Ala	
360 365 370	
cac gct ggt aac atc tac gcg ttc atc ggc ctg aag gac acc acc acc	1267
His Ala Gly Asn Ile Tyr Ala Phe Ile Gly Leu Lys Asp Thr Thr Thr	
375 380 385	
ggt gac acc ctc tgt gac gca aac gct cca atc att ctt gag tcc atg	1315
Gly Asp Thr Leu Cys Asp Ala Asn Ala Pro Ile Ile Leu Glu Ser Met	
390 395 400 405	
gac ttc ccg gat cca gtt atc cag gtt gct att gag cct aag acc aag	1363
Asp Phe Pro Asp Pro Val Ile Gln Val Ala Ile Glu Pro Lys Thr Lys	
410 415 420	
tct gac cag gag aag ctc ggc gta gct atc cag aag ctt gct gaa gaa	1411
Ser Asp Gln Glu Lys Leu Gly Val Ala Ile Gln Lys Leu Ala Glu Glu	
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Asp Pro Thr Phe Thr Val His Leu Asp Asp Glu Ser Gly Gln Thr Val	
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att ggc ggc atg ggc gag ctg cac ctc gat gtt ctt gtt gac cgc atg	1507
Ile Gly Gly Met Gly Glu Leu His Leu Asp Val Leu Val Asp Arg Met	
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Lys Arg Glu Phe Lys Val Glu Ala Asn Ile Gly Asp Pro Gln Val Ala	
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tac cgt gag acc atc cgt aag cct gtt gag tcc ctc agc tac acc cac	1603
Tyr Arg Glu Thr Ile Arg Lys Pro Val Glu Ser Leu Ser Tyr Thr His	
490 495 500	
aag aag cag act ggt ggt tcc ggt cag ttc gct aag gtc atc atc acc	1651
Lys Lys Gln Thr Gly Gly Ser Gly Gln Phe Ala Lys Val Ile Ile Thr	
505 510 515	
att gag cct tac gca cct gag gca gac gag ctt gaa gag ggc gag tcc	1699
Ile Glu Pro Tyr Ala Pro Glu Ala Asp Glu Leu Glu Glu Gly Glu Ser	
520 525 530	

gca atc tac aag ttc gag aac gct gtc acc ggt ggt cgt gtt cca cgt 1747  
 Ala Ile Tyr Lys Phe Glu Asn Ala Val Thr Gly Gly Arg Val Pro Arg  
 535 540 545  
  
 gaa tac atc cca tcc gtt gac gct ggt atc cag gac gca atg cag tac 1795  
 Glu Tyr Ile Pro Ser Val Asp Ala Gly Ile Gln Asp Ala Met Gln Tyr  
 550 555 560 565  
  
 ggc ttc ctg gct ggc tac cca ctg gtt aac gtc aag gca acc ctt gaa 1843  
 Gly Phe Leu Ala Gly Tyr Pro Leu Val Asn Val Lys Ala Thr Leu Glu  
 570 575 580  
  
 gat ggc gct tac cac gac gtt gac tcc tct gaa atg gcc ttc aag ctc 1891  
 Asp Gly Ala Tyr His Asp Val Asp Ser Ser Glu Met Ala Phe Lys Leu  
 585 590 595  
  
 gcc ggt tcc cag gcg ttc aag gaa gct gtt gca aag gca aag cca gtc 1939  
 Ala Gly Ser Gln Ala Phe Lys Glu Ala Val Ala Lys Ala Lys Pro Val  
 600 605 610  
  
 ctc ctc gag cca atc atg tcc gtt gaa atc acc act cct gag gag tac 1987  
 Leu Leu Glu Pro Ile Met Ser Val Glu Ile Thr Thr Pro Glu Glu Tyr  
 615 620 625  
  
 atg ggt gaa gtc atc ggt gac gtg aac tcc cgc cgt ggc cag atc gct 2035  
 Met Gly Glu Val Ile Gly Asp Val Asn Ser Arg Arg Gly Gln Ile Ala  
 630 635 640 645  
  
 tcc atg gat gac cgt gca ggc gcc aag ctg gtt aag gct aag gtt cca 2083  
 Ser Met Asp Asp Arg Ala Gly Ala Lys Leu Val Lys Ala Lys Val Pro  
 650 655 660  
  
 ctg tct cag atg ttc ggt tac gtc ggt gac ctt cgc tct aag acc cag 2131  
 Leu Ser Gln Met Phe Gly Tyr Val Gly Asp Leu Arg Ser Lys Thr Gln  
 665 670 675  
  
 ggt cgt gca aac tac tcc atg gtc ttc gat tcc tac gct gag gtc cca 2179  
 Gly Arg Ala Asn Tyr Ser Met Val Phe Asp Ser Tyr Ala Glu Val Pro  
 680 685 690  
  
 gcc aac gtt gca gca gat gtt att gct gag cgc aac ggc acc gct tcc 2227  
 Ala Asn Val Ala Ala Asp Val Ile Ala Glu Arg Asn Gly Thr Ala Ser  
 695 700 705  
  
 taaagatcgt ttagatccga agg 2250

&lt;210&gt; 2

&lt;211&gt; 709

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 2

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Ile Met Ala His Ile Asp Ala Gly Lys Thr Thr Thr Thr Glu Arg Ile  
 20 25 30

Leu Phe Tyr Thr Gly Ile Asn Arg Lys Val Gly Glu Thr His Asp Gly  
 35 40 45

Gly Ala Thr Thr Asp Trp Met Glu Gln Glu Lys Glu Arg Gly Ile Thr  
 50 55 60  
 Ile Thr Ser Ala Ala Val Thr Cys Phe Trp Asp Asn Asn Gln Val Asn  
 65 70 75 80  
 Ile Ile Asp Thr Pro Gly His Val Asp Phe Thr Val Glu Val Glu Arg  
 85 90 95  
 Ser Leu Arg Val Leu Asp Gly Ala Val Ala Val Phe Asp Gly Lys Glu  
 100 105 110  
 Gly Val Glu Pro Gln Ser Glu Gln Val Trp Arg Gln Ala Thr Lys Tyr  
 115 120 125  
 Asp Val Pro Arg Ile Cys Phe Val Asn Lys Met Asp Lys Leu Gly Ala  
 130 135 140  
 Asp Phe Tyr Phe Thr Val Gly Thr Ile Glu Asp Arg Leu Gly Ala Lys  
 145 150 155 160  
 Pro Leu Val Met Gln Leu Pro Ile Gly Ala Glu Asp Asn Phe Asp Gly  
 165 170 175  
 Val Ile Asp Leu Leu Glu Met Lys Ala Leu Thr Trp Arg Gly Val Thr  
 180 185 190  
 Pro Ile Gly Thr Glu Ala Thr Val Glu Glu Ile Pro Ala Glu Leu Ala  
 195 200 205  
 Asp Arg Ala Ala Glu Tyr Arg Glu Lys Leu Leu Glu Thr Val Ala Glu  
 210 215 220  
 Ser Asp Glu Glu Leu Met Glu Lys Tyr Phe Gly Gly Glu Glu Leu Ser  
 225 230 235 240  
 Ile Ala Glu Ile Lys Ala Ala Ile Arg Lys Met Val Val Asn Ser Glu  
 245 250 255  
 Ile Tyr Pro Val Tyr Cys Gly Thr Ala Tyr Lys Asn Lys Gly Ile Gln  
 260 265 270  
 Pro Leu Leu Asp Ala Val Val Asp Phe Leu Pro Ser Pro Leu Asp Leu  
 275 280 285  
 Gly Glu Thr Lys Gly Thr Asp Val Lys Asp Pro Glu Lys Val Leu Thr  
 290 295 300  
 Arg Lys Pro Ser Asp Glu Glu Pro Leu Ser Ala Leu Ala Phe Lys Ile  
 305 310 315 320  
 Ala Ala His Pro Phe Phe Gly Lys Leu Thr Phe Val Arg Leu Tyr Ser  
 325 330 335  
 Gly Lys Val Glu Pro Gly Glu Gln Val Leu Asn Ser Thr Lys Asn Lys  
 340 345 350  
 Lys Glu Arg Ile Gly Lys Leu Phe Gln Met His Ala Asn Lys Glu Asn  
 355 360 365

Pro Val Glu Val Ala His Ala Gly Asn Ile Tyr Ala Phe Ile Gly Leu  
 370 375 380  
 Lys Asp Thr Thr Thr Gly Asp Thr Leu Cys Asp Ala Asn Ala Pro Ile  
 385 390 395 400  
 Ile Leu Glu Ser Met Asp Phe Pro Asp Pro Val Ile Gln Val Ala Ile  
 405 410 415  
 Glu Pro Lys Thr Lys Ser Asp Gln Glu Lys Leu Gly Val Ala Ile Gln  
 420 425 430  
 Lys Leu Ala Glu Glu Asp Pro Thr Phe Thr Val His Leu Asp Asp Glu  
 435 440 445  
 Ser Gly Gln Thr Val Ile Gly Gly Met Gly Glu Leu His Leu Asp Val  
 450 455 460  
 Leu Val Asp Arg Met Lys Arg Glu Phe Lys Val Glu Ala Asn Ile Gly  
 465 470 475 480  
 Asp Pro Gln Val Ala Tyr Arg Glu Thr Ile Arg Lys Pro Val Glu Ser  
 485 490 495  
 Leu Ser Tyr Thr His Lys Lys Gln Thr Gly Gly Ser Gly Gln Phe Ala  
 500 505 510  
 Lys Val Ile Ile Thr Ile Glu Pro Tyr Ala Pro Glu Ala Asp Glu Leu  
 515 520 525  
 Glu Glu Gly Glu Ser Ala Ile Tyr Lys Phe Glu Asn Ala Val Thr Gly  
 530 535 540  
 Gly Arg Val Pro Arg Glu Tyr Ile Pro Ser Val Asp Ala Gly Ile Gln  
 545 550 555 560  
 Asp Ala Met Gln Tyr Gly Phe Leu Ala Gly Tyr Pro Leu Val Asn Val  
 565 570 575  
 Lys Ala Thr Leu Glu Asp Gly Ala Tyr His Asp Val Asp Ser Ser Glu  
 580 585 590  
 Met Ala Phe Lys Leu Ala Gly Ser Gln Ala Phe Lys Glu Ala Val Ala  
 595 600 605  
 Lys Ala Lys Pro Val Leu Leu Glu Pro Ile Met Ser Val Glu Ile Thr  
 610 615 620  
 Thr Pro Glu Glu Tyr Met Gly Glu Val Ile Gly Asp Val Asn Ser Arg  
 625 630 635 640  
 Arg Gly Gln Ile Ala Ser Met Asp Asp Arg Ala Gly Ala Lys Leu Val  
 645 650 655  
 Lys Ala Lys Val Pro Leu Ser Gln Met Phe Gly Tyr Val Gly Asp Leu  
 660 665 670  
 Arg Ser Lys Thr Gln Gly Arg Ala Asn Tyr Ser Met Val Phe Asp Ser  
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695

700

Asn Gly Thr Ala Ser  
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Met Ala Asn Tyr Thr  
1 5  
gct gcg gat gtt aag aag ctc cgc gaa ctc acc ggt tcc ggc atg ctc 163  
Ala Ala Asp Val Lys Lys Leu Arg Glu Thr Gly Ser Gly Met Leu  
10 15 20  
gat tgc aag aag gct ctg gag gag tcc gct ggc gac ttc gac aag gct 211  
Asp Cys Lys Lys Ala Leu Glu Glu Ser Ala Gly Asp Phe Asp Lys Ala  
25 30 35  
gtt gag atc ctg cgc gtc aag ggc gca aag gac gtc gga aag cgt gca 259  
Val Glu Ile Leu Arg Val Lys Gly Ala Lys Asp Val Gly Lys Arg Ala  
40 45 50  
gag cgt aac gct acc gaa ggt ctc gtt gca gtt tct ggc aac acc atg 307  
Glu Arg Asn Ala Thr Glu Gly Leu Val Ala Val Ser Gly Asn Thr Met  
55 60 65  
gtc gag gtc aac tct gag acc gac ttc gtt gca aag aac tct gac ttc 355  
Val Glu Val Asn Ser Glu Thr Asp Phe Val Ala Lys Asn Ser Asp Phe  
70 75 80 85  
aag gaa ttc gct gca aag gtt gca gac gca gca gca gct gca aag gct 403  
Lys Glu Phe Ala Ala Lys Val Ala Asp Ala Ala Ala Ala Ala Lys Ala  
90 95 100  
aac tcc cag gaa gag ctc gca gca gtt gac gtg gac gga cag acc gca 451  
Asn Ser Gln Glu Glu Leu Ala Ala Val Asp Val Asp Gly Gln Thr Ala  
105 110 115  
gac gca gct ctg cag gag ttc tcc gca aag atc ggc gag aag ctt gag 499  
Asp Ala Ala Leu Gln Glu Phe Ser Ala Lys Ile Gly Glu Lys Leu Glu  
120 125 130  
ctt cgt cgc gca gta acc ctc gag ggc gac aag acc gct gtt tac ctc 547  
Leu Arg Arg Ala Val Thr Leu Glu Gly Asp Lys Thr Ala Val Tyr Leu  
135 140 145  
cac cag cgt tcc gct gac ctg cca cca gca gtt ggc gtt ttg gtt gct 595  
His Gln Arg Ser Ala Asp Leu Pro Pro Ala Val Gly Val Leu Val Ala

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Phe Thr Gly Glu Gly Glu Ala Ala Glu Ala Ala Ala Arg Gln Ala Ala	170	175	180	
atg cag att gct gct ctg aag gct tct tac ctc acc cgt gag gac gtt				691
Met Gln Ile Ala Ala Leu Lys Ala Ser Tyr Leu Thr Arg Glu Asp Val	185	190	195	
cct gca gag atc atc gag aag gag cgc tcc atc gct gag cag atc act				739
Pro Ala Glu Ile Ile Glu Lys Glu Arg Ser Ile Ala Glu Gln Ile Thr	200	205	210	
cgc gaa gag ggc aag cca gag cag gct atc cct aag atc gtt gag ggt				787
Arg Glu Glu Gly Lys Pro Glu Gln Ala Ile Pro Lys Ile Val Glu Gly	215	220	225	
cgt ttg aat ggc ttc tac aag gag aac gta ctt ctt gag cag tcc tcg				835
Arg Leu Asn Gly Phe Tyr Lys Glu Asn Val Leu Leu Glu Gln Ser Ser	230	235	240	245
gta gct gac agc aag aag acc gtt aag gct ctt ctg gac gag gct ggc				883
Val Ala Asp Ser Lys Lys Thr Val Lys Ala Leu Leu Asp Glu Ala Gly	250	255	260	
gtt acc gtc acc tcc ttc gct cgc ttc gag gtc ggc cag gct				925
Val Thr Val Thr Ser Phe Ala Arg Phe Glu Val Gly Gln Ala	265	270	275	
taaggccact tgaaggttgt ggg				948

&lt;210&gt; 4

&lt;211&gt; 275

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 4

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Asp Phe Asp Lys Ala Val Glu Ile Leu Arg Val Lys Gly Ala Lys Asp			
35 40 45			

Val Gly Lys Arg Ala Glu Arg Asn Ala Thr Glu Gly Leu Val Ala Val			
50 55 60			

Ser Gly Asn Thr Met Val Glu Val Asn Ser Glu Thr Asp Phe Val Ala			
65 70 75 80			

Lys Asn Ser Asp Phe Lys Glu Phe Ala Ala Lys Val Ala Asp Ala Ala			
85 90 95			

Ala Ala Ala Lys Ala Asn Ser Gln Glu Glu Leu Ala Ala Val Asp Val			
100 105 110			

Asp Gly Gln Thr Ala Asp Ala Ala Leu Gln Glu Phe Ser Ala Lys Ile			
---	--	--	--

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Thr Ala Val Tyr Leu His Gln Arg Ser Ala Asp Leu Pro Pro Ala Val 145 150 155 160		
Gly Val Leu Val Ala Phe Thr Gly Glu Gly Glu Ala Ala Glu Ala Ala 165 170 175		
Ala Arg Gln Ala Ala Met Gln Ile Ala Ala Leu Lys Ala Ser Tyr Leu 180 185 190		
Thr Arg Glu Asp Val Pro Ala Glu Ile Ile Glu Lys Glu Arg Ser Ile 195 200 205		
Ala Glu Gln Ile Thr Arg Glu Glu Gly Lys Pro Glu Gln Ala Ile Pro 210 215 220		
Lys Ile Val Glu Gly Arg Leu Asn Gly Phe Tyr Lys Glu Asn Val Leu 225 230 235 240		
Leu Glu Gln Ser Ser Val Ala Asp Ser Lys Lys Thr Val Lys Ala Leu 245 250 255		
Leu Asp Glu Ala Gly Val Thr Val Thr Ser Phe Ala Arg Phe Glu Val 260 265 270		
Gly Gln Ala 275		

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 <213> Corynebacterium glutamicum

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 <223> RXN01559

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 Val Leu Ile Val Val  
 1 5  
 ggt gtt tat gcg ttg gtg ctg ttg aca ggc gat cgt tct gcc aca cca 163  
 Gly Val Tyr Ala Leu Val Leu Leu Thr Gly Asp Arg Ser Ala Thr Pro  
 10 15 20  
 aaa ttg ggt att gat ctg caa ggc gga acc cga gtg acc ctc gtg ccg 211  
 Lys Leu Gly Ile Asp Leu Gln Gly Gly Thr Arg Val Thr Leu Val Pro  
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 cag ggg cag gat cca act cag gac cag ctg aat cag gca cgc acc att 259  
 Gln Gly Gln Asp Pro Thr Gln Asp Gln Leu Asn Gln Ala Arg Thr Ile  
 40 45 50

ctg gaa aac cgt gtg aac ggc atg ggc gtt tca ggt gca agc gtg gtc	307
Leu Glu Asn Arg Val Asn Gly Met Gly Val Ser Gly Ala Ser Val Val	
55 60 65	
gct gac ggt aac acg ctg gtg atc act gtt ccc ggg gaa aat acc gca	355
Ala Asp Gly Asn Thr Leu Val Ile Thr Val Pro Gly Glu Asn Thr Ala	
70 75 80 85	
cag gcg caa tcc cta gga cag acc tcc cag ctg ctg ttc cgt ccc gtt	403
Gln Ala Gln Ser Leu Gly Gln Thr Ser Gln Leu Leu Phe Arg Pro Val	
90 95 100	
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Gly Gln Ala Gly Met Pro Asp Met Thr Thr Leu Met Pro Glu Leu Glu	
105 110 115	
gag atg gcc aac agg tgg gtt gaa tac ggc gtc atc acc gaa gag cag	499
Glu Met Ala Asn Arg Trp Val Glu Tyr Gly Val Ile Thr Glu Glu Gln	
120 125 130	
gca aat gcc tcc ttg gag gaa atg aac acc gct gtt gca tcg acc act	547
Ala Asn Ala Ser Leu Glu Glu Met Asn Thr Ala Val Ala Ser Thr Thr	
135 140 145	
gcg gtg gaa ggc gaa gaa gca act gag cca gaa ccc gtc acc gtg tcg	595
Ala Val Glu Gly Glu Glu Ala Thr Glu Pro Glu Pro Val Thr Val Ser	
150 155 160 165	
gcg acc cct atg gat gag cca gcc aac tcc att gag gca aca cag cga	643
Ala Thr Pro Met Asp Glu Pro Ala Asn Ser Ile Glu Ala Thr Gln Arg	
170 175 180	
cgc cag gaa atc acg gac atg ctg cgc acc gac cgc cag tcc acc gat	691
Arg Gln Glu Ile Thr Asp Met Leu Arg Thr Asp Arg Gln Ser Thr Asp	
185 190 195	
ccc act gtc cag atc gct gca agt tct ttg atg cag tgc acc act gat	739
Pro Thr Val Gln Ile Ala Ala Ser Ser Leu Met Gln Cys Thr Thr Asp	
200 205 210	
gag atg gat cct ttg gcc ggc acc gat gat cca cgc ctg cca ttg gtg	787
Glu Met Asp Pro Leu Ala Gly Thr Asp Asp Pro Arg Leu Pro Leu Val	
215 220 225	
gca tgt gat cca gct gta ggt ggc gtg tat gta ctt gat cct gca cct	835
Ala Cys Asp Pro Ala Val Gly Gly Val Tyr Val Leu Asp Pro Ala Pro	
230 235 240 245	
ttg ctc aac ggc gaa acc gat gag gaa aat ggt gcg cgc cta acc ggt	883
Leu Leu Asn Gly Glu Thr Asp Glu Glu Asn Gly Ala Arg Leu Thr Gly	
250 255 260	
aat gag atc gat acc aac cgt ccc atc acc ggt gga ttc aac gcc cag	931
Asn Glu Ile Asp Thr Asn Arg Pro Ile Thr Gly Gly Phe Asn Ala Gln	
265 270 275	
tcc ggc cag atg gaa atc agc ttt gcc ttc aaa tcc ggc gat ggg gaa	979
Ser Gly Gln Met Glu Ile Ser Phe Ala Phe Lys Ser Gly Asp Gly Glu	
280 285 290	

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Glu Gly Ser Ala Thr Trp Ser Ser Leu Thr Ser Gln Tyr Leu Gln Gln	
295 300 305	
cag atc gcc atc acc ctg gac tct cag gtg att tct gca ccc gtg att	1075
Gln Ile Ala Ile Thr Leu Asp Ser Gln Val Ile Ser Ala Pro Val Ile	
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Gln Ser Ala Thr Pro Val Gly Ser Ala Thr Ser Ile Thr Gly Asp Phe	
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Thr Gln Thr Glu Ala Gln Asp Leu Ala Asn Asn Leu Arg Tyr Gly Ala	
345 350 355	
ttg ccc ctg agc ttc gca ggt gaa aac ggc gag cgc ggc gga act acc	1219
Leu Pro Leu Ser Phe Ala Gly Glu Asn Gly Glu Arg Gly Gly Thr Thr	
360 365 370	
acc acc gtt ccg cca tca cta ggc gca gca tcc ttg aag gcc gga ctg	1267
Thr Thr Val Pro Pro Ser Leu Gly Ala Ala Ser Leu Lys Ala Gly Leu	
375 380 385	
atc gca ggc atc gtc ggc atc gcg ctg gtc gcc atc ttc gtg ttc gcc	1315
Ile Ala Gly Ile Val Gly Ile Ala Leu Val Ala Ile Phe Val Phe Ala	
390 395 400 405	
tac tac cgc gtc ttc gga ttc gtt tcc ctg ttc acc ctg ttt gcc gca	1363
Tyr Tyr Arg Val Phe Gly Phe Val Ser Leu Phe Thr Leu Phe Ala Ala	
410 415 420	
ggc gtg ttg gtc tac ggc ctt ctg gta ctg ctg gga cgc tgg atc gga	1411
Gly Val Leu Val Tyr Gly Leu Leu Val Leu Leu Gly Arg Trp Ile Gly	
425 430 435	
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Tyr Ser Leu Asp Leu Ala Gly Ile Ala Gly Leu Ile Ile Gly Ile Gly	
440 445 450	
acc acc gcc gac tcc ttc gtg gtg ttc tat gag cgc atc aag gat gag	1507
Thr Thr Ala Asp Ser Phe Val Val Phe Tyr Glu Arg Ile Lys Asp Glu	
455 460 465	
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Ile Arg Glu Gly Arg Ser Phe Arg Ser Ala Val Pro Arg Ala Trp Glu	
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agc gcc aag cgc acc atc gtc aca ggc aac atg gtc act ttg ctc ggc	1603
Ser Ala Lys Arg Thr Ile Val Thr Gly Asn Met Val Thr Leu Leu Gly	
490 495 500	
gct atc gtg att tac ttg ctc gcg gtc ggc gaa gtc aag ggc ttt gcc	1651
Ala Ile Val Ile Tyr Leu Leu Ala Val Gly Glu Val Lys Gly Phe Ala	
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ttc acc ctg ggt ctg acc acc gta ttc gat ctc gtt gtc acc ttc ctg	1699
Phe Thr Leu Gly Leu Thr Thr Val Phe Asp Leu Val Val Thr Phe Leu	
520 525 530	
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Ile Thr Ala Pro Leu Val Ile Leu Ala Ser Arg Asn Pro Phe Phe Ala  
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aag tca tcg gtc aac ggc atg gga cga gtg atg aag ctc gtt gaa gaa 1795  
 Lys Ser Ser Val Asn Gly Met Gly Arg Val Met Lys Leu Val Glu Glu  
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cgc cgc gcc aac ggt gaa ttg gat gag cct gag tac ctg aaa aag atc 1843  
 Arg Arg Ala Asn Gly Glu Leu Asp Glu Pro Glu Tyr Leu Lys Lys Ile  
 570 575 580

cat gcc aag aat gcg gca gct gat aag gct tcc act gac aat tct tcc 1891  
 His Ala Lys Asn Ala Ala Ala Asp Lys Ala Ser Thr Asp Asn Ser Ser  
 585 590 595

act gac aat tct gaa gca cct ggc acc gat acg aac caa gag gag gag 1939  
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 Lys

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 35 40 45

Gln Ala Arg Thr Ile Leu Glu Asn Arg Val Asn Gly Met Gly Val Ser  
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Gly Ala Ser Val Val Ala Asp Gly Asn Thr Leu Val Ile Thr Val Pro  
 65 70 75 80

Gly Glu Asn Thr Ala Gln Ala Gln Ser Leu Gly Gln Thr Ser Gln Leu  
 85 90 95

Leu Phe Arg Pro Val Gly Gln Ala Gly Met Pro Asp Met Thr Thr Leu  
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Met Pro Glu Leu Glu Glu Met Ala Asn Arg Trp Val Glu Tyr Gly Val  
 115 120 125

Ile Thr Glu Glu Gln Ala Asn Ala Ser Leu Glu Glu Met Asn Thr Ala  
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Val Ala Ser Thr Thr Ala Val Glu Gly Glu Glu Ala Thr Glu Pro Glu  
 145 150 155 160

Pro Val Thr Val Ser Ala Thr Pro Met Asp Glu Pro Ala Asn Ser Ile

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Glu	Ala	Thr	Gln	Arg	Arg	Gln	Glu	Ile	Thr	Asp	Met	Leu	Arg	Thr	Asp		
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Gln	Cys	Thr	Thr	Asp	Glu	Met	Asp	Pro	Leu	Ala	Gly	Thr	Asp	Asp	Pro		
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Leu	Asp	Pro	Ala	Pro	Leu	Leu	Asn	Gly	Glu	Thr	Asp	Glu	Glu	Asn	Gly		
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Ala	Arg	Leu	Thr	Gly	Asn	Glu	Ile	Asp	Thr	Asn	Arg	Pro	Ile	Thr	Gly		
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Ser	Gly	Asp	Gly	Glu	Glu	Gly	Ser	Ala	Thr	Trp	Ser	Ser	Leu	Thr	Ser		
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Arg	Gly	Gly	Thr	Thr	Thr	Thr	Val	Pro	Pro	Ser	Leu	Gly	Ala	Ala	Ser		
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Ile	Phe	Val	Phe	Ala	Tyr	Tyr	Arg	Val	Phe	Gly	Phe	Val	Ser	Leu	Phe		
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Thr	Leu	Phe	Ala	Ala	Gly	Val	Leu	Val	Tyr	Gly	Leu	Leu	Val	Leu	Leu		
			420					425					430				
Gly	Arg	Trp	Ile	Gly	Tyr	Ser	Leu	Asp	Leu	Ala	Gly	Ile	Ala	Gly	Leu		
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	450					455					460						
Arg	Ile	Lys	Asp	Glu	Ile	Arg	Glu	Gly	Arg	Ser	Phe	Arg	Ser	Ala	Val		
465					470					475					480		
Pro	Arg	Ala	Trp	Glu	Ser	Ala	Lys	Arg	Thr	Ile	Val	Thr	Gly	Asn	Met		
				485					490					495			

Val Thr Leu Leu Gly Ala Ile Val Ile Tyr Leu Leu Ala Val Gly Glu  
500 505 510

Val Lys Gly Phe Ala Phe Thr Leu Gly Leu Thr Thr Val Phe Asp Leu  
515 520 525

Val Val Thr Phe Leu Ile Thr Ala Pro Leu Val Ile Leu Ala Ser Arg  
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Asn Pro Phe Phe Ala Lys Ser Ser Val Asn Gly Met Gly Arg Val Met  
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Lys Leu Val Glu Glu Arg Arg Ala Asn Gly Glu Leu Asp Glu Pro Glu  
565 570 575

Tyr Leu Lys Lys Ile His Ala Lys Asn Ala Ala Ala Asp Lys Ala Ser  
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Thr Asp Asn Ser Ser Thr Asp Asn Ser Glu Ala Pro Gly Thr Asp Thr  
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Asn Gln Glu Glu Glu Lys  
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 Phe Val Leu Ile Val Val Gly Val Tyr Ala Leu Val Leu Leu Thr Gly  
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gat cgt tct gcc aca cca aaa ttg ggt att gat ctg caa ggc gga acc 144  
 Asp Arg Ser Ala Thr Pro Lys Leu Gly Ile Asp Leu Gln Gly Gly Thr  
 35 40 45

cga gtg acc ctc gtg ccg cag ggg cag gat cca act cag gac cag ctg 192  
 Arg Val Thr Leu Val Pro Gln Gly Gln Asp Pro Thr Gln Asp Gln Leu  
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aat cag gca cgc acc att ctg gaa aac cgt gtg aac ggc atg ggc gtt 240  
 Asn Gln Ala Arg Thr Ile Leu Glu Asn Arg Val Asn Gly Met Gly Val  
 65 70 75 80

tca ggt gca agc gtg gtc gct gac ggt aac acg ctg gtg atc act gtt 288  
 Ser Gly Ala Ser Val Val Ala Asp Gly Asn Thr Leu Val Ile Thr Val  
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ccc ggg gaa aat acc gca cag gcg caa tcc cta gga cag acc tcc cag 336  
 Pro Gly Glu Asn Thr Ala Gln Ala Gln Ser Leu Gly Gln Thr Ser Gln  
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ctg ctg ttc cgt ccc gtt ggt cag gca gga atg ccc gat atg acc acg 384  
 Leu Leu Phe Arg Pro Val Gly Gln Ala Gly Met Pro Asp Met Thr Thr  
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ttg atg cca gag ctg gaa gag atg gcc aac agg tgg gtt gaa tac ggc 432  
 Leu Met Pro Glu Leu Glu Glu Met Ala Asn Arg Trp Val Glu Tyr Gly  
 130 135 140

gtc atc acc gaa gag cag gca aat gcc tcc ttg gag gaa atg aac acc 480  
 Val Ile Thr Glu Glu Gln Ala Asn Ala Ser Leu Glu Glu Met Asn Thr  
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 Ala Val Ala Ser Thr Thr Ala Val Glu Gly Glu Glu Ala Thr Glu Pro  
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gaa ccc gtc acc gtg tcg gcg acc cct atg gat gag cca gcc aac tcc 576  
 Glu Pro Val Thr Val Ser Ala Thr Pro Met Asp Glu Pro Ala Asn Ser  
 180 185 190

att gag gca aca cag cga cgc cag gaa atc acg gac atg ctg cgc acc 624  
 Ile Glu Ala Thr Gln Arg Arg Gln Glu Ile Thr Asp Met Leu Arg Thr  
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 Asp Arg Gln Ser Thr Asp Pro Thr Val  
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Asp Arg Ser Ala Thr Pro Lys Leu Gly Ile Asp Leu Gln Gly Gly Thr  
 35 40 45

Arg Val Thr Leu Val Pro Gln Gly Gln Asp Pro Thr Gln Asp Gln Leu  
 50 55 60

Asn Gln Ala Arg Thr Ile Leu Glu Asn Arg Val Asn Gly Met Gly Val  
 65 70 75 80

Ser Gly Ala Ser Val Val Ala Asp Gly Asn Thr Leu Val Ile Thr Val  
 85 90 95

Pro Gly Glu Asn Thr Ala Gln Ala Gln Ser Leu Gly Gln Thr Ser Gln  
 100 105 110

Leu Leu Phe Arg Pro Val Gly Gln Ala Gly Met Pro Asp Met Thr Thr

115	120	125
Leu Met Pro Glu Leu Glu Glu Met Ala Asn Arg Trp Val Glu Tyr Gly		
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Val Ile Thr Glu Glu Gln Ala Asn Ala Ser Leu Glu Glu Met Asn Thr		
145	150	155
Ala Val Ala Ser Thr Thr Ala Val Glu Gly Glu Glu Ala Thr Glu Pro		
165	170	175
Glu Pro Val Thr Val Ser Ala Thr Pro Met Asp Glu Pro Ala Asn Ser		
180	185	190
Ile Glu Ala Thr Gln Arg Arg Gln Glu Ile Thr Asp Met Leu Arg Thr		
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Asp Arg Gln Ser Thr Asp Pro Thr Val		
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Lys Ser Ser Val Asn Gly Met Gly Arg Val Met Lys Leu Val Glu Glu	
20 25 30	
cgc cgc gcc aac ggt gaa ttg gat gag cct gag tac ctg aaa aag atc	144
Arg Arg Ala Asn Gly Glu Leu Asp Glu Pro Glu Tyr Leu Lys Lys Ile	
35 40 45	
cat gcc aag aat gcg gca gct gat aag gct tcc act gac aat tct tcc	192
His Ala Lys Asn Ala Ala Ala Asp Lys Ala Ser Thr Asp Asn Ser Ser	
50 55 60	
act gac aat tct gaa gca cct ggc acc gat acg aac caa gag gag gag	240
Thr Asp Asn Ser Glu Ala Pro Gly Thr Asp Thr Asn Gln Glu Glu Glu	
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Lys	

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Lys Ser Ser Val Asn Gly Met Gly Arg Val Met Lys Leu Val Glu Glu  
 20 25 30

Arg Arg Ala Asn Gly Glu Leu Asp Glu Pro Glu Tyr Leu Lys Lys Ile  
 35 40 45

His Ala Lys Asn Ala Ala Ala Asp Lys Ala Ser Thr Asp Asn Ser Ser  
 50 55 60

Thr Asp Asn Ser Glu Ala Pro Gly Thr Asp Thr Asn Gln Glu Glu Glu  
 65 70 75 80

Lys

&lt;210&gt; 11

&lt;211&gt; 1332

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

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&lt;222&gt; (101)..(1309)

&lt;223&gt; RXA01558

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cacctggcac cgatacgaac caagaggagg agaagtagcc atg act gat tcc cag 115  
 Met Thr Asp Ser Gln  
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act gaa tca ctg tca act cag agc gta aaa cca gcc aaa aaa cgc agt 163  
 Thr Glu Ser Leu Ser Thr Gln Ser Val Lys Pro Ala Lys Lys Arg Ser  
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tgg ttc aac agc ctc tac acc ggt gac ggc ggc att gac ttc atc gcc 211  
 Trp Phe Asn Ser Leu Tyr Thr Gly Asp Gly Gly Ile Asp Phe Ile Ala  
 25 30 35

aaa acc aaa ctg tgg tac tgg atc acc ggc att ttg ctg gtt atc tcg 259  
 Lys Thr Lys Leu Trp Tyr Trp Ile Thr Gly Ile Leu Leu Val Ile Ser  
 40 45 50

atc ctg ttc atc gcc atc cgt ggc ttc tcc ctg agc atc gat ttc cag 307  
 Ile Leu Phe Ile Ala Ile Arg Gly Phe Ser Leu Ser Ile Asp Phe Gln  
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ggc ggt acc aag atg agc atg cca gca tcg gat tac tcc acc gaa cag 355  
 Gly Gly Thr Lys Met Ser Met Pro Ala Ser Asp Tyr Ser Thr Glu Gln  
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gtg gag gaa acc ttt act gaa gcc acc ggc att act ccg gaa atc gtg 403  
 Val Glu Glu Thr Phe Thr Glu Ala Thr Gly Ile Thr Pro Glu Ile Val  
 90 95 100

cag atc gtc ggt tcc ggc gac gcc cgc acc ctg gag atc tac tcc gag	451
Gln Ile Val Gly Ser Gly Asp Ala Arg Thr Leu Glu Ile Tyr Ser Glu	
105 110 115	
cga ctc agc gat gag gat gta gaa aaa gcc cgc ctg gcg atc tac gag	499
Arg Leu Ser Asp Glu Asp Val Glu Lys Ala Arg Leu Ala Ile Tyr Glu	
120 125 130	
gaa tac caa ccc cta aac tct gag ggc cag cca agc cca gat gcc atc	547
Glu Tyr Gln Pro Leu Asn Ser Glu Gly Gln Pro Ser Pro Asp Ala Ile	
135 140 145	
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Gly Asn Ser Thr Val Ser Glu Ser Trp Gly Ser Thr Ile Thr Gln Arg	
150 155 160 165	
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Met Val Leu Ala Leu Ile Ala Phe Leu Val Ile Ala Ala Ile Tyr Ile	
170 175 180	
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Ala Phe Arg Leu Glu Arg Glu Met Ala Ile Ala Ala Met Ala Ala Leu	
185 190 195	
gtt gtt gac ggc atc gtc atc gcc ggc atc tac gcc gtc atc ggc ctc	739
Val Val Asp Gly Ile Val Ile Ala Gly Ile Tyr Ala Val Ile Gly Leu	
200 205 210	
gaa gta tcc cca gca acc gtc atc ggt ctg ctc acc gtg ctg acc ttc	787
Glu Val Ser Pro Ala Thr Val Ile Gly Leu Leu Thr Val Leu Thr Phe	
215 220 225	
tcc atc tac gac acc gtc gtg gtc ttt gac aag gtc aga gaa aac acc	835
Ser Ile Tyr Asp Thr Val Val Val Phe Asp Lys Val Arg Glu Asn Thr	
230 235 240 245	
gaa ggc ttc gaa ggc agc cgc aga cga acc tac gcc gaa caa gcc aac	883
Glu Gly Phe Glu Gly Ser Arg Arg Arg Thr Tyr Ala Glu Gln Ala Asn	
250 255 260	
ctg gcg gtc aac cag acc ttc atg cgt tcg atc tcc acg aca atc atc	931
Leu Ala Val Asn Gln Thr Phe Met Arg Ser Ile Ser Thr Thr Ile Ile	
265 270 275	
tct gca ctt ccg atc atc gct ttg atg gtt gtc gcc gtc tgg atg atg	979
Ser Ala Leu Pro Ile Ile Ala Leu Met Val Val Ala Val Trp Met Met	
280 285 290	
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Gly Val Gly Thr Leu Lys Asp Leu Ala Leu Ile Gln Leu Ile Gly Val	
295 300 305	
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Ile Glu Gly Thr Phe Ser Ser Val Phe Leu Ala Thr Pro Leu Leu Val	
310 315 320 325	
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Ser Leu Lys Asn Arg Leu Ser Lys Thr Lys Ala His Thr Ala Ser Val	
330 335 340	

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Met Lys Leu Arg Asp Gly Gln Ser Thr Leu Ile Asp Ala Thr Pro His  
345 350 355

acc aac gcc gac gcc ttc gcg cac ggc acc gaa agc gac act gac ggt 1219  
Thr Asn Ala Asp Ala Phe Ala His Gly Thr Glu Ser Asp Thr Asp Gly  
360 365 370

gtg acc ccc gaa gca cct gca aaa cgt aca gta agc aaa ccc att gtg 1267  
Val Thr Pro Glu Ala Pro Ala Lys Arg Thr Val Ser Lys Pro Ile Val  
375 380 385

gat gat cac cga tca agc gga acc tgg cga cca ggc aga agc 1309  
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Ile Asp Phe Ile Ala Lys Thr Lys Leu Trp Tyr Trp Ile Thr Gly Ile  
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Leu Leu Val Ile Ser Ile Leu Phe Ile Ala Ile Arg Gly Phe Ser Leu  
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Ser Ile Asp Phe Gln Gly Gly Thr Lys Met Ser Met Pro Ala Ser Asp  
65 70 75 80

Tyr Ser Thr Glu Gln Val Glu Glu Thr Phe Thr Glu Ala Thr Gly Ile  
85 90 95

Thr Pro Glu Ile Val Gln Ile Val Gly Ser Gly Asp Ala Arg Thr Leu  
100 105 110

Glu Ile Tyr Ser Glu Arg Leu Ser Asp Glu Asp Val Glu Lys Ala Arg  
115 120 125

Leu Ala Ile Tyr Glu Glu Tyr Gln Pro Leu Asn Ser Glu Gly Gln Pro  
130 135 140

Ser Pro Asp Ala Ile Gly Asn Ser Thr Val Ser Glu Ser Trp Gly Ser  
145 150 155 160

Thr Ile Thr Gln Arg Met Val Leu Ala Leu Ile Ala Phe Leu Val Ile  
165 170 175

Ala Ala Ile Tyr Ile Ala Phe Arg Leu Glu Arg Glu Met Ala Ile Ala  
180 185 190

Ala Met Ala Ala Leu Val Val Asp Gly Ile Val Ile Ala Gly Ile Tyr  
 195 200 205

Ala Val Ile Gly Leu Glu Val Ser Pro Ala Thr Val Ile Gly Leu Leu  
 210 215 220

Thr Val Leu Thr Phe Ser Ile Tyr Asp Thr Val Val Val Phe Asp Lys  
 225 230 235 240

Val Arg Glu Asn Thr Glu Gly Phe Glu Gly Ser Arg Arg Arg Thr Tyr  
 245 250 255

Ala Glu Gln Ala Asn Leu Ala Val Asn Gln Thr Phe Met Arg Ser Ile  
 260 265 270

Ser Thr Thr Ile Ile Ser Ala Leu Pro Ile Ile Ala Leu Met Val Val  
 275 280 285

Ala Val Trp Met Met Gly Val Gly Thr Leu Lys Asp Leu Ala Leu Ile  
 290 295 300

Gln Leu Ile Gly Val Ile Glu Gly Thr Phe Ser Ser Val Phe Leu Ala  
 305 310 315 320

Thr Pro Leu Leu Val Ser Leu Lys Asn Arg Leu Ser Lys Thr Lys Ala  
 325 330 335

His Thr Ala Ser Val Met Lys Leu Arg Asp Gly Gln Ser Thr Leu Ile  
 340 345 350

Asp Ala Thr Pro His Thr Asn Ala Asp Ala Phe Ala His Gly Thr Glu  
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 Val Ala Gly Phe Asp  
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Trp	Phe	Trp	Lys	Ala	Leu	Gly	Gly	Lys	Ser	Gly	Arg	Asn	Gln	Lys	Arg	
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agc	gtg	gca	att	gtc	aat	cag	gta	gaa	aac	cat	gca	gcg	gaa	tta	gac	211
Ser	Val	Ala	Ile	Val	Asn	Gln	Val	Glu	Asn	His	Ala	Ala	Glu	Leu	Asp	
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gcg	ctg	gat	gat	gtt	gca	ttg	gcg	cag	cgt	gcc	aag	gat	cta	gcc	agt	259
Ala	Leu	Asp	Asp	Val	Ala	Leu	Ala	Gln	Arg	Ala	Lys	Asp	Leu	Ala	Ser	
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ggc	gga	cgc	att	gac	aat	cat	gcg	gaa	ttc	ctc	gcc	att	ttg	ggc	gtg	307
Gly	Gly	Arg	Ile	Asp	Asn	His	Ala	Glu	Phe	Leu	Ala	Ile	Leu	Gly	Val	
	55					60					65					
gca	tcg	cag	cgg	aca	ttg	ggg	ctg	aag	ccg	tat	ccg	gtg	caa	tca	cag	355
Ala	Ser	Gln	Arg	Thr	Leu	Gly	Leu	Lys	Pro	Tyr	Pro	Val	Gln	Ser	Gln	
70					75				80						85	
gcg	gtg	ttg	cgt	ctc	att	gaa	ggc	gat	gtg	gtg	cac	atg	gct	acc	ggc	403
Ala	Val	Leu	Arg	Leu	Ile	Glu	Gly	Asp	Val	Val	His	Met	Ala	Thr	Gly	
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gag	ggc	aag	act	ttg	gtg	ggc	gcg	atg	gcg	gcc	acc	ggc	ctg	ggg	ttg	451
Glu	Gly	Lys	Thr	Leu	Val	Gly	Ala	Met	Ala	Ala	Thr	Gly	Leu	Gly	Leu	
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atg	ggc	aag	cga	gtc	cat	tcg	att	acc	gtc	aat	gat	tat	ttg	gcg	gtg	499
Met	Gly	Lys	Arg	Val	His	Ser	Ile	Thr	Val	Asn	Asp	Tyr	Leu	Ala	Val	
		120					125					130				
cgc	gat	gcc	gaa	tgg	atg	cgg	cca	ttg	gtc	gaa	ttt	ttc	ggc	ctg	agc	547
Arg	Asp	Ala	Glu	Trp	Met	Arg	Pro	Leu	Val	Glu	Phe	Phe	Gly	Leu	Ser	
	135					140					145					
gtg	gcg	agc	atc	agc	gag	aag	atg	gat	gca	ggg	gag	cgt	cga	caa	gca	595
Val	Ala	Ser	Ile	Ser	Glu	Lys	Met	Asp	Ala	Gly	Glu	Arg	Arg	Gln	Ala	
150					155					160					165	
tat	aaa	gcc	gca	att	gtc	tac	gga	cct	gtc	aat	gaa	atc	ggc	ttt	gac	643
Tyr	Lys	Ala	Ala	Ile	Val	Tyr	Gly	Pro	Val	Asn	Glu	Ile	Gly	Phe	Asp	
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Asp	Tyr	Thr	Ile	Asp	Asp	Asp	Arg	Arg	Asn	Val	Phe	Leu	Thr	Asp	Lys	

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Tyr	Ala	Thr	Met	Ala	Glu	Lys	Asn	Arg	Ala	Ile	Ile	Asp	Glu	Ile	Ala					
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Val	Ser	Val	Leu	Asn	Ala	Lys	Asn	Asp	Ala	Glu	Glu	Ala	Gln	Ile	Ile					
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Ala	Glu	Ala	Gly	Asp	Ile	Gly	Arg	Val	Thr	Val	Ser	Thr	Gln	Met	Ala					
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Cys	Gln	Arg	Val	Thr	Glu	Gly	Gln	Leu	Leu	Glu	Ile	His	Ser	Gln	Ser	
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Gln	His	Ala	Pro	Ala	Arg	Ala	Ala	Glu	Leu	Glu	Asp	Leu	Asp	Gln	Ser	
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Asn	Trp	Ser	Glu	His	Leu	Ala	Leu	Met	Asp	Asp	Val	Arg	Glu	Ser	Ile	
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His	Leu	Arg	Ala	Ile	Ala	Arg	Glu	Thr	Pro	Leu	Asp	Glu	Tyr	His	Arg	
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Ile	Ala	Val	Arg	Glu	Phe	Lys	Asp	Leu	Ala	Gln	Arg	Ala	Val	Asp	Asp	
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Ala	Val	Ser	Thr	Phe	Lys	Ser	Val	Thr	Ile	Asp	His	Glu	Gly	Ala	His	
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 Pro Val Gln Ser Gln Ala Val Leu Arg Leu Ile Glu Gly Asp Val Val  
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 His Met Ala Thr Gly Glu Gly Lys Thr Leu Val Gly Ala Met Ala Ala  
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 Thr Gly Leu Gly Leu Met Gly Lys Arg Val His Ser Ile Thr Val Asn  
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 Phe Phe Gly Leu Ser Val Ala Ser Ile Ser Glu Lys Met Asp Ala Gly  
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 Glu Arg Arg Gln Ala Tyr Lys Ala Ala Ile Val Tyr Gly Pro Val Asn  
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 Glu Ile Gly Phe Asp Val Leu Arg Asp Gln Leu Ile Thr Arg Arg Glu  
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 Asp Ala Val Gln His Gly Ala Asp Val Ala Ile Ile Asp Glu Ala Asp  
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 Ser Val Leu Val Asp Glu Ala Leu Val Pro Leu Val Leu Ala Gly Asn  
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 Gln Pro Gly His Ala Pro Arg Gly Lys Ile Thr Asp Val Val Arg Ser  
                   225                                  230                                  235                                  240  
 Leu Lys Glu Asn Asp Asp Tyr Thr Ile Asp Asp Asp Arg Arg Asn Val

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Ser	Ala	Gln	Pro	Asp	Ala	Thr	Gly	Leu	Ile	Asp	Ser	Asp	Arg	Ile	Arg			
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 Ile His Ser Gln Ser Trp Asn Tyr Asn Lys Leu Leu Ala Asp Gln Arg  
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 Val Ile Ile Asp Glu Arg Arg Glu Arg Leu Leu Asp Thr Ala Leu Ala  
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 Trp Glu Glu Leu Ala Gln His Ala Pro Ala Arg Ala Ala Glu Leu Glu  
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 Asp Leu Asp Gln Ser Val Arg Glu Gln Ala Ala Arg Asp Ile Met Leu  
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 Tyr His Leu Asp Tyr Asn Trp Ser Glu His Leu Ala Leu Met Asp Asp  
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 Val Arg Glu Ser Ile His Leu Arg Ala Ile Ala Arg Glu Thr Pro Leu  
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 His Glu Gly Ala His Leu Asp Asp Glu Gly Leu Ala Arg Pro Ser Ala  
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 Val Phe Glu Ser Leu  
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Pro	Ala	Gln	Gln	Val	Ile	Lys	Ile	Val	Asn	Glu	Glu	Leu	Val	Gln	Ile	
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Ala	Glu	Ala	Phe	Arg	Asp	Gly	Val	Asp	Phe	Thr	Gly	Val	Val	Leu	Thr	
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Asp Phe Asp Val Phe His Pro Glu Arg Met Ala Ser Arg Ile Leu Gly	
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Pro Ile Gly Asn Ile Leu Lys Met Leu Pro Gly Gly Lys Gln Met Ser	
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Asn Ala Ser Arg Arg Lys Arg Ile Ala Asn Gly Ser Gly Val Thr Val	
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Ser Glu Val Asn Lys Leu Val Glu Arg Phe Phe Glu Ala Arg Lys Met	
425 430 435	
atg ggt caa atg gct ggc cag ttt ggc atg ggt cct gga tcc cgc agt	1459
Met Gly Gln Met Ala Gly Gln Phe Gly Met Gly Pro Gly Ser Arg Ser	
440 445 450	
gca acc aag aag caa gcc aag ggc cgc aag ggt aag aac ggc aag cgt	1507
Ala Thr Lys Lys Gln Ala Lys Gly Arg Lys Gly Lys Asn Gly Lys Arg	
455 460 465	
aaa cca gcc aag aag ggc cca acc cag cca aag atg cca atg ggc ggt	1555
Lys Pro Ala Lys Lys Gly Pro Thr Gln Pro Lys Met Pro Met Gly Gly	
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Met Pro Gly Met Pro Gly Met Pro Gly Met Gly Gly Ala Gly Met Pro	
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gac ctt gct gaa cta cag aag cag ctt ggt gga gca ggt ggc ggt atg	1651
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Arg	Gly	Lys	Gly 20	Lys	Leu	Thr	Glu	Ala 25	Asp	Ile	Asn	Ala	Thr 30	Thr	Arg
Glu	Ile	Arg 35	Leu	Ala	Leu	Leu	Glu 40	Ala	Asp	Val	Ser	Leu 45	Thr	Val	Val
Arg	Ala 50	Phe	Ile	Asn	Arg	Ile 55	Lys	Glu	Arg	Ala	Ala 60	Gly	Ala	Glu	Val
Ser 65	Gln	Ala	Leu	Asn	Pro 70	Ala	Gln	Gln	Val	Ile 75	Lys	Ile	Val	Asn	Glu 80
Glu	Leu	Val	Gln	Ile 85	Leu	Gly	Gly	Glu	Thr 90	Arg	Arg	Leu	Ser	Leu 95	Ala
Lys	Asn	Pro	Pro 100	Thr	Val	Ile	Met	Leu 105	Ala	Gly	Leu	Gln 110	Gly	Ala	Gly
Lys	Thr	Thr 115	Leu	Ala	Gly	Lys	Leu 120	Ser	Lys	His	Leu	Val 125	Lys	Gln	Gly
His 130	Thr	Pro	Met	Leu	Val	Ala 135	Cys	Asp	Leu	Gln	Arg 140	Pro	Gly	Ala	Val
Gln 145	Gln	Leu	Gln	Ile	Val 150	Gly	Glu	Arg	Ala	Gly 155	Val	Thr	Thr	Phe	Ala 160
Pro	Asp	Pro	Gly	Thr 165	Ser	Ile	Asp	Ser	Leu 170	Glu	His	Glu	Met	Gly 175	Thr
Ser	His	Gly 180	Asp	Pro	Val	Glu	Val	Ala 185	Arg	Ala	Gly	Ile	Glu 190	Glu	Ala
Lys	Arg	Thr 195	Gln	His	Asp	Ile	Val 200	Ile	Val	Asp	Thr	Ala 205	Gly	Arg	Leu
Gly 210	Ile	Asp	Glu	Thr	Leu	Met 215	Thr	Gln	Ala	Arg	Asn 220	Ile	Arg	Glu	Ala
Ile 225	Asn	Pro	Asp	Glu	Val 230	Leu	Phe	Val	Ile	Asp 235	Ser	Met	Ile	Gly	Gln 240

Asp Ala Val Asp Thr Ala Glu Ala Phe Arg Asp Gly Val Asp Phe Thr  
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 Gly Val Val Leu Thr Lys Leu Asp Gly Asp Ala Arg Gly Gly Ala Ala  
 260 265 270  
 Leu Ser Ile Arg Glu Val Thr Gly Lys Pro Ile Met Phe Ala Ser Thr  
 275 280 285  
 Gly Glu Lys Leu Asp Asp Phe Asp Val Phe His Pro Glu Arg Met Ala  
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 Ser Arg Ile Leu Gly Met Gly Asp Val Leu Ser Leu Ile Glu Gln Ala  
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 Glu Ala Val Met Asp Gln Glu Lys Ala Glu Val Ala Ala Gln Lys Leu  
 325 330 335  
 Gly Ser Gly Glu Leu Thr Leu Glu Asp Phe Leu Asp Gln Met Leu Met  
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 Gly Lys Gln Met Ser Gln Met Ala Asp Met Val Asp Glu Lys Gln Leu  
 370 375 380  
 Asp Arg Ile Gln Ala Ile Ile Arg Gly Met Thr Pro Ala Glu Arg Asp  
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 420 425 430  
 Glu Ala Arg Lys Met Met Gly Gln Met Ala Gly Gln Phe Gly Met Gly  
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 Pro Gly Ser Arg Ser Ala Thr Lys Lys Gln Ala Lys Gly Arg Lys Gly  
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 Lys Asn Gly Lys Arg Lys Pro Ala Lys Lys Gly Pro Thr Gln Pro Lys  
 465 470 475 480  
 Met Pro Met Gly Gly Met Pro Gly Met Pro Gly Met Pro Gly Met Gly  
 485 490 495  
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 Ala Gly Gly Gly Met Gly Gly Leu Gly Gly Gly Leu Pro Gly Met Pro  
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 Gly Lys Lys  
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Val Asp Gly Lys Glu Val Asp Asp Ser Tyr Thr Leu Gln Pro Ala Gln  
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 Phe Pro Ile Asp Glu Thr Ser Gly Ser Thr Glu Cys Gly Gly Asn Tyr  
 185 190 195  
  
 ttc ggc ccc atc acc gtg cct ggc ggc aac tac ttc atg atg ggt gac 739  
 Phe Gly Pro Ile Thr Val Pro Gly Gly Asn Tyr Phe Met Met Gly Asp  
 200 205 210  
  
 aac cgc acc aac tcc atg gat tcc cgc tac cac ctg ggc gat cag tac 787  
 Asn Arg Thr Asn Ser Met Asp Ser Arg Tyr His Leu Gly Asp Gln Tyr  
 215 220 225  
  
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 Gln Gly Thr Ile Pro Glu Glu Asn Ile Lys Gly Lys Val Gln Ala Ile  
 230 235 240 245  
  
 atc ctg cca ttt agc cga atc ggt ggc gtc gac gac cct gcc atc aaa 883  
 Ile Leu Pro Phe Ser Arg Ile Gly Gly Val Asp Asp Pro Ala Ile Lys  
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 ggc tagtaattcg cttttcgacg ccc 909  
 Gly

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 <212> PRT  
 <213> Corynebacterium glutamicum

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 Leu Ile Phe Val Leu Gln Thr Phe Val Gly Arg Met Tyr Met Ile Pro  
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 Ser Gly Ser Met Glu Pro Thr Leu His Gly Cys Glu Gly Cys Thr Gly  
 65 70 75 80  
  
 Asp Arg Ile Leu Val Glu Lys Val Ser Tyr Tyr Phe Thr Asp Pro Glu  
 85 90 95  
  
 Pro Gly Asp Val Val Val Phe Lys Gly Thr Asp Ser Trp Asn Val Gly  
 100 105 110  
  
 Phe Thr Thr Gln Arg Ser Asp Asn Ser Val Ile Arg Gly Leu Gln Asn  
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Met Ser Asn Val Thr  
1 5  
  
att tac gcc aca gat tgg tgc cct tac tgc cga tcc ctc ctc aaa ggt 163  
Ile Tyr Ala Thr Asp Trp Cys Pro Tyr Cys Arg Ser Leu Leu Lys Gly  
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ctc gac ggc caa gag tac gac ctc atc gac gtc gac caa gat gag gaa 211  
Leu Asp Gly Gln Glu Tyr Asp Leu Ile Asp Val Asp Gln Asp Glu Glu  
25 30 35  
  
gcc ggc gag tgg gtt aag tca gtc aac gac ggc aac cgc atc gtc cca 259  
Ala Gly Glu Trp Val Lys Ser Val Asn Asp Gly Asn Arg Ile Val Pro  
40 45 50  
  
acc gtg cgc tac tcc gat ggc acc cac gca act aat ccc cta gct gcg 307  
Thr Val Arg Tyr Ser Asp Gly Thr His Ala Thr Asn Pro Leu Ala Ala  
55 60 65  
  
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Met Ser Glu Gln Pro																
1 5																
gct tcc att aag cat tat gac ctc atc atc att ggt acc ggc tct gga															163	
Ala Ser Ile Lys His Tyr Asp Leu Ile Ile Ile Gly Thr Gly Ser Gly																
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Asn Ser Ile Pro Gly Pro Glu Phe Asp Asp Lys Ser Ile Ala Ile Val																
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Glu Lys Gly Ala Phe Gly Gly Thr Cys Leu Asn Val Gly Cys Ile Pro																
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Thr Lys Met Tyr Val Tyr Ala Ala Asp Ile Ala Gln Glu Ile Gln Glu																
55 60 65																
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Ser Ala Arg Leu Gly Ile Asp Ala Thr Val Asn Ser Val Asp Trp Pro																
70 75 80 85																
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Ser Ile Val Ser Arg Val Phe Asp Lys Arg Ile Asp Leu Ile Ala Gln																

90										95					100					
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Gly	Gly	Glu	Ala	Tyr	Arg	Arg	Gly	Pro	Glu	Thr	Pro	Asn	Ile	Asp	Val					
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tat	gac	atg	cac	gca	tcg	ttt	gtt	gat	tcc	aag	aca	atc	tcc	act	ggt	499				
Tyr	Asp	Met	His	Ala	Ser	Phe	Val	Asp	Ser	Lys	Thr	Ile	Ser	Thr	Gly					
120			125				130													
att	gcc	ggc	caa	gaa	cag	ctg	atc	agc	ggt	act	gac	att	gta	atc	gca	547				
Ile	Ala	Gly	Gln	Glu	Gln	Leu	Ile	Ser	Gly	Thr	Asp	Ile	Val	Ile	Ala					
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acc	ggc	tcc	cgc	cct	tac	atc	cct	gaa	gct	att	gca	gag	tcc	ggc	gca	595				
Thr	Gly	Ser	Arg	Pro	Tyr	Ile	Pro	Glu	Ala	Ile	Ala	Glu	Ser	Gly	Ala					
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cgc	tac	tac	acc	aac	gaa	gac	atc	atg	cgc	ctg	gca	cag	cag	cct	gaa	643				
Arg	Tyr	Tyr	Thr	Asn	Glu	Asp	Ile	Met	Arg	Leu	Ala	Gln	Gln	Pro	Glu					
170				175				180												
tct	ttg	gtg	att	gtt	ggg	ggc	ggt	ttc	atc	gct	ttg	gaa	ttt	gct	cac	691				
Ser	Leu	Val	Ile	Val	Gly	Gly	Gly	Phe	Ile	Ala	Leu	Glu	Phe	Ala	His					
185			190				195													
gtt	ttt	gaa	gcg	ctt	ggc	acc	aag	gtc	acc	atc	ctc	aac	cgc	tct	gac	739				
Val	Phe	Glu	Ala	Leu	Gly	Thr	Lys	Val	Thr	Ile	Leu	Asn	Arg	Ser	Asp					
200			205				210													
gtg	ctg	ctg	cgc	gag	gca	gat	gca	gac	atc	tcc	gcg	aaa	atc	ctc	gag	787				
Val	Leu	Leu	Arg	Glu	Ala	Asp	Ala	Asp	Ile	Ser	Ala	Lys	Ile	Leu	Glu					
215			220				225													
ctt	tcc	aaa	aag	cgt	ttc	gac	gtc	cgc	ctc	agc	act	gcg	gtc	acc	gca	835				
Leu	Ser	Lys	Lys	Arg	Phe	Asp	Val	Arg	Leu	Ser	Thr	Ala	Val	Thr	Ala					
230	235				240				245											
gta	cac	aac	aag	gcc	gac	ggc	ggc	gtg	aag	atc	tcc	acc	gac	acc	ggc	883				
Val	His	Asn	Lys	Ala	Asp	Gly	Gly	Val	Lys	Ile	Ser	Thr	Asp	Thr	Gly					
250				255				260												
gac	gac	atc	gag	gca	gat	att	ttg	ctc	gtt	gcc	act	ggt	cgc	acc	cct	931				
Asp	Asp	Ile	Glu	Ala	Asp	Ile	Leu	Leu	Val	Ala	Thr	Gly	Arg	Thr	Pro					
265			270				275													
aac	ggc	aac	caa	atg	aac	ttg	gac	gcc	gca	ggc	atc	gag	atg	aac	ggt	979				
Asn	Gly	Asn	Gln	Met	Asn	Leu	Asp	Ala	Ala	Gly	Ile	Glu	Met	Asn	Gly					
280			285				290													
cgt	tcc	atc	aag	gtt	gat	gaa	ttc	ggt	cgc	acc	agt	gtt	gaa	ggc	gtg	1027				
Arg	Ser	Ile	Lys	Val	Asp	Glu	Phe	Gly	Arg	Thr	Ser	Val	Glu	Gly	Val					
295			300				305													
tgg	gcg	ctt	ggc	gat	gtc	tcc	tcc	cct	tac	aag	ctc	aag	cac	gta	gcc	1075				
Trp	Ala	Leu	Gly	Asp	Val	Ser	Ser	Pro	Tyr	Lys	Leu	Lys	His	Val	Ala					
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Asn	Ala	Glu	Met	Arg	Ala	Ile	Lys	His	Asn	Leu	Ala	Asn	Pro	Asn	Asp					
330				335				340												

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 345 350 355  
  
 cct cag atc tcg cag gtc ggc atg act gag cag gag gcg cgt gaa gct 1219  
 Pro Gln Ile Ser Gln Val Gly Met Thr Glu Gln Glu Ala Arg Glu Ala  
 360 365 370  
  
 ggc ctc gac atc act gtg aag atc cag aac tac tct gat gtg gct tat 1267  
 Gly Leu Asp Ile Thr Val Lys Ile Gln Asn Tyr Ser Asp Val Ala Tyr  
 375 380 385  
  
 ggc tgg gcc atg gaa gat aag gat gga ttc gtt aag ctc aat tgc cga 1315  
 Gly Trp Ala Met Glu Asp Lys Asp Gly Phe Val Lys Leu Asn Cys Arg  
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 taaggacacc ggcaagttgg tcg 1338

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 <212> PRT  
 <213> Corynebacterium glutamicum

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 Ser Ile Ala Ile Val Glu Lys Gly Ala Phe Gly Gly Thr Cys Leu Asn  
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 Val Gly Cys Ile Pro Thr Lys Met Tyr Val Tyr Ala Ala Asp Ile Ala  
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 Gln Glu Ile Gln Glu Ser Ala Arg Leu Gly Ile Asp Ala Thr Val Asn  
 65 70 75 80  
  
 Ser Val Asp Trp Pro Ser Ile Val Ser Arg Val Phe Asp Lys Arg Ile  
 85 90 95  
  
 Asp Leu Ile Ala Gln Gly Gly Glu Ala Tyr Arg Arg Gly Pro Glu Thr  
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 Pro Asn Ile Asp Val Tyr Asp Met His Ala Ser Phe Val Asp Ser Lys  
 115 120 125  
  
 Thr Ile Ser Thr Gly Ile Ala Gly Gln Glu Gln Leu Ile Ser Gly Thr  
 130 135 140  
  
 Asp Ile Val Ile Ala Thr Gly Ser Arg Pro Tyr Ile Pro Glu Ala Ile  
 145 150 155 160  
  
 Ala Glu Ser Gly Ala Arg Tyr Tyr Thr Asn Glu Asp Ile Met Arg Leu  
 165 170 175  
  
 Ala Gln Gln Pro Glu Ser Leu Val Ile Val Gly Gly Gly Phe Ile Ala  
 180 185 190

Leu Glu Phe Ala His Val Phe Glu Ala Leu Gly Thr Lys Val Thr Ile  
 195 200 205  
 Leu Asn Arg Ser Asp Val Leu Leu Arg Glu Ala Asp Ala Asp Ile Ser  
 210 215 220  
 Ala Lys Ile Leu Glu Leu Ser Lys Lys Arg Phe Asp Val Arg Leu Ser  
 225 230 235 240  
 Thr Ala Val Thr Ala Val His Asn Lys Ala Asp Gly Gly Val Lys Ile  
 245 250 255  
 Ser Thr Asp Thr Gly Asp Asp Ile Glu Ala Asp Ile Leu Leu Val Ala  
 260 265 270  
 Thr Gly Arg Thr Pro Asn Gly Asn Gln Met Asn Leu Asp Ala Ala Gly  
 275 280 285  
 Ile Glu Met Asn Gly Arg Ser Ile Lys Val Asp Glu Phe Gly Arg Thr  
 290 295 300  
 Ser Val Glu Gly Val Trp Ala Leu Gly Asp Val Ser Ser Pro Tyr Lys  
 305 310 315 320  
 Leu Lys His Val Ala Asn Ala Glu Met Arg Ala Ile Lys His Asn Leu  
 325 330 335  
 Ala Asn Pro Asn Asp Leu Gln Lys Met Pro His Asp Phe Val Pro Ser  
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 Ala Val Phe Thr Asn Pro Gln Ile Ser Gln Val Gly Met Thr Glu Gln  
 355 360 365  
 Glu Ala Arg Glu Ala Gly Leu Asp Ile Thr Val Lys Ile Gln Asn Tyr  
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 385 390 395 400  
 Lys Leu Asn Cys Arg  
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 <213> Corynebacterium glutamicum

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 <222> (101)..(577)  
 <223> RXA00539

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 Met Thr Ser Ile His  
 1 5

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			20					25					30		
Ala	Ser	Lys	Cys	Gly	Leu	Thr	Pro	Gln	Tyr	Glu	Gly	Leu	Gln	Lys	Leu
		35					40					45			
Tyr	Glu	Glu	Tyr	Gln	Asp	Arg	Gly	Phe	Phe	Val	Ile	Gly	Val	Pro	Cys
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Met Thr Asn Thr Leu															
1 5															
tgg aat tca gta gac gaa ctc ccc atc cac gac tcc tgg aaa cca gta															163
Trp Asn Ser Val Asp Glu Leu Pro Ile His Asp Ser Trp Lys Pro Val															
10 15 20															
ctc aaa cca gtc gaa gac gcc atc cga aaa ctc ggt gta ttc ctc gcg															211
Leu Lys Pro Val Glu Asp Ala Ile Arg Lys Leu Gly Val Phe Leu Ala															
25 30 35															
gaa gaa gaa ttc ctt cca cca gta gat gac gta ttc aga gca ttt agc															259
Glu Glu Glu Phe Leu Pro Pro Val Asp Asp Val Phe Arg Ala Phe Ser															
40 45 50															
tac ccc ttt gac gca gta aaa gta ctg atc atg gga caa gac cca tat															307
Tyr Pro Phe Asp Ala Val Lys Val Leu Ile Met Gly Gln Asp Pro Tyr															
55 60 65															
ccc acc cca gga cat gcc atg gga ctg agc ttt tcc acc caa cca gac															355
Pro Thr Pro Gly His Ala Met Gly Leu Ser Phe Ser Thr Gln Pro Asp															
70 75 80 85															
gta cga cca ctg cca cgg agc ctg aac aat atc ttc aaa gag ctg gtg															403
Val Arg Pro Leu Pro Arg Ser Leu Asn Asn Ile Phe Lys Glu Leu Val															
90 95 100															
agt gat gtc ggc tct tta ggc gat tgc gcg tca gag cag ggg gcc ttg															451
Ser Asp Val Gly Ser Leu Gly Asp Ser Ala Ser Glu Gln Gly Ala Leu															
105 110 115															

gac tta ggt att aac gcg ccg ggc tct gtc gct ggc aca caa gtt gcc 499  
 Asp Leu Gly Ile Asn Ala Pro Gly Ser Val Ala Gly Thr Gln Val Ala  
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ttg ccc gcg gac ggc gac ctc cgt gca tgg agc aac caa ggc gtc gca 547  
 Leu Pro Ala Asp Gly Asp Leu Arg Ala Trp Ser Asn Gln Gly Val Ala  
 135 140 145

ttg ttc aac cgc gta ctc acc gtc cac cca ggc cag gcc gga agc cac 595  
 Leu Phe Asn Arg Val Leu Thr Val His Pro Gly Gln Ala Gly Ser His  
 150 155 160 165

aag ggt aaa ggc tgg gaa gcg gta acc gaa cag gcg att aaa gcc ttg 643  
 Lys Gly Lys Gly Trp Glu Ala Val Thr Glu Gln Ala Ile Lys Ala Leu  
 170 175 180

gcg gag ccg gat caa ccc ttg gtg gca atc ctg tgg ggt aaa caa gcc 691  
 Ala Glu Arg Asp Gln Pro Leu Val Ala Ile Leu Trp Gly Lys Gln Ala  
 185 190 195

caa gag gta cag aaa ttc ctt gga gat acg ccg tgt atc tgc tca gtg 739  
 Gln Glu Val Gln Lys Phe Leu Gly Asp Thr Pro Cys Ile Cys Ser Val  
 200 205 210

cac cca tca ccg ctg tcg gcg tcg aga ggc ttt ttt ggc tct aag cct 787  
 His Pro Ser Pro Leu Ser Ala Ser Arg Gly Phe Phe Gly Ser Lys Pro  
 215 220 225

ttt agt cgt gcg aac gaa atc tta agc agc ctc ggt gcc acc gag atc 835  
 Phe Ser Arg Ala Asn Glu Ile Leu Ser Ser Leu Gly Ala Thr Glu Ile  
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gat tgg tcg ctg taaggtatct gattatgtcc agt 870  
 Asp Trp Ser Leu

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 <211> 249  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

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Gly Val Phe Leu Ala Glu Glu Glu Phe Leu Pro Pro Val Asp Asp Val  
 35 40 45

Phe Arg Ala Phe Ser Tyr Pro Phe Asp Ala Val Lys Val Leu Ile Met  
 50 55 60

Gly Gln Asp Pro Tyr Pro Thr Pro Gly His Ala Met Gly Leu Ser Phe  
 65 70 75 80

Ser Thr Gln Pro Asp Val Arg Pro Leu Pro Arg Ser Leu Asn Asn Ile  
 85 90 95

Phe Lys Glu Leu Val Ser Asp Val Gly Ser Leu Gly Asp Ser Ala Ser  
 100 105 110  
 Glu Gln Gly Ala Leu Asp Leu Gly Ile Asn Ala Pro Gly Ser Val Ala  
 115 120 125  
 Gly Thr Gln Val Ala Leu Pro Ala Asp Gly Asp Leu Arg Ala Trp Ser  
 130 135 140  
 Asn Gln Gly Val Ala Leu Phe Asn Arg Val Leu Thr Val His Pro Gly  
 145 150 155 160  
 Gln Ala Gly Ser His Lys Gly Lys Gly Trp Glu Ala Val Thr Glu Gln  
 165 170 175  
 Ala Ile Lys Ala Leu Ala Glu Arg Asp Gln Pro Leu Val Ala Ile Leu  
 180 185 190  
 Trp Gly Lys Gln Ala Gln Glu Val Gln Lys Phe Leu Gly Asp Thr Pro  
 195 200 205  
 Cys Ile Cys Ser Val His Pro Ser Pro Leu Ser Ala Ser Arg Gly Phe  
 210 215 220  
 Phe Gly Ser Lys Pro Phe Ser Arg Ala Asn Glu Ile Leu Ser Ser Leu  
 225 230 235 240  
 Gly Ala Thr Glu Ile Asp Trp Ser Leu  
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<210> 27  
 <211> 1203  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1180)  
 <223> RXN00484

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 Val Asp Ala Thr Leu  
 1 5  
 aaa aag aat ctc cgt gat aaa ggg att gaa gtg cat agc cac cca ggt 163  
 Lys Lys Asn Leu Arg Asp Lys Gly Ile Glu Val His Ser His Pro Gly  
 10 15 20  
 ttt tta ctc act gaa ccc tgg gaa gtc agt acc gct acc gga act ccc 211  
 Phe Leu Leu Thr Glu Pro Trp Glu Val Ser Thr Ala Thr Gly Thr Pro  
 25 30 35  
 tac aag gta ttt acc cct ttt tct aaa gcc gca tgg gaa gta gcc aga 259  
 Tyr Lys Val Phe Thr Pro Phe Ser Lys Ala Ala Trp Glu Val Ala Arg  
 40 45 50

gta cat gca tat gaa act gtt aaa aac aat gtg cct gtc ccc tct cac	307
Val His Ala Tyr Glu Thr Val Lys Asn Asn Val Pro Val Pro Ser His	
55 60 65	
cta aca gga cca gag gat gta gag ctg ccc atc cta gaa atg gag caa	355
Leu Thr Gly Pro Glu Asp Val Glu Leu Pro Ile Leu Glu Met Glu Gln	
70 75 80 85	
cct ttt tgg tca aca acg tta gtt aag gag tgt gct ccc ggt gaa aaa	403
Pro Phe Trp Ser Thr Thr Leu Val Lys Glu Cys Ala Pro Gly Glu Lys	
90 95 100	
aat gct tcg gaa aaa ctc ttt gat ttt ttg gaa cat cta cag gac tac	451
Asn Ala Ser Glu Lys Leu Phe Asp Phe Leu Glu His Leu Gln Asp Tyr	
105 110 115	
ccg caa gct cga gac agc tta gcc cga tcc gct aca agt aaa tta tct	499
Pro Gln Ala Arg Asp Ser Leu Ala Arg Ser Ala Thr Ser Lys Leu Ser	
120 125 130	
gct cat cta agg ttt ggt gag atc agc atc cac cgc gtg tgg gca gag	547
Ala His Leu Arg Phe Gly Glu Ile Ser Ile His Arg Val Trp Ala Glu	
135 140 145	
act gca gca ata gac tct gaa gga act gag tta ttt ctt aaa gaa ctt	595
Thr Ala Ala Ile Asp Ser Glu Gly Thr Glu Leu Phe Leu Lys Glu Leu	
150 155 160 165	
ctc tgg aga gat ttt gcg tgg cat cga ctt tat gcc ctg cca cac atg	643
Leu Trp Arg Asp Phe Ala Trp His Arg Leu Tyr Ala Leu Pro His Met	
170 175 180	
gac acg caa aac gtt cgt atg caa ttt aat cgt ttc gga tgg tcc tgg	691
Asp Thr Gln Asn Val Arg Met Gln Phe Asn Arg Phe Gly Trp Ser Trp	
185 190 195	
gat ccg agt gaa aaa gat aaa ctt aac act cca tcc acc cct ctt atc	739
Asp Pro Ser Glu Lys Asp Lys Leu Asn Thr Pro Ser Thr Pro Leu Ile	
200 205 210	
ccc acc aaa gct gac caa ttc cat gag gat tta gca gca tgg cgt gca	787
Pro Thr Lys Ala Asp Gln Phe His Glu Asp Leu Ala Ala Trp Arg Ala	
215 220 225	
gga aaa aca gga att ccg ctg gtc gat gca ggc atg cga gaa tta tgg	835
Gly Lys Thr Gly Ile Pro Leu Val Asp Ala Gly Met Arg Glu Leu Trp	
230 235 240 245	
gcc acc ggg tca atg cac aat cgc gtc aga atg gta gta gct agt ttt	883
Ala Thr Gly Ser Met His Asn Arg Val Arg Met Val Val Ala Ser Phe	
250 255 260	
tta acc aag aat ctc cag atc cat tgg cgt cat ggc gaa gaa tgg ttt	931
Leu Thr Lys Asn Leu Gln Ile His Trp Arg His Gly Glu Glu Trp Phe	
265 270 275	
tgg gaa act ctc gta gat gct gat cca gct tct aat gct ttc aac tgg	979
Trp Glu Thr Leu Val Asp Ala Asp Pro Ala Ser Asn Ala Phe Asn Trp	
280 285 290	
caa tgg gct gcg ggt agc gga gat gac gct tcg cct tat ttc cgt att	1027

Gln Trp Ala Ala Gly Ser Gly Asp Asp Ala Ser Pro Tyr Phe Arg Ile  
 295 300 305  
 ttt aat ccg gtc acc caa gcg aaa aaa ttt gat cca gat gaa act tat 1075  
 Phe Asn Pro Val Thr Gln Ala Lys Lys Phe Asp Pro Asp Glu Thr Tyr  
 310 315 320 325  
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 Ile Arg Arg Trp Val Pro Glu Tyr Gly Thr Pro Ser Tyr Pro Asp Pro  
 330 335 340  
 atc gtc gat ctg aaa gaa tcc cgt caa att gct tta gac gcc tac tct 1171  
 Ile Val Asp Leu Lys Glu Ser Arg Gln Ile Ala Leu Asp Ala Tyr Ser  
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 Ala Ile Lys  
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 <212> PRT  
 <213> Corynebacterium glutamicum

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 Ala Thr Gly Thr Pro Tyr Lys Val Phe Thr Pro Phe Ser Lys Ala Ala  
 35 40 45  
 Trp Glu Val Ala Arg Val His Ala Tyr Glu Thr Val Lys Asn Asn Val  
 50 55 60  
 Pro Val Pro Ser His Leu Thr Gly Pro Glu Asp Val Glu Leu Pro Ile  
 65 70 75 80  
 Leu Glu Met Glu Gln Pro Phe Trp Ser Thr Thr Leu Val Lys Glu Cys  
 85 90 95  
 Ala Pro Gly Glu Lys Asn Ala Ser Glu Lys Leu Phe Asp Phe Leu Glu  
 100 105 110  
 His Leu Gln Asp Tyr Pro Gln Ala Arg Asp Ser Leu Ala Arg Ser Ala  
 115 120 125  
 Thr Ser Lys Leu Ser Ala His Leu Arg Phe Gly Glu Ile Ser Ile His  
 130 135 140  
 Arg Val Trp Ala Glu Thr Ala Ala Ile Asp Ser Glu Gly Thr Glu Leu  
 145 150 155 160  
 Phe Leu Lys Glu Leu Leu Trp Arg Asp Phe Ala Trp His Arg Leu Tyr  
 165 170 175  
 Ala Leu Pro His Met Asp Thr Gln Asn Val Arg Met Gln Phe Asn Arg  
 180 185 190

Phe Gly Trp Ser Trp Asp Pro Ser Glu Lys Asp Lys Leu Asn Thr Pro  
 195 200 205  
 Ser Thr Pro Leu Ile Pro Thr Lys Ala Asp Gln Phe His Glu Asp Leu  
 210 215 220  
 Ala Ala Trp Arg Ala Gly Lys Thr Gly Ile Pro Leu Val Asp Ala Gly  
 225 230 235 240  
 Met Arg Glu Leu Trp Ala Thr Gly Ser Met His Asn Arg Val Arg Met  
 245 250 255  
 Val Val Ala Ser Phe Leu Thr Lys Asn Leu Gln Ile His Trp Arg His  
 260 265 270  
 Gly Glu Glu Trp Phe Trp Glu Thr Leu Val Asp Ala Asp Pro Ala Ser  
 275 280 285  
 Asn Ala Phe Asn Trp Gln Trp Ala Ala Gly Ser Gly Asp Asp Ala Ser  
 290 295 300  
 Pro Tyr Phe Arg Ile Phe Asn Pro Val Thr Gln Ala Lys Lys Phe Asp  
 305 310 315 320  
 Pro Asp Glu Thr Tyr Ile Arg Arg Trp Val Pro Glu Tyr Gly Thr Pro  
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 Leu Asp Ala Tyr Ser Ala Ile Lys  
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 <223> FRXA00484

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 Val His Ser His Pro  
 1 5  
 ggt ttt tta ctc act gaa ccc tgg gaa gtc agt acc gct acc gga act 163  
 Gly Phe Leu Leu Thr Glu Pro Trp Glu Val Ser Thr Ala Thr Gly Thr  
 10 15 20  
 ccc tac aag gta ttt acc cct ttt tct aaa gcc gca tgg gaa gta gcc 211  
 Pro Tyr Lys Val Phe Thr Pro Phe Ser Lys Ala Ala Trp Glu Val Ala  
 25 30 35  
 aga gta cat gca tat gaa act gtt aaa aac aat gtg cct gtc ccc tct 259

Arg	Val	His	Ala	Tyr	Glu	Thr	Val	Lys	Asn	Asn	Val	Pro	Val	Pro	Ser	
		40					45					50				
cac	cta	aca	gga	cca	gag	gat	gta	gag	ctg	ccc	atc	cta	gaa	atg	gag	307
His	Leu	Thr	Gly	Pro	Glu	Asp	Val	Glu	Leu	Pro	Ile	Leu	Glu	Met	Glu	
	55					60					65					
caa	cct	ttt	tgg	tca	aca	acg	tta	gtt	aag	gag	tgt	gct	ccc	ggg	gaa	355
Gln	Pro	Phe	Trp	Ser	Thr	Thr	Leu	Val	Lys	Glu	Cys	Ala	Pro	Gly	Glu	
70					75					80					85	
aaa	aat	gct	tcg	gaa	aaa	ctc	ttt	gat	ttt	ttg	gaa	cat	cta	cag	gac	403
Lys	Asn	Ala	Ser	Glu	Lys	Leu	Phe	Asp	Phe	Leu	Glu	His	Leu	Gln	Asp	
				90					95					100		
tac	ccg	caa	gct	cga	gac	agc	tta	gcc	cga	tcc	gct	aca	agt	aaa	tta	451
Tyr	Pro	Gln	Ala	Arg	Asp	Ser	Leu	Ala	Arg	Ser	Ala	Thr	Ser	Lys	Leu	
			105					110					115			
tct	gct	cat	cta	agg	ttt	ggg	gag	atc	agc	atc	cac	cgc	gtg	tgg	gca	499
Ser	Ala	His	Leu	Arg	Phe	Gly	Glu	Ile	Ser	Ile	His	Arg	Val	Trp	Ala	
		120					125					130				
gag	act	gca	gca	ata	gac	tct	gaa	gga	act	gag	tta	ttt	ctt	aaa	gaa	547
Glu	Thr	Ala	Ala	Ile	Asp	Ser	Glu	Gly	Thr	Glu	Leu	Phe	Leu	Lys	Glu	
	135					140					145					
ctt	ctc	tgg	aga	gat	ttt	gcg	tgg	cat	cga	ctt	tat	gcc	ctg	cca	cac	595
Leu	Leu	Trp	Arg	Asp	Phe	Ala	Trp	His	Arg	Leu	Tyr	Ala	Leu	Pro	His	
150					155					160					165	
atg	gac	acg	caa	aac	gtt	cgt	atg	caa	ttt	aat	cgt	ttc	gga	tgg	tcc	643
Met	Asp	Thr	Gln	Asn	Val	Arg	Met	Gln	Phe	Asn	Arg	Phe	Gly	Trp	Ser	
				170					175					180		
tgg	gat	ccg	agt	gaa	aaa	gat	aaa	ctt	aac	act	cca	tcc	acc	cct	ctt	691
Trp	Asp	Pro	Ser	Glu	Lys	Asp	Lys	Leu	Asn	Thr	Pro	Ser	Thr	Pro	Leu	
			185					190					195			
atc	ccc	acc	aaa	gct	gac	caa	ttc	cat	gag	gat	tta	gca	gca	tgg	cgt	739
Ile	Pro	Thr	Lys	Ala	Asp	Gln	Phe	His	Glu	Asp	Leu	Ala	Ala	Trp	Arg	
		200					205					210				
gca	gga	aaa	aca	gga	att	ccg	ctg	gtc	gat	gca	ggc	atg	cga	gaa	tta	787
Ala	Gly	Lys	Thr	Gly	Ile	Pro	Leu	Val	Asp	Ala	Gly	Met	Arg	Glu	Leu	
	215					220					225					
tgg	gcc	acc	ggg	tca	atg	cac	aat	cgc	gtc	aga	atg	gta	gta	gct	agt	835
Trp	Ala	Thr	Gly	Ser	Met	His	Asn	Arg	Val	Arg	Met	Val	Val	Ala	Ser	
230					235					240					245	
ttt	tta	acc	aag	aat	ctc	cag	atc	cat	tgg	cgt	cat	ggc	gaa	gaa	tgg	883
Phe	Leu	Thr	Lys	Asn	Leu	Gln	Ile	His	Trp	Arg	His	Gly	Glu	Glu	Trp	
				250					255					260		
ttt	tgg	gaa	act	ctc	gta	gat	gct	gat	cca	gct	tct	aat	gct	ttc	aac	931
Phe	Trp	Glu	Thr	Leu	Val	Asp	Ala	Asp	Pro	Ala	Ser	Asn	Ala	Phe	Asn	
			265					270					275			
tgg	caa	tgg	gct	gcg	ggg	agc	gga	gat	gac	gct	tcg	cct	tat	ttc	cgt	979
Trp	Gln	Trp	Ala	Ala	Gly	Ser	Gly	Asp	Asp	Ala	Ser	Pro	Tyr	Phe	Arg	

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Ile Phe Asn Pro Val Thr Gln Ala Lys Lys Phe Asp Pro Asp Glu Thr			
295	300	305	
tat att cgt cgc tgg gta ccc gaa tat gga aca cca tca tat ccg gat			1075
Tyr Ile Arg Arg Trp Val Pro Glu Tyr Gly Thr Pro Ser Tyr Pro Asp			
310	315	320	325
ccc atc gtc gat ctg aaa gaa tcc cgt caa att gct tta gac gcc tac			1123
Pro Ile Val Asp Leu Lys Glu Ser Arg Gln Ile Ala Leu Asp Ala Tyr			
	330	335	340
tct gcg att aag tgagtttacg cgcagctttt aaa			1158
Ser Ala Ile Lys			
345			

&lt;210&gt; 30

&lt;211&gt; 345

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 30

Val His Ser His Pro Gly Phe Leu Leu Thr Glu Pro Trp Glu Val Ser
1 5 10 15

Thr Ala Thr Gly Thr Pro Tyr Lys Val Phe Thr Pro Phe Ser Lys Ala
20 25 30

Ala Trp Glu Val Ala Arg Val His Ala Tyr Glu Thr Val Lys Asn Asn
35 40 45

Val Pro Val Pro Ser His Leu Thr Gly Pro Glu Asp Val Glu Leu Pro
50 55 60

Ile Leu Glu Met Glu Gln Pro Phe Trp Ser Thr Thr Leu Val Lys Glu
65 70 75 80

Cys Ala Pro Gly Glu Lys Asn Ala Ser Glu Lys Leu Phe Asp Phe Leu
85 90 95

Glu His Leu Gln Asp Tyr Pro Gln Ala Arg Asp Ser Leu Ala Arg Ser
100 105 110

Ala Thr Ser Lys Leu Ser Ala His Leu Arg Phe Gly Glu Ile Ser Ile
115 120 125

His Arg Val Trp Ala Glu Thr Ala Ala Ile Asp Ser Glu Gly Thr Glu
130 135 140

Leu Phe Leu Lys Glu Leu Leu Trp Arg Asp Phe Ala Trp His Arg Leu
145 150 155 160

Tyr Ala Leu Pro His Met Asp Thr Gln Asn Val Arg Met Gln Phe Asn
165 170 175

Arg Phe Gly Trp Ser Trp Asp Pro Ser Glu Lys Asp Lys Leu Asn Thr
180 185 190

Pro Ser Thr Pro Leu Ile Pro Thr Lys Ala Asp Gln Phe His Glu Asp  
 195 200 205  
 Leu Ala Ala Trp Arg Ala Gly Lys Thr Gly Ile Pro Leu Val Asp Ala  
 210 215 220  
 Gly Met Arg Glu Leu Trp Ala Thr Gly Ser Met His Asn Arg Val Arg  
 225 230 235 240  
 Met Val Val Ala Ser Phe Leu Thr Lys Asn Leu Gln Ile His Trp Arg  
 245 250 255  
 His Gly Glu Glu Trp Phe Trp Glu Thr Leu Val Asp Ala Asp Pro Ala  
 260 265 270  
 Ser Asn Ala Phe Asn Trp Gln Trp Ala Ala Gly Ser Gly Asp Asp Ala  
 275 280 285  
 Ser Pro Tyr Phe Arg Ile Phe Asn Pro Val Thr Gln Ala Lys Lys Phe  
 290 295 300  
 Asp Pro Asp Glu Thr Tyr Ile Arg Arg Trp Val Pro Glu Tyr Gly Thr  
 305 310 315 320  
 Pro Ser Tyr Pro Asp Pro Ile Val Asp Leu Lys Glu Ser Arg Gln Ile  
 325 330 335  
 Ala Leu Asp Ala Tyr Ser Ala Ile Lys  
 340 345

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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA02476

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 Met Ser Phe Thr Ala  
 1 5  
 ttt caa aca gcc ctg ctc gtg tgg ttt aga gca aat gcc cgc gat ctt 163  
 Phe Gln Thr Ala Leu Leu Val Trp Phe Arg Ala Asn Ala Arg Asp Leu  
 10 15 20  
 gcg tgg cgt gat ccc aat act tca gca tgg gga att ctc ctt tca gag 211  
 Ala Trp Arg Asp Pro Asn Thr Ser Ala Trp Gly Ile Leu Leu Ser Glu  
 25 30 35  
 gtg atg agc caa caa act ccc gtc gcg cga gtc gag ccg att tgg cgt 259  
 Val Met Ser Gln Gln Thr Pro Val Ala Arg Val Glu Pro Ile Trp Arg  
 40 45 50  
 gag tgg atg gaa aaa tgg ccc act ccg gaa gat ttc gcg aat gcg agc 307

Glu	Trp	Met	Glu	Lys	Trp	Pro	Thr	Pro	Glu	Asp	Phe	Ala	Asn	Ala	Ser	
	55					60					65					
acc	gat	gag	att	ttg	cgg	tcg	tgg	ggc	aag	ttg	ggc	tat	cca	cgt	agg	355
Thr	Asp	Glu	Ile	Leu	Arg	Ser	Trp	Gly	Lys	Leu	Gly	Tyr	Pro	Arg	Arg	
70					75				80						85	
gcg	ctg	agg	ttg	aag	gaa	tgt	gcg	gag	gtg	atc	gtc	gaa	aag	cat	gcc	403
Ala	Leu	Arg	Leu	Lys	Glu	Cys	Ala	Glu	Val	Ile	Val	Glu	Lys	His	Ala	
				90					95					100		
ggc	gag	gtg	ccg	gat	acg	gtg	gag	gcg	ctg	ctc	gcg	ttg	ccg	ggg	atc	451
Gly	Glu	Val	Pro	Asp	Thr	Val	Glu	Ala	Leu	Leu	Ala	Leu	Pro	Gly	Ile	
			105					110					115			
ggt	gat	tac	acg	gcg	cgc	gcg	gtc	gcg	gcg	ttt	cat	ttt	ggg	cag	cgc	499
Gly	Asp	Tyr	Thr	Ala	Arg	Ala	Val	Ala	Ala	Phe	His	Phe	Gly	Gln	Arg	
	120						125					130				
gtg	ccg	gtg	gtc	gat	acg	aac	gtg	cgt	cgc	gtg	tac	cag	cgc	gcg	gta	547
Val	Pro	Val	Val	Asp	Thr	Asn	Val	Arg	Arg	Val	Tyr	Gln	Arg	Ala	Val	
	135					140					145					
gcc	gga	cgt	tac	ctt	gcg	ggg	cct	gcg	aaa	aag	caa	gag	ctt	atc	gac	595
Ala	Gly	Arg	Tyr	Leu	Ala	Gly	Pro	Ala	Lys	Lys	Gln	Glu	Leu	Ile	Asp	
150					155				160					165		
gtc	tcc	ctt	ctc	ctt	ccc	aac	act	cac	gcc	cca	gaa	ttc	tct	gcc	gca	643
Val	Ser	Leu	Leu	Leu	Pro	Asn	Thr	His	Ala	Pro	Glu	Phe	Ser	Ala	Ala	
				170					175					180		
ata	atg	gag	ttg	ggt	gct	ctt	atc	tgc	acg	gcc	act	tcc	cca	aag	tgt	691
Ile	Met	Glu	Leu	Gly	Ala	Leu	Ile	Cys	Thr	Ala	Thr	Ser	Pro	Lys	Cys	
			185					190					195			
gac	acc	tgc	cca	ctg	ctt	gac	cag	tgt	caa	tgg	caa	aaa	ctt	ggc	tgt	739
Asp	Thr	Cys	Pro	Leu	Leu	Asp	Gln	Cys	Gln	Trp	Gln	Lys	Leu	Gly	Cys	
	200						205					210				
ccc	tcc	ccg	agt	gaa	gag	gag	ctg	gct	tca	gcg	aaa	aag	cgt	gtg	cag	787
Pro	Ser	Pro	Ser	Glu	Glu	Glu	Leu	Ala	Ser	Ala	Lys	Lys	Arg	Val	Gln	
	215					220					225					
aaa	ttt	gtg	gga	acc	gac	cga	caa	gtc	cgt	ggc	cta	atc	atg	gac	gta	835
Lys	Phe	Val	Gly	Thr	Asp	Arg	Gln	Val	Arg	Gly	Leu	Ile	Met	Asp	Val	
230					235					240				245		
ctg	cgc	aat	gcc	acc	gca	cct	gtg	cca	cta	tcc	gcg	att	gat	gtc	gtg	883
Leu	Arg	Asn	Ala	Thr	Ala	Pro	Val	Pro	Leu	Ser	Ala	Ile	Asp	Val	Val	
				250					255					260		
tgg	cct	gac	gat	gcc	caa	cgc	tcc	cgg	gcg	ctg	ttt	tcg	ctc	att	gag	931
Trp	Pro	Asp	Asp	Ala	Gln	Arg	Ser	Arg	Ala	Leu	Phe	Ser	Leu	Ile	Glu	
			265					270					275			
gac	gga	ctc	gcg	gaa	caa	aat	gag	gcg	ggt	tat	ttc	cac	ctg	cca	cgg	979
Asp	Gly	Leu	Ala	Glu	Gln	Asn	Glu	Ala	Gly	Tyr	Phe	His	Leu	Pro	Arg	
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taa	acc	act	g	cg	cg	cct	g	ca	aaa							1002

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 32

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Asn	Ala	Arg	Asp	Leu	Ala	Trp	Arg	Asp	Pro	Asn	Thr	Ser	Ala	Trp	Gly	20	25	30	
Ile	Leu	Leu	Ser	Glu	Val	Met	Ser	Gln	Gln	Thr	Pro	Val	Ala	Arg	Val	35	40	45	
Glu	Pro	Ile	Trp	Arg	Glu	Trp	Met	Glu	Lys	Trp	Pro	Thr	Pro	Glu	Asp	50	55	60	
Phe	Ala	Asn	Ala	Ser	Thr	Asp	Glu	Ile	Leu	Arg	Ser	Trp	Gly	Lys	Leu	65	70	75	80
Gly	Tyr	Pro	Arg	Arg	Ala	Leu	Arg	Leu	Lys	Glu	Cys	Ala	Glu	Val	Ile	85	90	95	
Val	Glu	Lys	His	Ala	Gly	Glu	Val	Pro	Asp	Thr	Val	Glu	Ala	Leu	Leu	100	105	110	
Ala	Leu	Pro	Gly	Ile	Gly	Asp	Tyr	Thr	Ala	Arg	Ala	Val	Ala	Ala	Phe	115	120	125	
His	Phe	Gly	Gln	Arg	Val	Pro	Val	Val	Asp	Thr	Asn	Val	Arg	Arg	Val	130	135	140	
Tyr	Gln	Arg	Ala	Val	Ala	Gly	Arg	Tyr	Leu	Ala	Gly	Pro	Ala	Lys	Lys	145	150	155	160
Gln	Glu	Leu	Ile	Asp	Val	Ser	Leu	Leu	Leu	Pro	Asn	Thr	His	Ala	Pro	165	170	175	
Glu	Phe	Ser	Ala	Ala	Ile	Met	Glu	Leu	Gly	Ala	Leu	Ile	Cys	Thr	Ala	180	185	190	
Thr	Ser	Pro	Lys	Cys	Asp	Thr	Cys	Pro	Leu	Leu	Asp	Gln	Cys	Gln	Trp	195	200	205	
Gln	Lys	Leu	Gly	Cys	Pro	Ser	Pro	Ser	Glu	Glu	Glu	Leu	Ala	Ser	Ala	210	215	220	
Lys	Lys	Arg	Val	Gln	Lys	Phe	Val	Gly	Thr	Asp	Arg	Gln	Val	Arg	Gly	225	230	235	240
Leu	Ile	Met	Asp	Val	Leu	Arg	Asn	Ala	Thr	Ala	Pro	Val	Pro	Leu	Ser	245	250	255	
Ala	Ile	Asp	Val	Val	Trp	Pro	Asp	Asp	Ala	Gln	Arg	Ser	Arg	Ala	Leu	260	265	270	
Phe	Ser	Leu	Ile	Glu	Asp	Gly	Leu	Ala	Glu	Gln	Asn	Glu	Ala	Gly	Tyr	275	280	285	

Phe His Leu Pro Arg  
290

<210> 33

<211> 891

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(868)

<223> RXA00102

<400> 33

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gacttttcgt ggaggcttcg gacggcgcta acctgatgac atg cca gaa ggt gat 115  
Met Pro Glu Gly Asp  
1 5

tcc gta ttc caa ctc tcc cgc aaa ctt caa ttc atg cgc gga aga gaa 163  
Ser Val Phe Gln Leu Ser Arg Lys Leu Gln Phe Met Arg Gly Arg Glu  
10 15 20

gtg ctg gaa acc tcc ctg cgt gtg cca tca gtg gca ctt cac gat ttc 211  
Val Leu Glu Thr Ser Leu Arg Val Pro Ser Val Ala Leu His Asp Phe  
25 30 35

acc ggt caa acc gtc aac cgc gta tgg ccc tac gga aaa cac ctc ttc 259  
Thr Gly Gln Thr Val Asn Arg Val Trp Pro Tyr Gly Lys His Leu Phe  
40 45 50

atg caa ttc ggt gaa gag atc ctc cac acc cac ctc aaa atg gaa ggg 307  
Met Gln Phe Gly Glu Glu Ile Leu His Thr His Leu Lys Met Glu Gly  
55 60 65

acg tgg gct gtc cac cgc aaa ggc gat cgc tgg cgc aaa cct gga cac 355  
Thr Trp Ala Val His Arg Lys Gly Asp Arg Trp Arg Lys Pro Gly His  
70 75 80 85

acc gcg agg gta gtg ctt gtg ctg tcg gaa aac atc gag gtg gtg ggg 403  
Thr Ala Arg Val Val Leu Val Leu Ser Glu Asn Ile Glu Val Val Gly  
90 95 100

cat tcc ctc ggc ttt gtc aga gtg ttc ccc gca aac cgc tac tcc gaa 451  
His Ser Leu Gly Phe Val Arg Val Phe Pro Ala Asn Arg Tyr Ser Glu  
105 110 115

gag atc gct tac ctc ggc ccc gac gtc ctt gcc gaa gaa ttc gac atc 499  
Glu Ile Ala Tyr Leu Gly Pro Asp Val Leu Ala Glu Glu Phe Asp Ile  
120 125 130

aac acc gca cgg aac aat att gca tcg aac cct tcc cga aca att ggc 547  
Asn Thr Ala Arg Asn Asn Ile Ala Ser Asn Pro Ser Arg Thr Ile Gly  
135 140 145

gaa gcc ctc ctc gac caa tcc aac ctc gct gga gta ggc aac gaa tac 595  
Glu Ala Leu Leu Asp Gln Ser Asn Leu Ala Gly Val Gly Asn Glu Tyr  
150 155 160 165

cgc gct gag atc tgc ttc ctc atg ggc gtc cac ccg gcg aca caa gta 643  
 Arg Ala Glu Ile Cys Phe Leu Met Gly Val His Pro Ala Thr Gln Val  
                   170                                  175                                  180

gga tac gtt gac gtc gaa aag gct ctg aag att acc cga aga ctc atg 691  
 Gly Tyr Val Asp Val Glu Lys Ala Leu Lys Ile Thr Arg Arg Leu Met  
                   185                                  190                                  195

tgg gaa aat cga aat tcg ccg att cga gtg acc acc ggg gtt cga cgc 739  
 Trp Glu Asn Arg Asn Ser Pro Ile Arg Val Thr Thr Gly Val Arg Arg  
                   200                                  205                                  210

gcc ggg gaa tcc acc tat gtg ttt ggg cgt aac aat aaa ccg tgc agg 787  
 Ala Gly Glu Ser Thr Tyr Val Phe Gly Arg Asn Asn Lys Pro Cys Arg  
                   215                                  220                                  225

aga tgc cga acc cca atc gtg aaa gcc gag ttg ggg gag cga ata atc 835  
 Arg Cys Arg Thr Pro Ile Val Lys Ala Glu Leu Gly Glu Arg Ile Ile  
 230                                  235                                  240                                  245

tgg tgg tgt ccg cgc tgc caa ccg cta aac tcg tgaagcatga gactaatact 888  
 Trp Trp Cys Pro Arg Cys Gln Pro Leu Asn Ser  
                   250                                  255

caa 891

<210> 34

<211> 256

<212> PRT

<213> Corynebacterium glutamicum

<400> 34

Met Pro Glu Gly Asp Ser Val Phe Gln Leu Ser Arg Lys Leu Gln Phe  
   1                                  5                                  10                                  15

Met Arg Gly Arg Glu Val Leu Glu Thr Ser Leu Arg Val Pro Ser Val  
                   20                                  25                                  30

Ala Leu His Asp Phe Thr Gly Gln Thr Val Asn Arg Val Trp Pro Tyr  
                   35                                  40                                  45

Gly Lys His Leu Phe Met Gln Phe Gly Glu Glu Ile Leu His Thr His  
                   50                                  55                                  60

Leu Lys Met Glu Gly Thr Trp Ala Val His Arg Lys Gly Asp Arg Trp  
                   65                                  70                                  75                                  80

Arg Lys Pro Gly His Thr Ala Arg Val Val Leu Val Leu Ser Glu Asn  
                   85                                  90                                  95

Ile Glu Val Val Gly His Ser Leu Gly Phe Val Arg Val Phe Pro Ala  
                   100                                  105                                  110

Asn Arg Tyr Ser Glu Glu Ile Ala Tyr Leu Gly Pro Asp Val Leu Ala  
                   115                                  120                                  125

Glu Glu Phe Asp Ile Asn Thr Ala Arg Asn Asn Ile Ala Ser Asn Pro  
                   130                                  135                                  140

Ser Arg Thr Ile Gly Glu Ala Leu Leu Asp Gln Ser Asn Leu Ala Gly

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ttttatcaaa tcggcacacc ggctactaag gttgggtgatt																
Met Pro Glu Gly His															115	
1 5																
gtg	att	cat	cga	cta	gct	ggg	gaa	ctc	acc	aag	aat	ttt	ggc	gat	acc	163
Val	Ile	His	Arg	Leu	Ala	Gly	Glu	Leu	Thr	Lys	Asn	Phe	Gly	Asp	Thr	
10 15 20																
att	ttg	gac	gcc	act	tca	cct	caa	gga	cgc	ttt	act	tct	gaa	gcg	gcg	211
Ile	Leu	Asp	Ala	Thr	Ser	Pro	Gln	Gly	Arg	Phe	Thr	Ser	Glu	Ala	Ala	
25 30 35																
atc	atc	aac	ggg	cac	cgc	atc	gcg	gtt	gcg	gag	gct	tac	ggc	aag	cac	259
Ile	Ile	Asn	Gly	His	Arg	Ile	Ala	Val	Ala	Glu	Ala	Tyr	Gly	Lys	His	
40 45 50																
ctg	ttg	gtc	gag	ttc	gat	gcg	gat	cac	cct	gag	cac	att	ttg	tat	atc	307
Leu	Phe	Val	Glu	Phe	Asp	Ala	Asp	His	Pro	Glu	His	Ile	Leu	Tyr	Ile	
55 60 65																
cat	ttg	ggg	ctg	att	ggc	acg	ttg	cag	ttt	gaa	cct	gcg	gaa	gaa	acc	355
His	Leu	Gly	Leu	Ile	Gly	Thr	Leu	Gln	Phe	Glu	Pro	Ala	Glu	Glu	Thr	
70 75 80 85																
gcg	ggg	cag	att	cgc	ctg	cac	ctt	tcc	gac	ggg	gag	atc	gca	gct	aat	403
Arg	Gly	Gln	Ile	Arg	Leu	His	Leu	Ser	Asp	Gly	Glu	Ile	Ala	Ala	Asn	
90 95 100																

ttg cgc gga ccc caa tgg tgc agg ttg atc acc gat gca gag cgc acc 451  
 Leu Arg Gly Pro Gln Trp Cys Arg Leu Ile Thr Asp Ala Glu Arg Thr  
 105 110 115  
  
 cag gcc att gga aaa ttg ggc gct gat ccg att cgc gat gat gcc gat 499  
 Gln Ala Ile Gly Lys Leu Gly Ala Asp Pro Ile Arg Asp Asp Ala Asp  
 120 125 130  
  
 ccg gaa cca att cgg att aag gtg cag cgc tca ggg cga agc att ggt 547  
 Pro Glu Pro Ile Arg Ile Lys Val Gln Arg Ser Gly Arg Ser Ile Gly  
 135 140 145  
  
 tcg ttg ttg atg gat cag aag ctt ttc gca ggt gtg gga aat atc tac 595  
 Ser Leu Leu Met Asp Gln Lys Leu Phe Ala Gly Val Gly Asn Ile Tyr  
 150 155 160 165  
  
 cgt gcg gag aca ctt ttc cgc ctg ggg att tca ccg ttc acc att gga 643  
 Arg Ala Glu Thr Leu Phe Arg Leu Gly Ile Ser Pro Phe Thr Ile Gly  
 170 175 180  
  
 aaa gac atc acc acg gca cag ttc cga tcc att tgg gcg gat ctt gtt 691  
 Lys Asp Ile Thr Thr Ala Gln Phe Arg Ser Ile Trp Ala Asp Leu Val  
 185 190 195  
  
 ggg ttg atg aaa gac ggt gtt gtg act ggt cgg att gat act gtg cgc 739  
 Gly Leu Met Lys Asp Gly Val Val Thr Gly Arg Ile Asp Thr Val Arg  
 200 205 210  
  
 ccg gaa cac aca ccg gag gcg atg ggt agg cca ccg cgg aaa gat gat 787  
 Pro Glu His Thr Pro Glu Ala Met Gly Arg Pro Pro Arg Lys Asp Asp  
 215 220 225  
  
 cac ggc ggt gag gtt tac acc tat cgg cga acc ggt caa gag tgc ttt 835  
 His Gly Gly Glu Val Tyr Thr Tyr Arg Arg Thr Gly Gln Glu Cys Phe  
 230 235 240 245  
  
 ctg tgc gca act ccc atc aag gag cag gtc atg gag ggt cgc aac tta 883  
 Leu Cys Ala Thr Pro Ile Lys Glu Gln Val Met Glu Gly Arg Asn Leu  
 250 255 260  
  
 ttt tgg tgt ccc ggc tgc caa cgc tagacagatt caccttttgc tgt 930  
 Phe Trp Cys Pro Gly Cys Gln Arg  
 265

&lt;210&gt; 36

&lt;211&gt; 269

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 36

Met Pro Glu Gly His Val Ile His Arg Leu Ala Gly Glu Leu Thr Lys  
 1 5 10 15  
  
 Asn Phe Gly Asp Thr Ile Leu Asp Ala Thr Ser Pro Gln Gly Arg Phe  
 20 25 30  
  
 Thr Ser Glu Ala Ala Ile Ile Asn Gly His Arg Ile Ala Val Ala Glu  
 35 40 45

Ala Tyr Gly Lys His Leu Phe Val Glu Phe Asp Ala Asp His Pro Glu  
50 55 60

His Ile Leu Tyr Ile His Leu Gly Leu Ile Gly Thr Leu Gln Phe Glu  
65 70 75 80

Pro Ala Glu Glu Thr Arg Gly Gln Ile Arg Leu His Leu Ser Asp Gly  
85 90 95

Glu Ile Ala Ala Asn Leu Arg Gly Pro Gln Trp Cys Arg Leu Ile Thr  
100 105 110

Asp Ala Glu Arg Thr Gln Ala Ile Gly Lys Leu Gly Ala Asp Pro Ile  
115 120 125

Arg Asp Asp Ala Asp Pro Glu Pro Ile Arg Ile Lys Val Gln Arg Ser  
130 135 140

Gly Arg Ser Ile Gly Ser Leu Leu Met Asp Gln Lys Leu Phe Ala Gly  
145 150 155 160

Val Gly Asn Ile Tyr Arg Ala Glu Thr Leu Phe Arg Leu Gly Ile Ser  
165 170 175

Pro Phe Thr Ile Gly Lys Asp Ile Thr Thr Ala Gln Phe Arg Ser Ile  
180 185 190

Trp Ala Asp Leu Val Gly Leu Met Lys Asp Gly Val Val Thr Gly Arg  
195 200 205

Ile Asp Thr Val Arg Pro Glu His Thr Pro Glu Ala Met Gly Arg Pro  
210 215 220

Pro Arg Lys Asp Asp His Gly Gly Glu Val Tyr Thr Tyr Arg Arg Thr  
225 230 235 240

Gly Gln Glu Cys Phe Leu Cys Ala Thr Pro Ile Lys Glu Gln Val Met  
245 250 255

Glu Gly Arg Asn Leu Phe Trp Cys Pro Gly Cys Gln Arg  
260 265

&lt;210&gt; 37

&lt;211&gt; 635

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(612)

&lt;223&gt; FRXA01670

&lt;400&gt; 37

cat ttt gta tat cat ttg ggg ctg att ggc acg ttg cag ttt gaa cct 48  
His Phe Val Tyr His Leu Gly Leu Ile Gly Thr Leu Gln Phe Glu Pro  
1 5 10 15

gcg gaa gaa acc cgc ggg cag att cgc ctg cac ctt tcc gac ggg gag 96  
Ala Glu Glu Thr Arg Gly Gln Ile Arg Leu His Leu Ser Asp Gly Glu  
20 25 30

atc gca gct aat ttg cgc gga ccc caa tgg tgc agg ttg atc acc gat 144  
 Ile Ala Ala Asn Leu Arg Gly Pro Gln Trp Cys Arg Leu Ile Thr Asp  
 35 40 45  
  
 gca gag cgc acc cag gcc att gga aaa ttg ggc gct gat ccg att cgc 192  
 Ala Glu Arg Thr Gln Ala Ile Gly Lys Leu Gly Ala Asp Pro Ile Arg  
 50 55 60  
  
 gat gat gcc gat ccg gaa cca att cgg att aag gtg cag cgc tca ggg 240  
 Asp Asp Ala Asp Pro Glu Pro Ile Arg Ile Lys Val Gln Arg Ser Gly  
 65 70 75 80  
  
 cga agc att ggt tgc ttg ttg atg gat cag aag ctt ttc gca ggt gtg 288  
 Arg Ser Ile Gly Ser Leu Leu Met Asp Gln Lys Leu Phe Ala Gly Val  
 85 90 95  
  
 gga aat atc tac cgt gcg gag aca ctt ttc cgc ctg ggg att tca ccg 336  
 Gly Asn Ile Tyr Arg Ala Glu Thr Leu Phe Arg Leu Gly Ile Ser Pro  
 100 105 110  
  
 ttc acc att gga aaa gac atc acc acg gca cag ttc cga tcc att tgg 384  
 Phe Thr Ile Gly Lys Asp Ile Thr Thr Ala Gln Phe Arg Ser Ile Trp  
 115 120 125  
  
 gcg gat ctt gtt ggg ttg atg aaa gac ggt gtt gtg act ggt cgg att 432  
 Ala Asp Leu Val Gly Leu Met Lys Asp Gly Val Val Thr Gly Arg Ile  
 130 135 140  
  
 gat act gtg cgc ccg gaa cac aca ccg gag gcg atg ggt agg cca ccg 480  
 Asp Thr Val Arg Pro Glu His Thr Pro Glu Ala Met Gly Arg Pro Pro  
 145 150 155 160  
  
 cgg aaa gat gat cac ggc ggt gag gtt tac acc tat cgg cga acc ggt 528  
 Arg Lys Asp Asp His Gly Gly Glu Val Tyr Thr Tyr Arg Arg Thr Gly  
 165 170 175  
  
 caa gag tgc ttt ctg tgc gca act ccc atc aag gag cag gtc atg gag 576  
 Gln Glu Cys Phe Leu Cys Ala Thr Pro Ile Lys Glu Gln Val Met Glu  
 180 185 190  
  
 ggt cgc aac tta ttt tgg tgt ccc ggc tgc caa cgc tagacagatt 622  
 Gly Arg Asn Leu Phe Trp Cys Pro Gly Cys Gln Arg  
 195 200  
  
 caccttttgc tgt 635

&lt;210&gt; 38

&lt;211&gt; 204

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 38

His Phe Val Tyr His Leu Gly Leu Ile Gly Thr Leu Gln Phe Glu Pro  
 1 5 10 15

Ala Glu Glu Thr Arg Gly Gln Ile Arg Leu His Leu Ser Asp Gly Glu  
 20 25 30

Ile Ala Ala Asn Leu Arg Gly Pro Gln Trp Cys Arg Leu Ile Thr Asp

35					40					45					
Ala	Glu	Arg	Thr	Gln	Ala	Ile	Gly	Lys	Leu	Gly	Ala	Asp	Pro	Ile	Arg
50					55					60					
Asp	Asp	Ala	Asp	Pro	Glu	Pro	Ile	Arg	Ile	Lys	Val	Gln	Arg	Ser	Gly
65					70					75					80
Arg	Ser	Ile	Gly	Ser	Leu	Leu	Met	Asp	Gln	Lys	Leu	Phe	Ala	Gly	Val
				85					90					95	
Gly	Asn	Ile	Tyr	Arg	Ala	Glu	Thr	Leu	Phe	Arg	Leu	Gly	Ile	Ser	Pro
			100					105					110		
Phe	Thr	Ile	Gly	Lys	Asp	Ile	Thr	Thr	Ala	Gln	Phe	Arg	Ser	Ile	Trp
			115				120					125			
Ala	Asp	Leu	Val	Gly	Leu	Met	Lys	Asp	Gly	Val	Val	Thr	Gly	Arg	Ile
130					135					140					
Asp	Thr	Val	Arg	Pro	Glu	His	Thr	Pro	Glu	Ala	Met	Gly	Arg	Pro	Pro
145					150					155					160
Arg	Lys	Asp	Asp	His	Gly	Gly	Glu	Val	Tyr	Thr	Tyr	Arg	Arg	Thr	Gly
				165					170					175	
Gln	Glu	Cys	Phe	Leu	Cys	Ala	Thr	Pro	Ile	Lys	Glu	Gln	Val	Met	Glu
			180					185					190		
Gly	Arg	Asn	Leu	Phe	Trp	Cys	Pro	Gly	Cys	Gln	Arg				
			195				200								

<210> 39  
 <211> 981  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(958)  
 <223> RXA02078

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 Val Pro Glu Leu Pro  
 1 5  
 gaa gtt gag gtg gtg cgc cgc ggt tta gaa gat cat atg gtc ggc cac 163  
 Glu Val Glu Val Val Arg Arg Gly Leu Glu Asp His Met Val Gly His  
 10 15 20  
 acc atc gtg tcc gcc aca gtg ctt cac ccg cgc gca gcc cgc aat caa 211  
 Thr Ile Val Ser Ala Thr Val Leu His Pro Arg Ala Ala Arg Asn Gln  
 25 30 35  
 ctc ggc ggt ggc ccc gaa atc gag gcc aac atc gca ggg ctt agg gtc 259  
 Leu Gly Gly Gly Pro Glu Ile Glu Ala Asn Ile Ala Gly Leu Arg Val  
 40 45 50

agc gct gcc aag cga cgc ggc aaa ttc ctc tgg ctt gag ctt atc gac	307
Ser Ala Ala Lys Arg Arg Gly Lys Phe Leu Trp Leu Glu Leu Ile Asp	
55 60 65	
gca ccc tcc ggc gaa acc cgt ccc gat tta ggg cta ctg gtt cac ctt	355
Ala Pro Ser Gly Glu Thr Arg Pro Asp Leu Gly Leu Leu Val His Leu	
70 75 80 85	
ggg atg agt gga caa atg ctc atc aaa gaa cca gat gca cca att agt	403
Gly Met Ser Gly Gln Met Leu Ile Lys Glu Pro Asp Ala Pro Ile Ser	
90 95 100	
cca cac ctt cga gcc aaa gtc gag cta gat aat ggc gat gaa gtg tgg	451
Pro His Leu Arg Ala Lys Val Glu Leu Asp Asn Gly Asp Glu Val Trp	
105 110 115	
ttt gtc gat caa cgc acc ttc ggt tat tgg tgg ctc ggc gac cta gtt	499
Phe Val Asp Gln Arg Thr Phe Gly Tyr Trp Trp Leu Gly Asp Leu Val	
120 125 130	
gat gga gta ccc gaa cgc gtc tct cac att gcc aca gat gta ttg gat	547
Asp Gly Val Pro Glu Arg Val Ser His Ile Ala Thr Asp Val Leu Asp	
135 140 145	
gag tct gct gat ttc tct gcg att gcg cgg aat ttg aaa tct cgg aaa	595
Glu Ser Ala Asp Phe Ser Ala Ile Ala Arg Asn Leu Lys Ser Arg Lys	
150 155 160 165	
tcg gag atc aaa cgc ctc ctg ctt aac caa gag atc gtc tcc ggc atc	643
Ser Glu Ile Lys Arg Leu Leu Leu Asn Gln Glu Ile Val Ser Gly Ile	
170 175 180	
gga aat atc tat gcc gat gaa atg ctc tgg caa gca aaa att cac cca	691
Gly Asn Ile Tyr Ala Asp Glu Met Leu Trp Gln Ala Lys Ile His Pro	
185 190 195	
ttg caa cgt gcc gat cga ctg tcc cta gct cgc ttg gaa gaa ctt ctt	739
Leu Gln Arg Ala Asp Arg Leu Ser Leu Ala Arg Leu Glu Glu Leu Leu	
200 205 210	
caa gct ggc aaa gac gtg atg acc aaa gca ctt gct caa ggt ggc acc	787
Gln Ala Gly Lys Asp Val Met Thr Lys Ala Leu Ala Gln Gly Gly Thr	
215 220 225	
tct ttc gac gcg ctc tat gtc aac gtc aat ggc aac tcc ggc tac ttt	835
Ser Phe Asp Ala Leu Tyr Val Asn Val Asn Gly Asn Ser Gly Tyr Phe	
230 235 240 245	
gcg ctg tca ttg aat gct tat gcg caa acc ggg gag ccg tgc gga cgc	883
Ala Leu Ser Leu Asn Ala Tyr Ala Gln Thr Gly Glu Pro Cys Gly Arg	
250 255 260	
tgc gga aca tta atc atc cgg gag agt ttc atg aac cgc ggc tcc cac	931
Cys Gly Thr Leu Ile Ile Arg Glu Ser Phe Met Asn Arg Gly Ser His	
265 270 275	
tac tgc cca aac tgc cag aag cgg cgc tagctgatga gcgaagcttt tga	981
Tyr Cys Pro Asn Cys Gln Lys Arg Arg	
280 285	

<210> 40  
 <211> 286  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 40

Val	Pro	Glu	Leu	Pro	Glu	Val	Glu	Val	Val	Arg	Arg	Gly	Leu	Glu	Asp
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His	Met	Val	Gly	His	Thr	Ile	Val	Ser	Ala	Thr	Val	Leu	His	Pro	Arg
			20					25					30		
Ala	Ala	Arg	Asn	Gln	Leu	Gly	Gly	Gly	Pro	Glu	Ile	Glu	Ala	Asn	Ile
		35					40					45			
Ala	Gly	Leu	Arg	Val	Ser	Ala	Ala	Lys	Arg	Arg	Gly	Lys	Phe	Leu	Trp
	50					55					60				
Leu	Glu	Leu	Ile	Asp	Ala	Pro	Ser	Gly	Glu	Thr	Arg	Pro	Asp	Leu	Gly
	65				70					75					80
Leu	Leu	Val	His	Leu	Gly	Met	Ser	Gly	Gln	Met	Leu	Ile	Lys	Glu	Pro
				85					90					95	
Asp	Ala	Pro	Ile	Ser	Pro	His	Leu	Arg	Ala	Lys	Val	Glu	Leu	Asp	Asn
			100					105					110		
Gly	Asp	Glu	Val	Trp	Phe	Val	Asp	Gln	Arg	Thr	Phe	Gly	Tyr	Trp	Trp
		115					120					125			
Leu	Gly	Asp	Leu	Val	Asp	Gly	Val	Pro	Glu	Arg	Val	Ser	His	Ile	Ala
	130					135					140				
Thr	Asp	Val	Leu	Asp	Glu	Ser	Ala	Asp	Phe	Ser	Ala	Ile	Ala	Arg	Asn
	145				150					155					160
Leu	Lys	Ser	Arg	Lys	Ser	Glu	Ile	Lys	Arg	Leu	Leu	Leu	Asn	Gln	Glu
				165					170					175	
Ile	Val	Ser	Gly	Ile	Gly	Asn	Ile	Tyr	Ala	Asp	Glu	Met	Leu	Trp	Gln
			180					185					190		
Ala	Lys	Ile	His	Pro	Leu	Gln	Arg	Ala	Asp	Arg	Leu	Ser	Leu	Ala	Arg
		195					200					205			
Leu	Glu	Glu	Leu	Leu	Gln	Ala	Gly	Lys	Asp	Val	Met	Thr	Lys	Ala	Leu
	210					215					220				
Ala	Gln	Gly	Gly	Thr	Ser	Phe	Asp	Ala	Leu	Tyr	Val	Asn	Val	Asn	Gly
	225				230					235					240
Asn	Ser	Gly	Tyr	Phe	Ala	Leu	Ser	Leu	Asn	Ala	Tyr	Ala	Gln	Thr	Gly
				245					250					255	
Glu	Pro	Cys	Gly	Arg	Cys	Gly	Thr	Leu	Ile	Ile	Arg	Glu	Ser	Phe	Met
			260					265					270		
Asn	Arg	Gly	Ser	His	Tyr	Cys	Pro	Asn	Cys	Gln	Lys	Arg	Arg		
		275					280					285			

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Met Leu Val Asp Ile 5																
gct att gag aac ctc gga gtt att cca gcg gcc tca gct gag ttc agc 163																
Ala Ile Glu Asn Leu Gly Val Ile Pro Ala Ala Ser Ala Glu Phe Ser 20																
tca ggt tta aca gtg ctc acc ggt gag acc ggc gcc gga aag acc atg 211																
Ser Gly Leu Thr Val Leu Thr Gly Glu Thr Gly Ala Gly Lys Thr Met 35																
gta gtg aca ggt tta cgc ctg tta tcc ggc ggt cgc gcc gac gct tca 259																
Val Val Thr Gly Leu Arg Leu Leu Ser Gly Gly Arg Ala Asp Ala Ser 50																
cgc gtg cgc aca gga tcc cct caa gct gtt gtg gag ggg cgc ttt gtt 307																
Arg Val Arg Thr Gly Ser Pro Gln Ala Val Val Glu Gly Arg Phe Val 65																
acg caa ggc gtg ccc tgc gac att gtc gaa cgt gca acc gga atc gtt 355																
Thr Gln Gly Val Pro Cys Asp Ile Val Glu Arg Ala Thr Gly Ile Val 85																
tcg aac gcc gga ggt gcc gca gat gaa aat gga gag ttt tta gct gtc 403																
Ser Asn Ala Gly Gly Ala Ala Asp Glu Asn Gly Glu Phe Leu Ala Val 100																
cgt tcc gtc ggc gcc aac ggc cgt tca aaa gct cat ctc ggt ggt cgc 451																
Arg Ser Val Gly Ala Asn Gly Arg Ser Lys Ala His Leu Gly Gly Arg 115																
tcc gta cct gcg gca acg ctg tcc gag ttc tct gat gag ctg ttg acc 499																
Ser Val Pro Ala Ala Thr Leu Ser Glu Phe Ser Asp Glu Leu Leu Thr 130																
atc cac ggt caa aat gac caa ctc cgg ttg ctc tcc cca gaa cgc caa 547																
Ile His Gly Gln Asn Asp Gln Leu Arg Leu Leu Ser Pro Glu Arg Gln 145																
cta gag gcg ctt gat cgt ttt gat cca gag ctg gcc caa ctg cgc aaa 595																
Leu Glu Ala Leu Asp Arg Phe Asp Pro Glu Leu Ala Gln Leu Arg Lys 165																
aac tac aac gcc aag tac ctc act tgg aag tcc ttg gat aaa gat ctg 643																
Asn Tyr Asn Ala Lys Tyr Leu Thr Trp Lys Ser Leu Asp Lys Asp Leu 180																

cag aag cgc ctg agt agt agg cga gag ctg gct caa gaa gtc gat cgc	691
Gln Lys Arg Leu Ser Ser Arg Arg Glu Leu Ala Gln Glu Val Asp Arg	
185 190 195	
ctg caa ttc gcg att aat gag atc gag gaa gtc tcg cca cag cca ggc	739
Leu Gln Phe Ala Ile Asn Glu Ile Glu Glu Val Ser Pro Gln Pro Gly	
200 205 210	
gaa gac gcc gaa ctg gtt gag cag atc cgc agg ctc cag gac gtg gac	787
Glu Asp Ala Glu Leu Val Glu Gln Ile Arg Arg Leu Gln Asp Val Asp	
215 220 225	
acc ctg cgg gag caa gct gca acc gca ttg gct gcg att gat ggt gcc	835
Thr Leu Arg Glu Gln Ala Ala Thr Ala Leu Ala Ala Ile Asp Gly Ala	
230 235 240 245	
ggc tct ctc agc gac gcc atg ggt ggt tcc ggc ggc ttt gat gaa tcc	883
Gly Ser Leu Ser Asp Ala Met Gly Gly Ser Gly Gly Phe Asp Glu Ser	
250 255 260	
cag gag tca gcc tct gac cag ctc ggc cag gcg gag tcc gcg ctg gca	931
Gln Glu Ser Ala Ser Asp Gln Leu Gly Gln Ala Glu Ser Ala Leu Ala	
265 270 275	
ggc agt gat gac tca aag ctg aaa gat att gcc gtt cag ctt gcg gaa	979
Gly Ser Asp Asp Ser Lys Leu Lys Asp Ile Ala Val Gln Leu Ala Glu	
280 285 290	
atc acc agc cag ctc agc caa gtg tcc atg gaa ttg ggc ggg ttc ctc	1027
Ile Thr Ser Gln Leu Ser Gln Val Ser Met Glu Leu Gly Gly Phe Leu	
295 300 305	
tct gat ctc ccc gca gac ccc caa gca ctc gat gac atg ctc acc cgc	1075
Ser Asp Leu Pro Ala Asp Pro Gln Ala Leu Asp Asp Met Leu Thr Arg	
310 315 320 325	
caa cag caa ttg aaa ctg ctc acg cgt aaa tac gct gca gat att gac	1123
Gln Gln Gln Leu Lys Leu Leu Thr Arg Lys Tyr Ala Ala Asp Ile Asp	
330 335 340	
ggc gtg att gag tgg cag cgg aaa gcc caa atc cgc cta gac agc att	1171
Gly Val Ile Glu Trp Gln Arg Lys Ala Gln Ile Arg Leu Asp Ser Ile	
345 350 355	
gac att tcc tcc gaa gcg ctt gac aag ctg aaa gaa gac gcg aaa aag	1219
Asp Ile Ser Ser Glu Ala Leu Asp Lys Leu Lys Glu Asp Ala Lys Lys	
360 365 370	
gcg cag gcc tcc atg atg cgt gcc gct aag aag ctt tca gct gtc cgt	1267
Ala Gln Ala Ser Met Met Arg Ala Ala Lys Lys Leu Ser Ala Val Arg	
375 380 385	
gca aag gca gca acc aag ttg ggg aca act gtc acc gag gag ctt cag	1315
Ala Lys Ala Ala Thr Lys Leu Gly Thr Thr Val Thr Glu Glu Leu Gln	
390 395 400 405	
ggc ctg gcc atg caa aaa gcc cgc ttt gag gtt gct ttg acc tcc att	1363
Gly Leu Ala Met Gln Lys Ala Arg Phe Glu Val Ala Leu Thr Ser Ile	
410 415 420	

gag gcg tgc gcc agc ggt atc gac cag gtg gaa ttc cag ctc gca gca 1411  
 Glu Ala Cys Ala Ser Gly Ile Asp Gln Val Glu Phe Gln Leu Ala Ala  
 425 430 435

aat gcc ttt gca cag cct cgt cca ctt gca tcc tct gcg tct ggt ggt 1459  
 Asn Ala Phe Ala Gln Pro Arg Pro Leu Ala Ser Ser Ala Ser Gly Gly  
 440 445 450

gaa ctt tcc cgc gtt atg ttg gcg ctc gag gtg atc ttg gct gct gga 1507  
 Glu Leu Ser Arg Val Met Leu Ala Leu Glu Val Ile Leu Ala Ala Gly  
 455 460 465

acc acg ggc acc acc ttg gtg ttc gac gag gtt gat gca ggt gtg ggc 1555  
 Thr Thr Gly Thr Thr Leu Val Phe Asp Glu Val Asp Ala Gly Val Gly  
 470 475 480 485

gga cgc gca gcg gtg gaa atc ggt cgc cgc ctg gcc cgc ctt gcc acc 1603  
 Gly Arg Ala Ala Val Glu Ile Gly Arg Arg Leu Ala Arg Leu Ala Thr  
 490 495 500

aaa aac caa gtc atc gtg gtc acc cat ctc cca cag gtc gct gct tac 1651  
 Lys Asn Gln Val Ile Val Val Thr His Leu Pro Gln Val Ala Ala Tyr  
 505 510 515

gcc gac acg cac ctg cac gtt gcc aag aat gta gga gaa gcc tcc gtg 1699  
 Ala Asp Thr His Leu His Val Ala Lys Asn Val Gly Glu Ala Ser Val  
 520 525 530

acc tca gga gtg gag tca ctg acc ttc gac cga cgc gtg gaa gag ctc 1747  
 Thr Ser Gly Val Glu Ser Leu Thr Phe Asp Arg Arg Val Glu Glu Leu  
 535 540 545

tcc cgc atg ctc gct ggc ctc gac gac acc gcc acc ggc cga gcc cac 1795  
 Ser Arg Met Leu Ala Gly Leu Asp Asp Thr Ala Thr Gly Arg Ala His  
 550 555 560 565

gca acg gag ctg ctc gag cgt gca cag cgt gaa aag gaa gat att aac 1843  
 Ala Thr Glu Leu Leu Glu Arg Ala Gln Arg Glu Lys Glu Asp Ile Asn  
 570 575 580

gag gag cga gta gaa cca ctt ctc gcc gcc agt gca taagagtttt 1889  
 Glu Glu Arg Val Glu Pro Leu Leu Ala Ala Ser Ala  
 585 590

cttggaattt ttt 1902

&lt;210&gt; 42

&lt;211&gt; 593

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 42

Met Leu Val Asp Ile Ala Ile Glu Asn Leu Gly Val Ile Pro Ala Ala  
 1 5 10 15

Ser Ala Glu Phe Ser Ser Gly Leu Thr Val Leu Thr Gly Glu Thr Gly  
 20 25 30

Ala Gly Lys Thr Met Val Val Thr Gly Leu Arg Leu Leu Ser Gly Gly  
 35 40 45

Arg Ala Asp Ala Ser Arg Val Arg Thr Gly Ser Pro Gln Ala Val Val  
 50 55 60  
 Glu Gly Arg Phe Val Thr Gln Gly Val Pro Cys Asp Ile Val Glu Arg  
 65 70 75 80  
 Ala Thr Gly Ile Val Ser Asn Ala Gly Gly Ala Ala Asp Glu Asn Gly  
 85 90 95  
 Glu Phe Leu Ala Val Arg Ser Val Gly Ala Asn Gly Arg Ser Lys Ala  
 100 105 110  
 His Leu Gly Gly Arg Ser Val Pro Ala Ala Thr Leu Ser Glu Phe Ser  
 115 120 125  
 Asp Glu Leu Leu Thr Ile His Gly Gln Asn Asp Gln Leu Arg Leu Leu  
 130 135 140  
 Ser Pro Glu Arg Gln Leu Glu Ala Leu Asp Arg Phe Asp Pro Glu Leu  
 145 150 155 160  
 Ala Gln Leu Arg Lys Asn Tyr Asn Ala Lys Tyr Leu Thr Trp Lys Ser  
 165 170 175  
 Leu Asp Lys Asp Leu Gln Lys Arg Leu Ser Ser Arg Arg Glu Leu Ala  
 180 185 190  
 Gln Glu Val Asp Arg Leu Gln Phe Ala Ile Asn Glu Ile Glu Glu Val  
 195 200 205  
 Ser Pro Gln Pro Gly Glu Asp Ala Glu Leu Val Glu Gln Ile Arg Arg  
 210 215 220  
 Leu Gln Asp Val Asp Thr Leu Arg Glu Gln Ala Ala Thr Ala Leu Ala  
 225 230 235 240  
 Ala Ile Asp Gly Ala Gly Ser Leu Ser Asp Ala Met Gly Gly Ser Gly  
 245 250 255  
 Gly Phe Asp Glu Ser Gln Glu Ser Ala Ser Asp Gln Leu Gly Gln Ala  
 260 265 270  
 Glu Ser Ala Leu Ala Gly Ser Asp Asp Ser Lys Leu Lys Asp Ile Ala  
 275 280 285  
 Val Gln Leu Ala Glu Ile Thr Ser Gln Leu Ser Gln Val Ser Met Glu  
 290 295 300  
 Leu Gly Gly Phe Leu Ser Asp Leu Pro Ala Asp Pro Gln Ala Leu Asp  
 305 310 315 320  
 Asp Met Leu Thr Arg Gln Gln Gln Leu Lys Leu Leu Thr Arg Lys Tyr  
 325 330 335  
 Ala Ala Asp Ile Asp Gly Val Ile Glu Trp Gln Arg Lys Ala Gln Ile  
 340 345 350  
 Arg Leu Asp Ser Ile Asp Ile Ser Ser Glu Ala Leu Asp Lys Leu Lys  
 355 360 365

Glu Asp Ala Lys Lys Ala Gln Ala Ser Met Met Arg Ala Ala Lys Lys  
 370 375 380  
 Leu Ser Ala Val Arg Ala Lys Ala Ala Thr Lys Leu Gly Thr Thr Val  
 385 390 395 400  
 Thr Glu Glu Leu Gln Gly Leu Ala Met Gln Lys Ala Arg Phe Glu Val  
 405 410 415  
 Ala Leu Thr Ser Ile Glu Ala Cys Ala Ser Gly Ile Asp Gln Val Glu  
 420 425 430  
 Phe Gln Leu Ala Ala Asn Ala Phe Ala Gln Pro Arg Pro Leu Ala Ser  
 435 440 445  
 Ser Ala Ser Gly Gly Glu Leu Ser Arg Val Met Leu Ala Leu Glu Val  
 450 455 460  
 Ile Leu Ala Ala Gly Thr Thr Gly Thr Thr Leu Val Phe Asp Glu Val  
 465 470 475 480  
 Asp Ala Gly Val Gly Gly Arg Ala Ala Val Glu Ile Gly Arg Arg Leu  
 485 490 495  
 Ala Arg Leu Ala Thr Lys Asn Gln Val Ile Val Val Thr His Leu Pro  
 500 505 510  
 Gln Val Ala Ala Tyr Ala Asp Thr His Leu His Val Ala Lys Asn Val  
 515 520 525  
 Gly Glu Ala Ser Val Thr Ser Gly Val Glu Ser Leu Thr Phe Asp Arg  
 530 535 540  
 Arg Val Glu Glu Leu Ser Arg Met Leu Ala Gly Leu Asp Asp Thr Ala  
 545 550 555 560  
 Thr Gly Arg Ala His Ala Thr Glu Leu Leu Glu Arg Ala Gln Arg Glu  
 565 570 575  
 Lys Glu Asp Ile Asn Glu Glu Arg Val Glu Pro Leu Leu Ala Ala Ser  
 580 585 590  
 Ala

<210> 43  
 <211> 1434  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1411)  
 <223> RXA01493

<400> 43  
 cctgctgcag gctataccgc tcgtggtacg gaaatcgaag cctcgcatac gttgattgaa 60  
 gcaaccgta ccttggggga gtctttgcga agctcggcgc atg tcg atg tct aac 115  
 Met Ser Met Ser Asn

															1																5	
aac	gac	ttt	gag	cat	gag	tcc	cat	gat	gtt	tct	gca	aag	cag	atc	ttc	163																
Asn	Asp	Phe	Glu	His	Glu	Ser	His	Asp	Val	Ser	Ala	Lys	Gln	Ile	Phe																	
				10					15					20																		
ggg	ctc	gcg	ttc	ccc	gca	ctg	ggt	gtt	cta	gct	gcg	atg	ccg	ctg	tat	211																
Gly	Leu	Ala	Phe	Pro	Ala	Leu	Gly	Val	Leu	Ala	Ala	Met	Pro	Leu	Tyr																	
				25					30					35																		
ctc	ttg	ttg	gat	aca	gcg	gtt	gtt	ggc	act	ttg	ggt	ggc	ttc	gaa	ttg	259																
Leu	Leu	Leu	Asp	Thr	Ala	Val	Val	Gly	Thr	Leu	Gly	Gly	Phe	Glu	Leu																	
				40					45					50																		
gct	gcg	ttg	ggc	gca	gca	aca	aca	att	caa	gct	caa	gtg	aca	aca	cag	307																
Ala	Ala	Leu	Gly	Ala	Ala	Thr	Thr	Ile	Gln	Ala	Gln	Val	Thr	Thr	Gln																	
				55					60					65																		
ctg	aca	ttc	ttg	tcc	tat	gga	act	acc	gcg	aga	tca	tcg	aga	att	ttc	355																
Leu	Thr	Phe	Leu	Ser	Tyr	Gly	Thr	Thr	Ala	Arg	Ser	Ser	Arg	Ile	Phe																	
				70					75					80																		
gga	atg	ggt	gat	cgc	cgg	gga	gca	att	gcc	gaa	ggt	gtg	caa	gca	acc	403																
Gly	Met	Gly	Asp	Arg	Arg	Gly	Ala	Ile	Ala	Glu	Gly	Val	Gln	Ala	Thr																	
				90					95					100																		
tgg	gtg	gca	ctc	ttt	gta	ggc	ttg	ggc	atc	tta	acg	ctg	atg	ctc	att	451																
Trp	Val	Ala	Leu	Phe	Val	Gly	Leu	Gly	Ile	Leu	Thr	Leu	Met	Leu	Ile																	
				105					110					115																		
gga	gcc	ccg	act	ttc	gcg	ttg	tgg	ctc	agt	ggt	gat	gaa	gct	cta	gcc	499																
Gly	Ala	Pro	Thr	Phe	Ala	Leu	Trp	Leu	Ser	Gly	Asp	Glu	Ala	Leu	Ala																	
				120					125					130																		
caa	gaa	gca	ggg	cat	tgg	ctc	cgg	gtc	gct	gct	ttt	gcg	gtg	cca	cta	547																
Gln	Glu	Ala	Gly	His	Trp	Leu	Arg	Val	Ala	Ala	Phe	Ala	Val	Pro	Leu																	
				135					140					145																		
att	ctc	atg	atc	atg	gct	ggc	aac	ggt	tgg	tta	aga	ggt	att	caa	aac	595																
Ile	Leu	Met	Ile	Met	Ala	Gly	Asn	Gly	Trp	Leu	Arg	Gly	Ile	Gln	Asn																	
				150					155					160																		
acc	aag	ctg	cca	ctc	tat	ttc	acc	ttg	gcg	gga	gtc	atc	ccc	ggc	gcg	643																
Thr	Lys	Leu	Pro	Leu	Tyr	Phe	Thr	Leu	Ala	Gly	Val	Ile	Pro	Gly	Ala																	
				170					175					180																		
atc	ttg	att	ccg	ata	ttc	gtg	gct	aag	ttt	gga	ctt	gtg	ggc	tct	gcc	691																
Ile	Leu	Ile	Pro	Ile	Phe	Val	Ala	Lys	Phe	Gly	Leu	Val	Gly	Ser	Ala																	
				185					190					195																		
tgg	gca	aac	ctc	att	gca	gaa	gca	att	act	gct	tcg	ctg	ttt	ttg	ggt	739																
Trp	Ala	Asn	Leu	Ile	Ala	Glu	Ala	Ile	Thr	Ala	Ser	Leu	Phe	Leu	Gly																	
				200					205					210																		
gca	ttg	atc	aag	cac	cac	gaa	ggt	tcg	tgg	aag	ccg	agc	tgg	acg	gtg	787																
Ala	Leu	Ile	Lys	His	His	Glu	Gly	Ser	Trp	Lys	Pro	Ser	Trp	Thr	Val																	
				215					220					225																		
atg	aaa	aat	cag	ttg	gtt	ctt	gga	cgt	gat	ttg	atc	atg	cgg	tca	atg	835																
Met	Lys	Asn	Gln	Leu	Val	Leu	Gly	Arg	Asp	Leu	Ile	Met	Arg	Ser	Met																	
				230					235					240																		
														245																		

tcg ttc cag gtt gct ttt ctt tcc gcg gcc gct gtg gct gca cga ttt	883
Ser Phe Gln Val Ala Phe Leu Ser Ala Ala Ala Val Ala Ala Arg Phe	
250 255 260	
ggc acg gca tcc ttg gcg gcc cac cag gtg ttg ctt cag ctg tgg aat	931
Gly Thr Ala Ser Leu Ala Ala His Gln Val Leu Leu Gln Leu Trp Asn	
265 270 275	
ttc atc aca ttg gtg ctg gat tct cta gct atc gcg gcg cag acc tta	979
Phe Ile Thr Leu Val Leu Asp Ser Leu Ala Ile Ala Ala Gln Thr Leu	
280 285 290	
act ggt gca gcc ctg ggc gct gga act gcg aag gtc gcc cgc agg gtg	1027
Thr Gly Ala Ala Leu Gly Ala Gly Thr Ala Lys Val Ala Arg Arg Val	
295 300 305	
ggt aat cag gtg att aag tac tct ctg att ttc gct ggt ggc tta ggt	1075
Gly Asn Gln Val Ile Lys Tyr Ser Leu Ile Phe Ala Gly Gly Leu Gly	
310 315 320 325	
ttg gtg ttc gtg gtc tta cac tcg tgg att ccg cgt att ttc act cag	1123
Leu Val Phe Val Val Leu His Ser Trp Ile Pro Arg Ile Phe Thr Gln	
330 335 340	
gac gcc gac gtt tta gat gcg att gct tcc ccg tgg tgg atc atg gtc	1171
Asp Ala Asp Val Leu Asp Ala Ile Ala Ser Pro Trp Trp Ile Met Val	
345 350 355	
gcg atg atc att ttg ggt ggc att gtc ttt gct att gat ggt gtg ctg	1219
Ala Met Ile Ile Leu Gly Gly Ile Val Phe Ala Ile Asp Gly Val Leu	
360 365 370	
ttg ggt gct gct gac gcg gtg ttc ctc cga aat gcc tct atc ttg gcg	1267
Leu Gly Ala Ala Asp Ala Val Phe Leu Arg Asn Ala Ser Ile Leu Ala	
375 380 385	
gtt gtg gtc gga ttc tta cca ggc gtc tgg att tcc tat gca tta gat	1315
Val Val Val Gly Phe Leu Pro Gly Val Trp Ile Ser Tyr Ala Leu Asp	
390 395 400 405	
gca ggg ctg aca ggc gtg tgg tgt ggt ttg ctg gcg ttt att ctg atc	1363
Ala Gly Leu Thr Gly Val Trp Cys Gly Leu Leu Ala Phe Ile Leu Ile	
410 415 420	
cga cta ttt gcg gtg att tgg cgg ttt aag tct atg aag tgg gcg cgt	1411
Arg Leu Phe Ala Val Ile Trp Arg Phe Lys Ser Met Lys Trp Ala Arg	
425 430 435	
tagcttcggc gcgtggcaaa cca	1434

&lt;210&gt; 44

&lt;211&gt; 437

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 44

Met Ser Met Ser Asn Asn Asp Phe Glu His Glu Ser His Asp Val Ser
1 5 10 15

Ala Lys Gln Ile Phe Gly Leu Ala Phe Pro Ala Leu Gly Val Leu Ala  
                     20                    25                    30  
 Ala Met Pro Leu Tyr Leu Leu Leu Asp Thr Ala Val Val Gly Thr Leu  
                     35                    40                    45  
 Gly Gly Phe Glu Leu Ala Ala Leu Gly Ala Ala Thr Thr Ile Gln Ala  
                     50                    55                    60  
 Gln Val Thr Thr Gln Leu Thr Phe Leu Ser Tyr Gly Thr Thr Ala Arg  
                     65                    70                    75                    80  
 Ser Ser Arg Ile Phe Gly Met Gly Asp Arg Arg Gly Ala Ile Ala Glu  
                     85                    90                    95  
 Gly Val Gln Ala Thr Trp Val Ala Leu Phe Val Gly Leu Gly Ile Leu  
                     100                    105                    110  
 Thr Leu Met Leu Ile Gly Ala Pro Thr Phe Ala Leu Trp Leu Ser Gly  
                     115                    120                    125  
 Asp Glu Ala Leu Ala Gln Glu Ala Gly His Trp Leu Arg Val Ala Ala  
                     130                    135                    140  
 Phe Ala Val Pro Leu Ile Leu Met Ile Met Ala Gly Asn Gly Trp Leu  
                     145                    150                    155                    160  
 Arg Gly Ile Gln Asn Thr Lys Leu Pro Leu Tyr Phe Thr Leu Ala Gly  
                     165                    170                    175  
 Val Ile Pro Gly Ala Ile Leu Ile Pro Ile Phe Val Ala Lys Phe Gly  
                     180                    185                    190  
 Leu Val Gly Ser Ala Trp Ala Asn Leu Ile Ala Glu Ala Ile Thr Ala  
                     195                    200                    205  
 Ser Leu Phe Leu Gly Ala Leu Ile Lys His His Glu Gly Ser Trp Lys  
                     210                    215                    220  
 Pro Ser Trp Thr Val Met Lys Asn Gln Leu Val Leu Gly Arg Asp Leu  
                     225                    230                    235                    240  
 Ile Met Arg Ser Met Ser Phe Gln Val Ala Phe Leu Ser Ala Ala Ala  
                     245                    250                    255  
 Val Ala Ala Arg Phe Gly Thr Ala Ser Leu Ala Ala His Gln Val Leu  
                     260                    265                    270  
 Leu Gln Leu Trp Asn Phe Ile Thr Leu Val Leu Asp Ser Leu Ala Ile  
                     275                    280                    285  
 Ala Ala Gln Thr Leu Thr Gly Ala Ala Leu Gly Ala Gly Thr Ala Lys  
                     290                    295                    300  
 Val Ala Arg Arg Val Gly Asn Gln Val Ile Lys Tyr Ser Leu Ile Phe  
                     305                    310                    315                    320  
 Ala Gly Gly Leu Gly Leu Val Phe Val Val Leu His Ser Trp Ile Pro  
                     325                    330                    335  
 Arg Ile Phe Thr Gln Asp Ala Asp Val Leu Asp Ala Ile Ala Ser Pro

340	345	350
Trp Trp Ile Met Val Ala Met Ile Ile Leu Gly Gly Ile Val Phe Ala		
355	360	365
Ile Asp Gly Val Leu Leu Gly Ala Ala Asp Ala Val Phe Leu Arg Asn		
370	375	380
Ala Ser Ile Leu Ala Val Val Val Gly Phe Leu Pro Gly Val Trp Ile		
385	390	395
Ser Tyr Ala Leu Asp Ala Gly Leu Thr Gly Val Trp Cys Gly Leu Leu		
405	410	415
Ala Phe Ile Leu Ile Arg Leu Phe Ala Val Ile Trp Arg Phe Lys Ser		
420	425	430
Met Lys Trp Ala Arg		
435		

<210> 45  
 <211> 702  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(679)  
 <223> RXA02671

<400> 45  
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 Met Lys Ser Gly Cys  
 1 5  
 ttc gaa caa caa tcc gac ggc atc aaa gaa gtc ccc gat ccc tcc gga 163  
 Phe Glu Gln Gln Ser Asp Gly Ile Lys Glu Val Pro Asp Pro Ser Gly  
 10 15 20  
 ctc ttc ctc tcc cac cgc ggc tct acc cca gac ggc acc gcg gtc acc 211  
 Leu Phe Leu Ser His Arg Gly Ser Thr Pro Asp Gly Thr Ala Val Thr  
 25 30 35  
 gtc gcc atg gat ggc gtg cgc ccg cta tta gcg gag gtt caa agc ttg 259  
 Val Ala Met Asp Gly Val Arg Pro Leu Leu Ala Glu Val Gln Ser Leu  
 40 45 50  
 ctt gtc gac gcc ccc tcc aag aat cca cgc agg gtc gtc acg ggc ctc 307  
 Leu Val Asp Ala Pro Ser Lys Asn Pro Arg Arg Val Val Thr Gly Leu  
 55 60 65  
 gac gcc aat cgg gtc ccc atg gtc ctt gcg gtg tta tcc gca cgc gcc 355  
 Asp Ala Asn Arg Val Pro Met Val Leu Ala Val Leu Ser Ala Arg Ala  
 70 75 80 85  
 gga cgc caa acc caa gga aaa gac gct tac gtg gca acc gtt ggt ggc 403  
 Gly Arg Gln Thr Gln Gly Lys Asp Ala Tyr Val Ala Thr Val Gly Gly  
 90 95 100

atg aaa gtt ggc gaa cca gca aca gac ctc gct gtc gcg ctc gct act 451  
 Met Lys Val Gly Glu Pro Ala Thr Asp Leu Ala Val Ala Leu Ala Thr  
 105 110 115  
  
 gcc tcg gct tta gcc aag aaa cca cta cca gat aaa aca gtg gta ctc 499  
 Ala Ser Ala Leu Ala Lys Lys Pro Leu Pro Asp Lys Thr Val Val Leu  
 120 125 130  
  
 ggt gaa gtc ggc ttg gcc gga gaa atc cgt cgc gtc ccc aac gtt gat 547  
 Gly Glu Val Gly Leu Ala Gly Glu Ile Arg Arg Val Pro Asn Val Asp  
 135 140 145  
  
 cgc aga cta gcc gag gcg gaa cgt tta ggt tat gaa aaa gca gtc atc 595  
 Arg Arg Leu Ala Glu Ala Glu Arg Leu Gly Tyr Glu Lys Ala Val Ile  
 150 155 160 165  
  
 ccc gga ggc tca ggc atc aaa caa aca agc ctg aga gtc atc gaa gct 643  
 Pro Gly Gly Ser Gly Ile Lys Gln Thr Ser Leu Arg Val Ile Glu Ala  
 170 175 180  
  
 tca aca ctt gcc gaa gca ctt gca gca gta agc tta taaagcatga 689  
 Ser Thr Leu Ala Glu Ala Leu Ala Ala Val Ser Leu  
 185 190  
  
 caccaacaac cac 702

<210> 46  
 <211> 193  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 46  
 Met Lys Ser Gly Cys Phe Glu Gln Gln Ser Asp Gly Ile Lys Glu Val  
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 Pro Asp Pro Ser Gly Leu Phe Leu Ser His Arg Gly Ser Thr Pro Asp  
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 Gly Thr Ala Val Thr Val Ala Met Asp Gly Val Arg Pro Leu Leu Ala  
 35 40 45  
  
 Glu Val Gln Ser Leu Leu Val Asp Ala Pro Ser Lys Asn Pro Arg Arg  
 50 55 60  
  
 Val Val Thr Gly Leu Asp Ala Asn Arg Val Pro Met Val Leu Ala Val  
 65 70 75 80  
  
 Leu Ser Ala Arg Ala Gly Arg Gln Thr Gln Gly Lys Asp Ala Tyr Val  
 85 90 95  
  
 Ala Thr Val Gly Gly Met Lys Val Gly Glu Pro Ala Thr Asp Leu Ala  
 100 105 110  
  
 Val Ala Leu Ala Thr Ala Ser Ala Leu Ala Lys Lys Pro Leu Pro Asp  
 115 120 125  
  
 Lys Thr Val Val Leu Gly Glu Val Gly Leu Ala Gly Glu Ile Arg Arg  
 130 135 140

Val Pro Asn Val Asp Arg Arg Leu Ala Glu Ala Glu Arg Leu Gly Tyr  
145 150 155 160

Glu Lys Ala Val Ile Pro Gly Gly Ser Gly Ile Lys Gln Thr Ser Leu  
165 170 175

Arg Val Ile Glu Ala Ser Thr Leu Ala Glu Ala Leu Ala Ala Val Ser  
180 185 190

Leu

<210> 47

<211> 777

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(754)

<223> RXN02291

<400> 47

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ccaccaactt cccagaccac cgcgcagggt tgcagctggc gtg gtg cac ctg ccc 115  
Val Val His Leu Pro  
1 5

aac ttc ctc ggc ttg gcc gag caa aag gca ctg gtc gcc cag gct cga 163  
Asn Phe Leu Gly Leu Ala Glu Gln Lys Ala Leu Val Ala Gln Ala Arg  
10 15 20

gac ctt gcg cgt gaa gtt gtg ggc aca ccg ttg gcg atg gtc cga ccc 211  
Asp Leu Ala Arg Glu Val Val Gly Thr Pro Leu Ala Met Val Arg Pro  
25 30 35

aag ctg aaa agt ggt cag atg agt gtc cat atg ttg cat tta gga aag 259  
Lys Leu Lys Ser Gly Gln Met Ser Val His Met Leu His Leu Gly Lys  
40 45 50

tac tgg gca tcc aat cct tat cgc tat gtg gat gtc gtt gat ggt ttt 307  
Tyr Trp Ala Ser Asn Pro Tyr Arg Tyr Val Asp Val Val Asp Gly Phe  
55 60 65

cca gtg cca cca ctg ccg gat tct ttc gtg gac ttg gca cac cga gca 355  
Pro Val Pro Pro Leu Pro Asp Ser Phe Val Asp Leu Ala His Arg Ala  
70 75 80 85

ttg ctg tct gca gga tct tta agc aat tca ctt cag tct tgg tcg gag 403  
Leu Leu Ser Ala Gly Ser Leu Ser Asn Ser Leu Gln Ser Trp Ser Glu  
90 95 100

gca tat cga gca gaa gcg gca ttg gtg aat tac tac tcg cca gat gct 451  
Ala Tyr Arg Ala Glu Ala Ala Leu Val Asn Tyr Tyr Ser Pro Asp Ala  
105 110 115

tca atg ggc atg cac caa gac gct aat gaa gaa tcg gaa gcc cct gtg 499  
Ser Met Gly Met His Gln Asp Ala Asn Glu Glu Ser Glu Ala Pro Val  
120 125 130

atc tcc cta tcg atc ggt gat acc gga atc ttt cga ctg ggc ggc act 547  
 Ile Ser Leu Ser Ile Gly Asp Thr Gly Ile Phe Arg Leu Gly Gly Thr  
 135 140 145

cta aac cgc aat aaa ccg tgg aca gat atc cca cta atg agt ggt gat 595  
 Leu Asn Arg Asn Lys Pro Trp Thr Asp Ile Pro Leu Met Ser Gly Asp  
 150 155 160 165

ctc atc gtt ttc gga ggt gca aac agg caa gca ttt cat ggc att ccc 643  
 Leu Ile Val Phe Gly Gly Ala Asn Arg Gln Ala Phe His Gly Ile Pro  
 170 175 180

tct att gag gcc aat act gca cct gca gga tgc ggg ttg aaa gaa ggg 691  
 Ser Ile Glu Ala Asn Thr Ala Pro Ala Gly Cys Gly Leu Lys Glu Gly  
 185 190 195

gaa tca aca tca cga tcc gcc aac ttg cac tat aaa act cca ggt aga 739  
 Glu Ser Thr Ser Arg Ser Ala Asn Leu His Tyr Lys Thr Pro Gly Arg  
 200 205 210

ggt atg tct cgg ggg tgaaatagcc ccgcaatgtc cca 777  
 Gly Met Ser Arg Gly  
 215

<210> 48

<211> 218

<212> PRT

<213> Corynebacterium glutamicum

<400> 48

Val Val His Leu Pro Asn Phe Leu Gly Leu Ala Glu Gln Lys Ala Leu  
 1 5 10 15

Val Ala Gln Ala Arg Asp Leu Ala Arg Glu Val Val Gly Thr Pro Leu  
 20 25 30

Ala Met Val Arg Pro Lys Leu Lys Ser Gly Gln Met Ser Val His Met  
 35 40 45

Leu His Leu Gly Lys Tyr Trp Ala Ser Asn Pro Tyr Arg Tyr Val Asp  
 50 55 60

Val Val Asp Gly Phe Pro Val Pro Pro Leu Pro Asp Ser Phe Val Asp  
 65 70 75 80

Leu Ala His Arg Ala Leu Leu Ser Ala Gly Ser Leu Ser Asn Ser Leu  
 85 90 95

Gln Ser Trp Ser Glu Ala Tyr Arg Ala Glu Ala Ala Leu Val Asn Tyr  
 100 105 110

Tyr Ser Pro Asp Ala Ser Met Gly Met His Gln Asp Ala Asn Glu Glu  
 115 120 125

Ser Glu Ala Pro Val Ile Ser Leu Ser Ile Gly Asp Thr Gly Ile Phe  
 130 135 140

Arg Leu Gly Gly Thr Leu Asn Arg Asn Lys Pro Trp Thr Asp Ile Pro  
 145 150 155 160

<400> 49																
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ccaccaactt cccagaccac cgcgcagggt tgcagctggc																
Val Val His Leu Pro																115
1 5																
aac ttc ctc ggc ttg gcc gag caa aag gca ctg gtc gcc cag gct cga																163
Asn Phe Leu Gly Leu Ala Glu Gln Lys Ala Leu Val Ala Gln Ala Arg																
10 15 20																
gac ctt gcg cgt gaa gtt gtg ggc aca ccg ttg gcg atg gtc cga ccc																211
Asp Leu Ala Arg Glu Val Val Gly Thr Pro Leu Ala Met Val Arg Pro																
25 30 35																
aag ctg aaa agt ggt cag atg agt gtc cat atg ttg cat tta gga aag																259
Lys Leu Lys Ser Gly Gln Met Ser Val His Met Leu His Leu Gly Lys																
40 45 50																
tac tgg gca tcc aat cct tat cgc tat gtg gat gtc gtt gat ggt ttt																307
Tyr Trp Ala Ser Asn Pro Tyr Arg Tyr Val Asp Val Val Asp Gly Phe																
55 60 65																
cca gtg cca cca ctg ccg gat tct ttc gtg gac ttg gca cac cga gca																355
Pro Val Pro Pro Leu Pro Asp Ser Phe Val Asp Leu Ala His Arg Ala																
70 75 80 85																
ttg ctg tct gca gga tct tta agc aat tca ctt cag tct tgg tcg gag																403
Leu Leu Ser Ala Gly Ser Leu Ser Asn Ser Leu Gln Ser Trp Ser Glu																
90 95 100																
gca tat cga gca gaa gcg gca ttg gtg aat tac tac tcg cca gat gct																451
Ala Tyr Arg Ala Glu Ala Ala Leu Val Asn Tyr Tyr Ser Pro Asp Ala																
105 110 115																
tca atg ggc atg cac caa gac gct aat gaa gaa tcg gaa gcc cct gtg																499
Ser Met Gly Met His Gln Asp Ala Asn Glu Glu Ser Glu Ala Pro Val																

120	125	130	
atc tcc cta tcg atc ggt gat	acc gga atc ttt cga ctg ggc ggc act	547	
Ile Ser Leu Ser Ile Gly Asp Thr Gly Ile Phe Arg Leu Gly Gly Thr			
135	140 145		
cta aac cgc aat aaa ccg tgg aca gat atc cca cta atg agt ggt gat	595		
Leu Asn Arg Asn Lys Pro Trp Thr Asp Ile Pro Leu Met Ser Gly Asp			
150	155 160 165		
ctc atc gtt ttc gga ggt gca aac agg caa gca ttt cat ggc att ccc	643		
Leu Ile Val Phe Gly Gly Ala Asn Arg Gln Ala Phe His Gly Ile Pro			
170	175 180		
tct att gag gcc aat act gca cct gca gga tgc ggg ttg aaa gaa ggg	691		
Ser Ile Glu Ala Asn Thr Ala Pro Ala Gly Cys Gly Leu Lys Glu Gly			
185	190 195		
gaa tca aca tca cga tcc gcc aac ttg cac tat aaa act cca ggt aga	739		
Glu Ser Thr Ser Arg Ser Ala Asn Leu His Tyr Lys Thr Pro Gly Arg			
200	205 210		
ggt atg tct cgg ggg tgaaatagcc ccgcaatgtc cca	777		
Gly Met Ser Arg Gly			
215			

&lt;210&gt; 50

&lt;211&gt; 218

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 50

Val Val His Leu Pro Asn Phe Leu Gly Leu Ala Glu Gln Lys Ala Leu
1 5 10 15

Val Ala Gln Ala Arg Asp Leu Ala Arg Glu Val Val Gly Thr Pro Leu
20 25 30

Ala Met Val Arg Pro Lys Leu Lys Ser Gly Gln Met Ser Val His Met
35 40 45

Leu His Leu Gly Lys Tyr Trp Ala Ser Asn Pro Tyr Arg Tyr Val Asp
50 55 60

Val Val Asp Gly Phe Pro Val Pro Pro Leu Pro Asp Ser Phe Val Asp
65 70 75 80

Leu Ala His Arg Ala Leu Leu Ser Ala Gly Ser Leu Ser Asn Ser Leu
85 90 95

Gln Ser Trp Ser Glu Ala Tyr Arg Ala Glu Ala Ala Leu Val Asn Tyr
100 105 110

Tyr Ser Pro Asp Ala Ser Met Gly Met His Gln Asp Ala Asn Glu Glu
115 120 125

Ser Glu Ala Pro Val Ile Ser Leu Ser Ile Gly Asp Thr Gly Ile Phe
130 135 140

Arg Leu Gly Gly Thr Leu Asn Arg Asn Lys Pro Trp Thr Asp Ile Pro
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145		150		155		160
Leu Met Ser Gly Asp	Leu Ile Val Phe Gly Gly Ala Asn Arg Gln Ala					
	165			170		175
Phe His Gly Ile Pro Ser Ile Glu Ala Asn Thr Ala Pro Ala Gly Cys						
	180		185		190	
Gly Leu Lys Glu Gly Glu Ser Thr Ser Arg Ser Ala Asn Leu His Tyr						
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Lys Thr Pro Gly Arg Gly Met Ser Arg Gly						
	210		215			

<210> 51  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXN01733

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 Met His Ile Arg Ser Leu Glu Leu Arg Asp Tyr Arg Ser Trp  
 1 5 10

cct gaa ctc aaa gtg gat ttg gaa cct gga att aca gtt ttt atc ggc 159  
 Pro Glu Leu Lys Val Asp Leu Glu Pro Gly Ile Thr Val Phe Ile Gly  
 15 20 25 30

cgc aac ggt ttt ggt aaa acc aac atc gtc gag gcc atc ggc tat ctt 207  
 Arg Asn Gly Phe Gly Lys Thr Asn Ile Val Glu Ala Ile Gly Tyr Leu  
 35 40 45

gcg cat ttg tca tgc cat cgg gtg tcc tct gat gcg cca ttg gtg cgg 255  
 Ala His Leu Ser Ser His Arg Val Ser Ser Asp Ala Pro Leu Val Arg  
 50 55 60

gcg cac gct gaa aac gcc cga gtt tgc gcg gtt gct gtt aat caa ggc 303  
 Ala His Ala Glu Asn Ala Arg Val Ser Ala Val Ala Val Asn Gln Gly  
 65 70 75

cga gaa ttg gca gct cac ttg ctg atc aaa ccc cat gct gcg aat cag 351  
 Arg Glu Leu Ala Ala His Leu Leu Ile Lys Pro His Ala Ala Asn Gln  
 80 85 90

gca agt ttg aat cgc aca aaa gtc agg act ccc cgg gag ctg ctt ggt 399  
 Ala Ser Leu Asn Arg Thr Lys Val Arg Thr Pro Arg Glu Leu Leu Gly  
 95 100 105 110

gtg gtg aaa acg gtg ctg ttt gcg ccg gaa gat ttg gca tta gtc aaa 447  
 Val Val Lys Thr Val Leu Phe Ala Pro Glu Asp Leu Ala Leu Val Lys  
 115 120 125

ggc gag cca gca gaa cgt cgc cgc tat tta gat gac att att gcc act 495

Gly	Glu	Pro	Ala	Glu	Arg	Arg	Arg	Tyr	Leu	Asp	Asp	Ile	Ile	Ala	Thr		
			130					135					140				
cgc	cag	cct	cgg	atg	gcg	ggg	gtc	aag	gcc	gac	tac	gac	aag	gtg	ctg	543	
Arg	Gln	Pro	Arg	Met	Ala	Gly	Val	Lys	Ala	Asp	Tyr	Asp	Lys	Val	Leu		
		145					150					155					
aaa	caa	agg	aac	gcc	ctg	ctc	aag	acc	gcc	acc	att	gcg	ctt	cgt	cga	591	
Lys	Gln	Arg	Asn	Ala	Leu	Leu	Lys	Thr	Ala	Thr	Ile	Ala	Leu	Arg	Arg		
	160					165					170						
ggg	tac	ggc	acc	gag	gaa	ggc	gca	gct	gcg	ctg	agt	act	ttg	gat	acc	639	
Gly	Tyr	Gly	Thr	Glu	Glu	Gly	Ala	Ala	Ala	Leu	Ser	Thr	Leu	Asp	Thr		
175					180					185					190		
tgg	gat	ggc	cag	ttg	gca	cgc	ctg	ggg	gct	gaa	gtg	atg	gca	gcc	aga	687	
Trp	Asp	Gly	Gln	Leu	Ala	Arg	Leu	Gly	Ala	Glu	Val	Met	Ala	Ala	Arg		
				195					200					205			
ttt	gcc	ctg	ctc	aat	gag	ttg	ggg	ccg	aaa	atc	tat	gag	gct	tac	acc	735	
Phe	Ala	Leu	Leu	Asn	Glu	Leu	Gly	Pro	Lys	Ile	Tyr	Glu	Ala	Tyr	Thr		
			210					215					220				
acg	atc	gcc	ccg	gaa	tcc	cgg	cca	gct	gcg	gtg	aat	tac	aaa	acc	acc	783	
Thr	Ile	Ala	Pro	Glu	Ser	Arg	Pro	Ala	Ala	Val	Asn	Tyr	Lys	Thr	Thr		
		225					230					235					
atc	gat	caa	ggc	ctg	tcg	cag	ttt	tcc	gaa	ttc	gat	gcc	ggc	atc	atc	831	
Ile	Asp	Gln	Gly	Leu	Ser	Gln	Phe	Ser	Glu	Phe	Asp	Ala	Gly	Ile	Ile		
	240					245					250						
gaa	gcc	acg	ctg	ctg	aca	gaa	ttg	gca	gcg	aaa	cgt	caa	cga	gaa	atc	879	
Glu	Ala	Thr	Leu	Leu	Thr	Glu	Leu	Ala	Ala	Lys	Arg	Gln	Arg	Glu	Ile		
255					260					265					270		
gaa	cgc	ggc	tca	agc	ctg	gtc	ggc	ccc	cac	cgc	gat	gat	gtc	gat	tta	927	
Glu	Arg	Gly	Ser	Ser	Leu	Val	Gly	Pro	His	Arg	Asp	Asp	Val	Asp	Leu		
				275					280					285			
atg	ctc	ggc	gat	cag	ccc	gcc	aaa	ggc	ttt	gcc	agc	cac	ggc	gag	acc	975	
Met	Leu	Gly	Asp	Gln	Pro	Ala	Lys	Gly	Phe	Ala	Ser	His	Gly	Glu	Thr		
			290					295					300				
tgg	tct	ttc	gcg	ctt	tca	ctg	cga	att	gca	gaa	ttt	aac	ctg	ctg	aaa	1023	
Trp	Ser	Phe	Ala	Leu	Ser	Leu	Arg	Ile	Ala	Glu	Phe	Asn	Leu	Leu	Lys		
		305					310					315					
tcc	gat	ggc	acc	gac	ccg	atc	ctc	atc	ttg	gat	gat	gtg	ttt	tcc	gag	1071	
Ser	Asp	Gly	Thr	Asp	Pro	Ile	Leu	Ile	Leu	Asp	Asp	Val	Phe	Ser	Glu		
		320				325					330						
ctc	gac	gcc	ggc	cgt	cgc	gaa	aaa	ctc	gtg	ggc	ata	gcg	caa	gag	gtg	1119	
Leu	Asp	Ala	Gly	Arg	Arg	Glu	Lys	Leu	Val	Gly	Ile	Ala	Gln	Glu	Val		
335					340					345					350		
gaa	cag	gtg	ctc	atc	acc	gct	gca	gtc	cac	gac	gat	ctg	ccg	gag	aat	1167	
Glu	Gln	Val	Leu	Ile	Thr	Ala	Ala	Val	His	Asp	Asp	Leu	Pro	Glu	Asn		
				355				360						365			
ctc	aag	aaa	gtg	ctc	act	gcg	cag	cac	acc	gtc	acc	gtc	caa	gac	acc	1215	
Leu	Lys	Lys	Val	Leu	Thr	Ala	Gln	His	Thr	Val	Thr	Val	Gln	Asp	Thr		

370 375 380  
 ggc acc ggg cgg att tca ctc ctg gat gtg caa cca tgacagatcc 1261  
 Gly Thr Gly Arg Ile Ser Leu Leu Asp Val Gln Pro  
 385 390

aattgagcag gca 1274

<210> 52  
 <211> 394  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 52  
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 Gly Phe Gly Lys Thr Asn Ile Val Glu Ala Ile Gly Tyr Leu Ala His  
 35 40 45  
 Leu Ser Ser His Arg Val Ser Ser Asp Ala Pro Leu Val Arg Ala His  
 50 55 60  
 Ala Glu Asn Ala Arg Val Ser Ala Val Ala Val Asn Gln Gly Arg Glu  
 65 70 75 80  
 Leu Ala Ala His Leu Leu Ile Lys Pro His Ala Ala Asn Gln Ala Ser  
 85 90 95  
 Leu Asn Arg Thr Lys Val Arg Thr Pro Arg Glu Leu Leu Gly Val Val  
 100 105 110  
 Lys Thr Val Leu Phe Ala Pro Glu Asp Leu Ala Leu Val Lys Gly Glu  
 115 120 125  
 Pro Ala Glu Arg Arg Arg Tyr Leu Asp Asp Ile Ile Ala Thr Arg Gln  
 130 135 140  
 Pro Arg Met Ala Gly Val Lys Ala Asp Tyr Asp Lys Val Leu Lys Gln  
 145 150 155 160  
 Arg Asn Ala Leu Leu Lys Thr Ala Thr Ile Ala Leu Arg Arg Gly Tyr  
 165 170 175  
 Gly Thr Glu Glu Gly Ala Ala Ala Leu Ser Thr Leu Asp Thr Trp Asp  
 180 185 190  
 Gly Gln Leu Ala Arg Leu Gly Ala Glu Val Met Ala Ala Arg Phe Ala  
 195 200 205  
 Leu Leu Asn Glu Leu Gly Pro Lys Ile Tyr Glu Ala Tyr Thr Thr Ile  
 210 215 220  
 Ala Pro Glu Ser Arg Pro Ala Ala Val Asn Tyr Lys Thr Thr Ile Asp  
 225 230 235 240  
 Gln Gly Leu Ser Gln Phe Ser Glu Phe Asp Ala Gly Ile Ile Glu Ala

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Gly	Pro	Lys	Ile	Tyr	Glu	Ala	Tyr	Thr	Thr	Ile	Ala	Pro	Glu	Ser	Arg	
1				5					10					15		
cca gct gcg gtg aat tac aaa acc acc atc gat caa ggc ctg tcg cag																96
Pro	Ala	Ala	Val	Asn	Tyr	Lys	Thr	Thr	Ile	Asp	Gln	Gly	Leu	Ser	Gln	
			20					25					30			
ttt tcc gaa ttc gat gcc ggc atc atc gaa gcc acg ctg ctg aca gaa																144
Phe	Ser	Glu	Phe	Asp	Ala	Gly	Ile	Ile	Glu	Ala	Thr	Leu	Leu	Thr	Glu	
		35					40					45				
ttg gca gcg aaa cgt caa cga gaa atc gaa cgc ggc tca agc ctg gtc																192
Leu	Ala	Ala	Lys	Arg	Gln	Arg	Glu	Ile	Glu	Arg	Gly	Ser	Ser	Leu	Val	
	50					55					60					
ggc ccc cac cgc gat gat gtc gat tta atg ctc ggc gat cag ccc gcc																240
Gly	Pro	His	Arg	Asp	Asp	Val	Asp	Leu	Met	Leu	Gly	Asp	Gln	Pro	Ala	
65					70					75					80	

aaa ggc ttt gcc agc cac ggc gag acc tgg tct ttc gcg ctt tca ctg 288  
 Lys Gly Phe Ala Ser His Gly Glu Thr Trp Ser Phe Ala Leu Ser Leu  
                     85                    90                    95

cga att gca gaa ttt aac ctg ctg aaa tcc gat ggc acc gac ccg atc 336  
 Arg Ile Ala Glu Phe Asn Leu Leu Lys Ser Asp Gly Thr Asp Pro Ile  
                     100                    105                    110

ctc atc ttg gat gat gtg ttt tcc gag ctc gac gcc ggc cgt cgc gaa 384  
 Leu Ile Leu Asp Asp Val Phe Ser Glu Leu Asp Ala Gly Arg Arg Glu  
                     115                    120                    125

aaa ctc gtg ggc ata gcg caa gag gtg gaa cag gtg ctc atc acc gct 432  
 Lys Leu Val Gly Ile Ala Gln Glu Val Glu Gln Val Leu Ile Thr Ala  
                     130                    135                    140

gca gtc cac gac gat ctg ccg gag aat ctc aag aaa gtg ctc act gcg 480  
 Ala Val His Asp Asp Leu Pro Glu Asn Leu Lys Lys Val Leu Thr Ala  
 145                    150                    155                    160

cag cac acc gtc acc gtc caa gac acc ggc acc ggg cgg att tca ctc 528  
 Gln His Thr Val Thr Val Gln Asp Thr Gly Thr Gly Arg Ile Ser Leu  
                     165                    170                    175

ctg gat gtg caa cca tgacagatcc aattgagcag gca 566  
 Leu Asp Val Gln Pro  
                     180

&lt;210&gt; 54

&lt;211&gt; 181

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 54

Gly Pro Lys Ile Tyr Glu Ala Tyr Thr Thr Ile Ala Pro Glu Ser Arg  
   1                    5                    10                    15

Pro Ala Ala Val Asn Tyr Lys Thr Thr Ile Asp Gln Gly Leu Ser Gln  
                     20                    25                    30

Phe Ser Glu Phe Asp Ala Gly Ile Ile Glu Ala Thr Leu Leu Thr Glu  
                     35                    40                    45

Leu Ala Ala Lys Arg Gln Arg Glu Ile Glu Arg Gly Ser Ser Leu Val  
                     50                    55                    60

Gly Pro His Arg Asp Asp Val Asp Leu Met Leu Gly Asp Gln Pro Ala  
   65                    70                    75                    80

Lys Gly Phe Ala Ser His Gly Glu Thr Trp Ser Phe Ala Leu Ser Leu  
                     85                    90                    95

Arg Ile Ala Glu Phe Asn Leu Leu Lys Ser Asp Gly Thr Asp Pro Ile  
                     100                    105                    110

Leu Ile Leu Asp Asp Val Phe Ser Glu Leu Asp Ala Gly Arg Arg Glu  
                     115                    120                    125

Lys Leu Val Gly Ile Ala Gln Glu Val Glu Gln Val Leu Ile Thr Ala  
                     130                    135                    140

Ala Val His Asp Asp Leu Pro Glu Asn Leu Lys Lys Val Leu Thr Ala  
145 150 155 160

Gln His Thr Val Thr Val Gln Asp Thr Gly Thr Gly Arg Ile Ser Leu  
165 170 175

Leu Asp Val Gln Pro  
180

<210> 55

<211> 777

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(754)

<223> RXA01252

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Val Phe Glu Gly Pro  
1 5

ctc cag gat ctc atc gac gaa ctt tct cgt ctc ccc ggc gtc ggc ccc 163  
Leu Gln Asp Leu Ile Asp Glu Leu Ser Arg Leu Pro Gly Val Gly Pro  
10 15 20

aaa agt gcc caa cgc atc gca ttt cac ctg ctc aac gta gat cct tcc 211  
Lys Ser Ala Gln Arg Ile Ala Phe His Leu Leu Asn Val Asp Pro Ser  
25 30 35

gac att acc cgc ctt cag gaa gcc ctc gga ggc gtg cgt gat ggc gtc 259  
Asp Ile Thr Arg Leu Gln Glu Ala Leu Gly Gly Val Arg Asp Gly Val  
40 45 50

caa ttc tgc cgc atc tgc tgc aac att tcc cgc gaa gaa gtc tgt cgc 307  
Gln Phe Cys Arg Ile Cys Cys Asn Ile Ser Arg Glu Glu Val Cys Arg  
55 60 65

atc tgc tcc gac tcc gga cgt gac ggc gga aca atc tgt gtc gtc gaa 355  
Ile Cys Ser Asp Ser Gly Arg Asp Gly Gly Thr Ile Cys Val Val Glu  
70 75 80 85

gaa cca aaa gac atc caa gtt atc gag cgc acc ggc gaa ttc tcc ggc 403  
Glu Pro Lys Asp Ile Gln Val Ile Glu Arg Thr Gly Glu Phe Ser Gly  
90 95 100

cgc tac cac gtc ctc ggc ggc gcc ctc gac ccg ctg gcc aac atc ggc 451  
Arg Tyr His Val Leu Gly Gly Ala Leu Asp Pro Leu Ala Asn Ile Gly  
105 110 115

ccc cgc gaa ctc aac att tcc acg ctc ctg cag cgc atc ggc ggc gtc 499  
Pro Arg Glu Leu Asn Ile Ser Thr Leu Leu Gln Arg Ile Gly Gly Val  
120 125 130

ctg cca gac cgt gag ctc gca gat tcc acg cct gaa aat aag ctt ttc 547

Leu Pro Asp Arg Glu Leu Ala Asp Ser Thr Pro Glu Asn Lys Leu Phe  
 135 140 145  
 gac gcc acc ccc acc gtc cgc gaa gtc atc ctc gca aca gac ccc aac 595  
 Asp Ala Thr Pro Thr Val Arg Glu Val Ile Leu Ala Thr Asp Pro Asn  
 150 155 160 165  
 acc gaa ggc gaa gcc acc gcc tca tac ctc ggc cgc ctc ttg aaa gac 643  
 Thr Glu Gly Glu Ala Thr Ala Ser Tyr Leu Gly Arg Leu Leu Lys Asp  
 170 175 180  
 ttc cca gat ctg gta att tcc cgc ctc gca tcc gga atg cca cta ggc 691  
 Phe Pro Asp Leu Val Ile Ser Arg Leu Ala Ser Gly Met Pro Leu Gly  
 185 190 195  
 ggc gac ctc gaa ttc gtc gac gaa ctc act ctc tcc cga gca ttg agt 739  
 Gly Asp Leu Glu Phe Val Asp Glu Leu Thr Leu Ser Arg Ala Leu Ser  
 200 205 210  
 ggc cgc ctg cag atc tagccccctcc tttacaggct ggc 777  
 Gly Arg Leu Gln Ile  
 215

<210> 56  
 <211> 218  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 56  
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 Asn Val Asp Pro Ser Asp Ile Thr Arg Leu Gln Glu Ala Leu Gly Gly  
 35 40 45  
 Val Arg Asp Gly Val Gln Phe Cys Arg Ile Cys Cys Asn Ile Ser Arg  
 50 55 60  
 Glu Glu Val Cys Arg Ile Cys Ser Asp Ser Gly Arg Asp Gly Gly Thr  
 65 70 75 80  
 Ile Cys Val Val Glu Glu Pro Lys Asp Ile Gln Val Ile Glu Arg Thr  
 85 90 95  
 Gly Glu Phe Ser Gly Arg Tyr His Val Leu Gly Gly Ala Leu Asp Pro  
 100 105 110  
 Leu Ala Asn Ile Gly Pro Arg Glu Leu Asn Ile Ser Thr Leu Leu Gln  
 115 120 125  
 Arg Ile Gly Gly Val Leu Pro Asp Arg Glu Leu Ala Asp Ser Thr Pro  
 130 135 140  
 Glu Asn Lys Leu Phe Asp Ala Thr Pro Thr Val Arg Glu Val Ile Leu  
 145 150 155 160  
 Ala Thr Asp Pro Asn Thr Glu Gly Glu Ala Thr Ala Ser Tyr Leu Gly

	165		170		175
Arg Leu Leu Lys Asp Phe Pro Asp Leu Val Ile Ser Arg Leu Ala Ser	180	185	190		
Gly Met Pro Leu Gly Gly Asp Leu Glu Phe Val Asp Glu Leu Thr Leu	195	200	205		
Ser Arg Ala Leu Ser Gly Arg Leu Gln Ile	210	215			

<210> 57  
 <211> 1002  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(979)  
 <223> RXA01878

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 Met Glu Glu Pro Ser 5  
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 ggt gca cag ctg ctc ggc ccg gta gaa atc cgt gcg ctg gca gaa aag 163  
 Gly Ala Gln Leu Leu Gly Pro Val Glu Ile Arg Ala Leu Ala Glu Lys 20  
 10 15  
 ctc gac gtc aca cca act aag aag ttg ggg cag aac ttt gtt cac gat 211  
 Leu Asp Val Thr Pro Thr Lys Lys Leu Gly Gln Asn Phe Val His Asp 35  
 25 30  
 ccc aac acg gtg cgt cgc att gtt gct gcg gca gag ctc acc cca aac 259  
 Pro Asn Thr Val Arg Arg Ile Val Ala Ala Ala Glu Leu Thr Pro Asn 50  
 40 45  
 gac cac gtg gtg gaa gtt ggc cct ggt ctg ggc tct ctg acc ctt gcc 307  
 Asp His Val Val Glu Val Gly Pro Gly Leu Gly Ser Leu Thr Leu Ala 65  
 55 60  
 ctg gtg gaa tct gct gct tca gta act gcg gtg gaa att gat ccc cgt 355  
 Leu Val Glu Ser Ala Ala Ser Val Thr Ala Val Glu Ile Asp Pro Arg 85  
 70 75 80  
 ttg gct gcg gaa ttg ccg gag act ttt cag tgg cgc gcg ccg gcc ctt 403  
 Leu Ala Ala Glu Leu Pro Glu Thr Phe Gln Trp Arg Ala Pro Ala Leu 100  
 90 95 100  
 gct cac aag ttg agc atc gtg ctg aaa gac gcc ctg aag gtt caa caa 451  
 Ala His Lys Leu Ser Ile Val Leu Lys Asp Ala Leu Lys Val Gln Gln 115  
 105 110  
 tcc gat atg gct gtt caa ccc acc gcc ttg gtg gct aac ttg ccg tac 499  
 Ser Asp Met Ala Val Gln Pro Thr Ala Leu Val Ala Asn Leu Pro Tyr 130  
 120 125

aac gtc tct gtc cct gtc ttg ttg cac atg atg gag gag ttt ccc acc 547  
 Asn Val Ser Val Pro Val Leu Leu His Met Met Glu Glu Phe Pro Thr  
 135 140 145

atc aac aag gtg ctt gtc atg gtg cag gca gag gtt gct gat cgt ttg 595  
 Ile Asn Lys Val Leu Val Met Val Gln Ala Glu Val Ala Asp Arg Leu  
 150 155 160 165

gct gcg gat cca gga tgc aag att tat ggt gtg cct agc gtg aag gcg 643  
 Ala Ala Asp Pro Gly Ser Lys Ile Tyr Gly Val Pro Ser Val Lys Ala  
 170 175 180

tcc ttc tac ggt cca gtt act cgc gcc ggg tgc att ggt aag aat gtc 691  
 Ser Phe Tyr Gly Pro Val Thr Arg Ala Gly Ser Ile Gly Lys Asn Val  
 185 190 195

ttt tgg cca gct cca aag atc gaa tcc ggt ttg gtg aag atc gtg cgc 739  
 Phe Trp Pro Ala Pro Lys Ile Glu Ser Gly Leu Val Lys Ile Val Arg  
 200 205 210

gaa gac acc gcg tgg aag cag gac gat gag acg cgt aag aag gtg tgg 787  
 Glu Asp Thr Ala Trp Lys Gln Asp Asp Glu Thr Arg Lys Lys Val Trp  
 215 220 225

ccg atc att gat gct gct ttc ttg cag cgc cgt aaa acc cta aga gct 835  
 Pro Ile Ile Asp Ala Ala Phe Leu Gln Arg Arg Lys Thr Leu Arg Ala  
 230 235 240 245

gcg ctt tct gga cac tac ggt tct ggc cag gca gct gag gaa gct ttg 883  
 Ala Leu Ser Gly His Tyr Gly Ser Gly Gln Ala Ala Glu Glu Ala Leu  
 250 255 260

cgg gcc gct gat att gat cca acg ctt cgt ggc gaa aag ctt gat gtc 931  
 Arg Ala Ala Asp Ile Asp Pro Thr Leu Arg Gly Glu Lys Leu Asp Val  
 265 270 275

act gac tat gtg cgc cta gct ggg gtg ttg cag caa aag gat gag aag 979  
 Thr Asp Tyr Val Arg Leu Ala Gly Val Leu Gln Gln Lys Asp Glu Lys  
 280 285 290

tgaaaattac cgctaaggcg tgg 1002

&lt;210&gt; 58

&lt;211&gt; 293

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 58

Met Glu Glu Pro Ser Gly Ala Gln Leu Leu Gly Pro Val Glu Ile Arg  
 1 5 10 15

Ala Leu Ala Glu Lys Leu Asp Val Thr Pro Thr Lys Lys Leu Gly Gln  
 20 25 30

Asn Phe Val His Asp Pro Asn Thr Val Arg Arg Ile Val Ala Ala Ala  
 35 40 45

Glu Leu Thr Pro Asn Asp His Val Val Glu Val Gly Pro Gly Leu Gly  
 50 55 60

Ser Leu Thr Leu Ala Leu Val Glu Ser Ala Ala Ser Val Thr Ala Val  
 65 70 75 80  
 Glu Ile Asp Pro Arg Leu Ala Ala Glu Leu Pro Glu Thr Phe Gln Trp  
 85 90 95  
 Arg Ala Pro Ala Leu Ala His Lys Leu Ser Ile Val Leu Lys Asp Ala  
 100 105 110  
 Leu Lys Val Gln Gln Ser Asp Met Ala Val Gln Pro Thr Ala Leu Val  
 115 120 125  
 Ala Asn Leu Pro Tyr Asn Val Ser Val Pro Val Leu Leu His Met Met  
 130 135 140  
 Glu Glu Phe Pro Thr Ile Asn Lys Val Leu Val Met Val Gln Ala Glu  
 145 150 155 160  
 Val Ala Asp Arg Leu Ala Ala Asp Pro Gly Ser Lys Ile Tyr Gly Val  
 165 170 175  
 Pro Ser Val Lys Ala Ser Phe Tyr Gly Pro Val Thr Arg Ala Gly Ser  
 180 185 190  
 Ile Gly Lys Asn Val Phe Trp Pro Ala Pro Lys Ile Glu Ser Gly Leu  
 195 200 205  
 Val Lys Ile Val Arg Glu Asp Thr Ala Trp Lys Gln Asp Asp Glu Thr  
 210 215 220  
 Arg Lys Lys Val Trp Pro Ile Ile Asp Ala Ala Phe Leu Gln Arg Arg  
 225 230 235 240  
 Lys Thr Leu Arg Ala Ala Leu Ser Gly His Tyr Gly Ser Gly Gln Ala  
 245 250 255  
 Ala Glu Glu Ala Leu Arg Ala Ala Asp Ile Asp Pro Thr Leu Arg Gly  
 260 265 270  
 Glu Lys Leu Asp Val Thr Asp Tyr Val Arg Leu Ala Gly Val Leu Gln  
 275 280 285  
 Gln Lys Asp Glu Lys  
 290

&lt;210&gt; 59

&lt;211&gt; 872

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(849)

&lt;223&gt; RXA01556

&lt;400&gt; 59

aac atc cgc ttt gag acc ctc aac atc atg gga cct gcg cgt cgc atc 48  
 Asn Ile Arg Phe Glu Thr Leu Asn Ile Met Gly Pro Ala Arg Arg Ile  
 1 5 10 15

cac ctg ggt cac gtg tgg aat gat cgc ctg acc ttt gaa tac agt cgc	96
His Leu Gly His Val Trp Asn Asp Arg Leu Thr Phe Glu Tyr Ser Arg	
20 25 30	
tcg ctg ttc ggt aaa gag acc ctg tcg cca gac atc gcg cgc ctg ttc	144
Ser Leu Phe Gly Lys Glu Thr Leu Ser Pro Asp Ile Ala Arg Leu Phe	
35 40 45	
acc gac cgc gtt ccc acc cct ccg ctg cca gct ccg cgt aaa gcg cgc	192
Thr Asp Arg Val Pro Thr Pro Pro Leu Pro Ala Pro Arg Lys Ala Arg	
50 55 60	
gca gtg gcg cag gtg ctg gtg tcc aac cct gcg gat cag acc agt ttg	240
Ala Val Ala Gln Val Leu Val Ser Asn Pro Ala Asp Gln Thr Ser Leu	
65 70 75 80	
gaa gaa ttt gcg gag atc caa ggc gtt tcg gcg cgt act ttg cag cgc	288
Glu Glu Phe Ala Glu Ile Gln Gly Val Ser Ala Arg Thr Leu Gln Arg	
85 90 95	
cag ttc ctc aaa tcc acg ggc tat tca ttc agc gaa tgg cgt gct gcg	336
Gln Phe Leu Lys Ser Thr Gly Tyr Ser Phe Ser Glu Trp Arg Ala Ala	
100 105 110	
cag cgc gtc tgc gtc gcc gcg agc ctg ctg gcc cac gac ttc agc att	384
Gln Arg Val Cys Val Ala Ala Ser Leu Leu Ala His Asp Phe Ser Ile	
115 120 125	
tca gtg gtt gcg aac ctc gtc ggg ttc gcc gcg acc agc agc ttg acc	432
Ser Val Val Ala Asn Leu Val Gly Phe Ala Ala Thr Ser Ser Leu Thr	
130 135 140	
aga gct ttt cga cgc cac acc ggt gca act ccg tcc acc ttt act act	480
Arg Ala Phe Arg Arg His Thr Gly Ala Thr Pro Ser Thr Phe Thr Thr	
145 150 155 160	
gga cag atc ggc atg ggc tcc gca ggt cac cca cca cgc atc cca gca	528
Gly Gln Ile Gly Met Gly Ser Ala Gly His Pro Pro Arg Ile Pro Ala	
165 170 175	
acc acc acg ttt gcc gaa gcg cat cag gac cag cag ctg tgg att tac	576
Thr Thr Thr Phe Ala Glu Ala His Gln Asp Gln Gln Leu Trp Ile Tyr	
180 185 190	
agc gga acc gca acc gtc acc acc ccc ggc tac tgc cga ttc atg gga	624
Ser Gly Thr Ala Thr Val Thr Thr Pro Gly Tyr Cys Arg Phe Met Gly	
195 200 205	
caa ggt gac atg gtg acc atc cct gcc ggc acc caa acc cgc att gac	672
Gln Gly Asp Met Val Thr Ile Pro Ala Gly Thr Gln Thr Arg Ile Asp	
210 215 220	
gtg gca gcc gga tcc atc gca ttc cca gtc cca gtt gga ctc gac gaa	720
Val Ala Ala Gly Ser Ile Ala Phe Pro Val Pro Val Gly Leu Asp Glu	
225 230 235 240	
tgg gga atg gac cta acc cgc gtc gtg gct gtt aat aac cag cag cca	768
Trp Gly Met Asp Leu Thr Arg Val Val Ala Val Asn Asn Gln Gln Pro	
245 250 255	
aag cca ctg acc att ttg gaa cag tct gaa tgg tcc aag ctc agc gaa	816

Lys Pro Leu Thr Ile Leu Glu Gln Ser Glu Trp Ser Lys Leu Ser Glu  
 260 265 270

gaa ctt ctg aac act cct gta cct gta caa atg tgaaggtagt aaagggtgtga 869  
 Glu Leu Leu Asn Thr Pro Val Pro Val Gln Met  
 275 280

aaa

872

<210> 60

<211> 283

<212> PRT

<213> Corynebacterium glutamicum

<400> 60

Asn Ile Arg Phe Glu Thr Leu Asn Ile Met Gly Pro Ala Arg Arg Ile  
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His Leu Gly His Val Trp Asn Asp Arg Leu Thr Phe Glu Tyr Ser Arg  
 20 25 30

Ser Leu Phe Gly Lys Glu Thr Leu Ser Pro Asp Ile Ala Arg Leu Phe  
 35 40 45

Thr Asp Arg Val Pro Thr Pro Pro Leu Pro Ala Pro Arg Lys Ala Arg  
 50 55 60

Ala Val Ala Gln Val Leu Val Ser Asn Pro Ala Asp Gln Thr Ser Leu  
 65 70 75 80

Glu Glu Phe Ala Glu Ile Gln Gly Val Ser Ala Arg Thr Leu Gln Arg  
 85 90 95

Gln Phe Leu Lys Ser Thr Gly Tyr Ser Phe Ser Glu Trp Arg Ala Ala  
 100 105 110

Gln Arg Val Cys Val Ala Ala Ser Leu Leu Ala His Asp Phe Ser Ile  
 115 120 125

Ser Val Val Ala Asn Leu Val Gly Phe Ala Ala Thr Ser Ser Leu Thr  
 130 135 140

Arg Ala Phe Arg Arg His Thr Gly Ala Thr Pro Ser Thr Phe Thr Thr  
 145 150 155 160

Gly Gln Ile Gly Met Gly Ser Ala Gly His Pro Pro Arg Ile Pro Ala  
 165 170 175

Thr Thr Thr Phe Ala Glu Ala His Gln Asp Gln Gln Leu Trp Ile Tyr  
 180 185 190

Ser Gly Thr Ala Thr Val Thr Thr Pro Gly Tyr Cys Arg Phe Met Gly  
 195 200 205

Gln Gly Asp Met Val Thr Ile Pro Ala Gly Thr Gln Thr Arg Ile Asp  
 210 215 220

Val Ala Ala Gly Ser Ile Ala Phe Pro Val Pro Val Gly Leu Asp Glu  
 225 230 235 240

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gtagcattg ggtttctgac cagtagttct gaggagaatc gtg aag aaa cgc atc 115															
Val Lys Lys Arg Ile 5															
aat gta acc ggc gcc gtc cta gtc aag gaa aac cgt atc ctt gca gca 163															
Asn Val Thr Gly Ala Val Leu Val Lys Glu Asn Arg Ile Leu Ala Ala 20															
caa cgt ggt cca gag atg tca ctt ccc gga tat tgg gag ttt ccg gga 211															
Gln Arg Gly Pro Glu Met Ser Leu Pro Gly Tyr Trp Glu Phe Pro Gly 35															
gga aag atc gag cag ggc gaa act cca gaa gct tca ctt gca cga gag 259															
Gly Lys Ile Glu Gln Gly Glu Thr Pro Glu Ala Ser Leu Ala Arg Glu 50															
ctc aaa gaa gaa ttg ctt tgc gac gcc acc gta ggc gaa cac ctc acc 307															
Leu Lys Glu Glu Leu Leu Cys Asp Ala Thr Val Gly Glu His Leu Thr 65															
act aca gag cac gag tac gac ttt gga atc gtc gtg ctt tcc acc tac 355															
Thr Thr Glu His Glu Tyr Asp Phe Gly Ile Val Val Leu Ser Thr Tyr 85															
ttc tgc aca cta aat gat gca gag cct caa ttg acc gag cat gct gag 403															
Phe Cys Thr Leu Asn Asp Ala Glu Pro Gln Leu Thr Glu His Ala Glu 100															
atc cgc tgg gtg gca cca cac gaa ttg gaa tct ttg gag tgg gca cct 451															
Ile Arg Trp Val Ala Pro His Glu Leu Glu Ser Leu Glu Trp Ala Pro 115															
gct gat att cct gcg gtg aaa ctt ctc gtc gag cag ctt gct 493															
Ala Asp Ile Pro Ala Val Lys Leu Leu Val Glu Gln Leu Ala 130															
taatgagccc attcgattca aag 516															

<210> 62  
 <211> 131  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 62  
 Val Lys Lys Arg Ile Asn Val Thr Gly Ala Val Leu Val Lys Glu Asn  
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 Arg Ile Leu Ala Ala Gln Arg Gly Pro Glu Met Ser Leu Pro Gly Tyr  
           20                    25                    30  
 Trp Glu Phe Pro Gly Gly Lys Ile Glu Gln Gly Glu Thr Pro Glu Ala  
           35                    40                    45  
 Ser Leu Ala Arg Glu Leu Lys Glu Glu Leu Leu Cys Asp Ala Thr Val  
           50                    55                    60  
 Gly Glu His Leu Thr Thr Thr Glu His Glu Tyr Asp Phe Gly Ile Val  
       65                    70                    75                    80  
 Val Leu Ser Thr Tyr Phe Cys Thr Leu Asn Asp Ala Glu Pro Gln Leu  
                     85                    90                    95  
 Thr Glu His Ala Glu Ile Arg Trp Val Ala Pro His Glu Leu Glu Ser  
           100                    105                    110  
 Leu Glu Trp Ala Pro Ala Asp Ile Pro Ala Val Lys Leu Leu Val Glu  
       115                    120                    125  
 Gln Leu Ala  
       130

<210> 63  
 <211> 624  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(601)  
 <223> RXA00280

<400> 63  
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 attggctacc ttgatgaata cccccagcgt ttagcctaat gtg gac acc atg aaa 115  
   Val Asp Thr Met Lys  
   1                    5  
 ggc gac ggc gat gga tgg gca gca gca ccc aat ggc ggg gca gta tgg 163  
 Gly Asp Gly Asp Gly Trp Ala Ala Ala Pro Asn Gly Gly Ala Val Trp  
                     10                    15                    20  
 ggc aaa aac gga gca gca gga ttg ttg ttg gta gca gat aaa caa atg 211  
 Gly Lys Asn Gly Ala Ala Gly Leu Leu Leu Val Ala Asp Lys Gln Met  
                     25                    30                    35  
 ctc atg cag cac cga gcc gca tgg acc aac aac ggc gac acc tgg gca 259

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<400> 64
Val Asp Thr Met Lys Gly Asp Gly Asp Gly Trp Ala Ala Ala Pro Asn
  1                      5                      10                      15

Gly Gly Ala Val Trp Gly Lys Asn Gly Ala Ala Gly Leu Leu Leu Val
      20                      25                      30

Ala Asp Lys Gln Met Leu Met Gln His Arg Ala Ala Trp Thr Asn Asn
      35                      40                      45

Gly Asp Thr Trp Ala Leu Pro Gly Gly Ala Arg Asp Ser His Glu Thr
  50                      55                      60

Ala Ala Glu Ser Ala Leu Arg Glu Ala Phe Glu Glu Thr Gly Ile Leu
  65                      70                      75                      80

Pro Asp Asp Val Glu Val Leu Asp Ser Ile Val Thr Ala Gly Pro Phe
      85                      90                      95

Pro Ala Asp Pro Glu Arg Pro Glu Leu Ala Gly Asn Trp Thr Tyr Thr

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100	105	110	
Thr Val Ile Ala Arg Thr Lys Thr Gly Glu Thr Leu Asp Thr Thr Ala			
115	120	125	
Asn Glu Glu Ser Leu Glu Leu Arg Trp Val Asp Ile Ala Ala Val Asp			
130	135	140	
Ser Leu Ala Leu Met Pro Ala Phe Ala Lys Ala Trp Pro Ser Leu Arg			
145	150	155	160
Lys Leu Leu Asn Thr Thr Glu			
165			
<210> 65			
<211> 657			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(634)			
<223> RXA00333			
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cctgggagtc aaagattacc aattggagag gttttgctgc	atg gcg gtt cca gag	115	
	Met Ala Val Pro Glu		
	1 5		
ttc att gtt agt ttg cgg gag aag gtc ggt cag gat ccg ttg tgg ttg		163	
Phe Ile Val Ser Leu Arg Glu Lys Val Gly Gln Asp Pro Leu Trp Leu			
10	15 20		
ccg gct gta act gcg gtt gtt att cgt gat gtt cct ccg ggg tct cct		211	
Pro Ala Val Thr Ala Val Val Ile Arg Asp Val Pro Pro Gly Ser Pro			
25	30 35		
ttc cat gtg gtt ccg gat gtg ttg ttg gtc aag cgc gct gat act ggt		259	
Phe His Val Val Pro Asp Val Leu Leu Val Lys Arg Ala Asp Thr Gly			
40	45 50		
gag tgg act cca ccg acc ggt att tgt gat ccg gat gag cag cct cat		307	
Glu Trp Thr Pro Pro Thr Gly Ile Cys Asp Pro Asp Glu Gln Pro His			
55	60 65		
gtg act gcg gtg cgt gaa gtc aag gag gaa acc ggc ctt gat gtc agc		355	
Val Thr Ala Val Arg Glu Val Lys Glu Glu Thr Gly Leu Asp Val Ser			
70	75 80 85		
gtt gag gcg ttg ctt ggc gtg ggc gcg gtg ggg cct gtg acc tat caa		403	
Val Glu Ala Leu Leu Gly Val Gly Ala Val Gly Pro Val Thr Tyr Gln			
90	95 100		
aat ggt gat gtg gcg agc tac atg gat acg acc atg cgt tgc gtt gtt		451	
Asn Gly Asp Val Ala Ser Tyr Met Asp Thr Thr Met Arg Cys Val Val			
105	110 115		
tct ggt gat tcc gat gag cct cac gtc ggc gat gac gag aac gtg gat		499	

Ser Gly Asp Ser Asp Glu Pro His Val Gly Asp Asp Glu Asn Val Asp  
 120 125 130  
 gtt gca tgg ttc ccg att tct aag atg cct gtc act aat cag cgt ttc 547  
 Val Ala Trp Phe Pro Ile Ser Lys Met Pro Val Thr Asn Gln Arg Phe  
 135 140 145  
 cgc atg gtc atc gct gat gcg gtg gca cag ttg aag cat ccg caa ggt 595  
 Arg Met Val Ile Ala Asp Ala Val Ala Gln Leu Lys His Pro Gln Gly  
 150 155 160 165  
 tat aag ccc cgc atg gga tat gag aaa agg aat gca cga tgagtattga 644  
 Tyr Lys Pro Arg Met Gly Tyr Glu Lys Arg Asn Ala Arg  
 170 175  
 atttccgtta ggt 657  
 <210> 66  
 <211> 178  
 <212> PRT  
 <213> Corynebacterium glutamicum  
 <400> 66  
 Met Ala Val Pro Glu Phe Ile Val Ser Leu Arg Glu Lys Val Gly Gln  
 1 5 10 15  
 Asp Pro Leu Trp Leu Pro Ala Val Thr Ala Val Val Ile Arg Asp Val  
 20 25 30  
 Pro Pro Gly Ser Pro Phe His Val Val Pro Asp Val Leu Leu Val Lys  
 35 40 45  
 Arg Ala Asp Thr Gly Glu Trp Thr Pro Pro Thr Gly Ile Cys Asp Pro  
 50 55 60  
 Asp Glu Gln Pro His Val Thr Ala Val Arg Glu Val Lys Glu Glu Thr  
 65 70 75 80  
 Gly Leu Asp Val Ser Val Glu Ala Leu Leu Gly Val Gly Ala Val Gly  
 85 90 95  
 Pro Val Thr Tyr Gln Asn Gly Asp Val Ala Ser Tyr Met Asp Thr Thr  
 100 105 110  
 Met Arg Cys Val Val Ser Gly Asp Ser Asp Glu Pro His Val Gly Asp  
 115 120 125  
 Asp Glu Asn Val Asp Val Ala Trp Phe Pro Ile Ser Lys Met Pro Val  
 130 135 140  
 Thr Asn Gln Arg Phe Arg Met Val Ile Ala Asp Ala Val Ala Gln Leu  
 145 150 155 160  
 Lys His Pro Gln Gly Tyr Lys Pro Arg Met Gly Tyr Glu Lys Arg Asn  
 165 170 175  
 Ala Arg

<400> 67															60			
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										Met Ala Val Ser Thr								
										1	5							
atc atc ttc gcg ctg cgc ccc ggc ccc cag gat ctg ccc agc ctg tgg															163			
Ile Ile Phe Ala Leu Arg Pro Gly Pro Gln Asp Leu Pro Ser Leu Trp																		
															10	15	20	
gcc ccc ttc gtt ccg cgc acc cgc gaa cca cat tta aat aaa tgg gca															211			
Ala Pro Phe Val Pro Arg Thr Arg Glu Pro His Leu Asn Lys Trp Ala																		
															25	30	35	
ctg ccc ggc ggt tgg ctg cca cca cat gaa gaa ctt gaa gat gct gct															259			
Leu Pro Gly Gly Trp Leu Pro Pro His Glu Glu Leu Glu Asp Ala Ala																		
															40	45	50	
gcc cgc aca ctg gca gaa acc acc ggc ctg cac ccc agc tat cta gaa															307			
Ala Arg Thr Leu Ala Glu Thr Thr Gly Leu His Pro Ser Tyr Leu Glu																		
															55	60	65	
cag ctg tac act ttc gga aaa gtc gac cgc tcc cca acc gga cgc gtg															355			
Gln Leu Tyr Thr Phe Gly Lys Val Asp Arg Ser Pro Thr Gly Arg Val																		
															70	75	80	85
atc tct gtg gtg tat tgg gca ctt gtc cga gcc gat gaa gcg ttg aaa															403			
Ile Ser Val Val Tyr Trp Ala Leu Val Arg Ala Asp Glu Ala Leu Lys																		
															90	95	100	
gcc atc cca gga gaa aac gtc cag tgg ttt ccc gcc gat cat ctg cct															451			
Ala Ile Pro Gly Glu Asn Val Gln Trp Phe Pro Ala Asp His Leu Pro																		
															105	110	115	
gag ctg gca ttt gac cac aat aac atc gtc aaa tat gca cta gaa cga															499			
Glu Leu Ala Phe Asp His Asn Asn Ile Val Lys Tyr Ala Leu Glu Arg																		
															120	125	130	
ctt cgc acc aag gtg gaa tac tcc gaa atc gcc cac tcc ttc ctg gga															547			
Leu Arg Thr Lys Val Glu Tyr Ser Glu Ile Ala His Ser Phe Leu Gly																		
															135	140	145	
gaa acc ttc acc atc gcc cag ctt cga tcc gtg cat gag gca gtc ctt															595			
Glu Thr Phe Thr Ile Ala Gln Leu Arg Ser Val His Glu Ala Val Leu																		
															150	155	160	165
gga cac aaa ctg gat gcc gcc aac ttc cga aga tcc gtg gcc acc tcg															643			
Gly His Lys Leu Asp Ala Ala Asn Phe Arg Arg Ser Val Ala Thr Ser																		
															170	175	180	

ccc gat ctg atc gac acc ggc gaa gtg ctt gcg gga aca ccg cac cgc 691  
 Pro Asp Leu Ile Asp Thr Gly Glu Val Leu Ala Gly Thr Pro His Arg  
                   185                                  190                                  195

cca ccc aaa ctg ttc aga ttc caa aga taaattctga cgctcattcc agc 741  
 Pro Pro Lys Leu Phe Arg Phe Gln Arg  
                   200                                  205

<210> 68

<211> 206

<212> PRT

<213> Corynebacterium glutamicum

<400> 68

Met Ala Val Ser Thr Ile Ile Phe Ala Leu Arg Pro Gly Pro Gln Asp  
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Leu Pro Ser Leu Trp Ala Pro Phe Val Pro Arg Thr Arg Glu Pro His  
                   20                                  25                                  30

Leu Asn Lys Trp Ala Leu Pro Gly Gly Trp Leu Pro Pro His Glu Glu  
                   35                                  40                                  45

Leu Glu Asp Ala Ala Ala Arg Thr Leu Ala Glu Thr Thr Gly Leu His  
   50                                  55                                  60

Pro Ser Tyr Leu Glu Gln Leu Tyr Thr Phe Gly Lys Val Asp Arg Ser  
   65                                  70                                  75                                  80

Pro Thr Gly Arg Val Ile Ser Val Val Tyr Trp Ala Leu Val Arg Ala  
                   85                                  90                                  95

Asp Glu Ala Leu Lys Ala Ile Pro Gly Glu Asn Val Gln Trp Phe Pro  
                   100                                  105                                  110

Ala Asp His Leu Pro Glu Leu Ala Phe Asp His Asn Asn Ile Val Lys  
                   115                                  120                                  125

Tyr Ala Leu Glu Arg Leu Arg Thr Lys Val Glu Tyr Ser Glu Ile Ala  
   130                                  135                                  140

His Ser Phe Leu Gly Glu Thr Phe Thr Ile Ala Gln Leu Arg Ser Val  
   145                                  150                                  155                                  160

His Glu Ala Val Leu Gly His Lys Leu Asp Ala Ala Asn Phe Arg Arg  
                   165                                  170                                  175

Ser Val Ala Thr Ser Pro Asp Leu Ile Asp Thr Gly Glu Val Leu Ala  
                   180                                  185                                  190

Gly Thr Pro His Arg Pro Pro Lys Leu Phe Arg Phe Gln Arg  
                   195                                  200                                  205

<210> 69

<211> 522

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<400> 70
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Val Gly Val Thr Trp His Ala Val Leu Ser Lys Arg Glu Gly Phe Arg
                      20                      25                      30

Gln Ala Phe Ala Gln Phe Asp Val Ala Lys Val Ala Ala Phe Asn Glu
      35                      40                      45

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ttgggggatat cccgagaccc ggccgccccca aggagaatcc																
												atg agt tca tta atc	115			
												Met Ser Ser Leu Ile				
												1 5				
gtt ggc acg gac ggc ctc agt cgc ccg agt tgg gct gcg caa gat ccc								163								
Val Gly Thr Asp Gly Leu Ser Arg Pro Ser Trp Ala Ala Gln Asp Pro																
							10 15 20									
ctg atg cgc gat tat tac gac acc gag tgg gga atg ccg att cgc gat								211								
Leu Met Arg Asp Tyr Tyr Asp Thr Glu Trp Gly Met Pro Ile Arg Asp																
							25 30 35									
gaa cag gga tta ttc gaa aga gtt agt ctg gaa gct ttt caa tcc ggg								259								
Glu Gln Gly Leu Phe Glu Arg Val Ser Leu Glu Ala Phe Gln Ser Gly																
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ctg tcc tgg gcg acg att ttg cgc aag cgc gat agt ttc cgc gca gct								307								
Leu Ser Trp Ala Thr Ile Leu Arg Lys Arg Asp Ser Phe Arg Ala Ala																
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ttc tct cag ttt gat ccg gaa tta gtc gca aaa ttc acc gat gct gac								355								
Phe Ser Gln Phe Asp Pro Glu Leu Val Ala Lys Phe Thr Asp Ala Asp																
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atc gaa cgc ctc atg gag gac gcc gcc atc gtg cgc aac aaa cgt aaa								403								
Ile Glu Arg Leu Met Glu Asp Ala Gly Ile Val Arg Asn Lys Arg Lys																
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att ttg gcc acc att aac aac gcc aaa gcc acc ctt caa ttg cgt gag								451								

Ile Leu Ala Thr Ile Asn Asn Ala Lys Ala Thr Leu Gln Leu Arg Glu  
 105 110 115  
 aag ggt ggc ttg gtg gaa ttt gta tgg ggt ttc aaa ccg att gat acc 499  
 Lys Gly Gly Leu Val Glu Phe Val Trp Gly Phe Lys Pro Ile Asp Thr  
 120 125 130  
 cca cag ccg gag acc ctg gag gag att ccg acg cag tcg ccg gag tca 547  
 Pro Gln Pro Glu Thr Leu Glu Glu Ile Pro Thr Gln Ser Pro Glu Ser  
 135 140 145  
 gtt gca ctg tct aag gcg ctg aag aag gaa ggt ttt tcc ttc gtt ggt 595  
 Val Ala Leu Ser Lys Ala Leu Lys Lys Glu Gly Phe Ser Phe Val Gly  
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 ccc acg acg atg ttt gcc ctt atg gaa gcc ata gga atc gtc gac acc 643  
 Pro Thr Thr Met Phe Ala Leu Met Glu Ala Ile Gly Ile Val Asp Thr  
 170 175 180  
 cat ttg gtg ggc agc cat cgc cgc gga agt tct ggg gtg tgg gct 688  
 His Leu Val Gly Ser His Arg Arg Gly Ser Ser Gly Val Trp Ala  
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 <212> PRT  
 <213> Corynebacterium glutamicum  
  
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 Ala Ala Gln Asp Pro Leu Met Arg Asp Tyr Tyr Asp Thr Glu Trp Gly  
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 35 40 45  
 Ala Phe Gln Ser Gly Leu Ser Trp Ala Thr Ile Leu Arg Lys Arg Asp  
 50 55 60  
 Ser Phe Arg Ala Ala Phe Ser Gln Phe Asp Pro Glu Leu Val Ala Lys  
 65 70 75 80  
 Phe Thr Asp Ala Asp Ile Glu Arg Leu Met Glu Asp Ala Gly Ile Val  
 85 90 95  
 Arg Asn Lys Arg Lys Ile Leu Ala Thr Ile Asn Asn Ala Lys Ala Thr  
 100 105 110  
 Leu Gln Leu Arg Glu Lys Gly Gly Leu Val Glu Phe Val Trp Gly Phe  
 115 120 125  
 Lys Pro Ile Asp Thr Pro Gln Pro Glu Thr Leu Glu Glu Ile Pro Thr  
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ttcgaacagt ccagaatagc cctgacctag acttagagct atg tcc gaa caa aga 115
               Met Ser Glu Gln Arg

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Leu	Asp	Gln	Leu	Glu	Arg	Arg	Leu	Ser	Glu	Leu	Glu	Arg	Glu	Ile	Ala		
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gcg	att	cgt	cag	gag	atc	cgc	cag	gaa	cgc	cta	gtg	ctt	ccg	gaa	ccg	211	
Ala	Ile	Arg	Gln	Glu	Ile	Arg	Gln	Glu	Arg	Leu	Val	Leu	Pro	Glu	Pro		
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gaa	cct	gtg	aaa	gtt	gat	aca	gtc	atc	gcc	acc	gaa	gcg	acc	gga	gtc	259	
Glu	Pro	Val	Lys	Val	Asp	Thr	Val	Ile	Ala	Thr	Glu	Ala	Thr	Gly	Val		
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aat	gca	tcg	tcg	ggt	ccg	gag	gcg	aag	atc	gct	ttg	ttc	atg	gag	agg	307	
Asn	Ala	Ser	Ser	Gly	Pro	Glu	Ala	Lys	Ile	Ala	Leu	Phe	Met	Glu	Arg		
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ttt	agt	ggt	cgc	cac	gat	gtg	tat	gcg	cgg	cgc	tgg	acc	agc	aga	aaa	355	
Phe	Ser	Gly	Arg	His	Asp	Val	Tyr	Ala	Arg	Arg	Trp	Thr	Ser	Arg	Lys		
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acg	ggc	aaa	agt	gga	tgg	tcg	ccg	gct	act	cgc	cag	ggt	ttt	tac	tca	403	
Thr	Gly	Lys	Ser	Gly	Trp	Ser	Pro	Ala	Thr	Arg	Gln	Gly	Phe	Tyr	Ser		
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aaa	gac	acc	aca	ccg	aag	gac	tat	ctc	ccc	ttc	acc	gtt	gac	acc	gtc	451	
Lys	Asp	Thr	Thr	Pro	Lys	Asp	Tyr	Leu	Pro	Phe	Thr	Val	Asp	Thr	Val		
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aat	gcg	cat	ctg	cgc	cgg	ggc	ggc	gac	cat	atc	ggt	ctc	tat	gtg	atg	499	
Asn	Ala	His	Leu	Arg	Arg	Gly	Gly	Asp	His	Ile	Gly	Leu	Tyr	Val	Met		
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gtc	ccc	atc	gac	acg	tgc	aaa	ctt	ctc	gcc	tgc	gat	ttc	gac	gat	ggc	547	
Val	Pro	Ile	Asp	Thr	Cys	Lys	Leu	Leu	Ala	Cys	Asp	Phe	Asp	Asp	Gly		
		135					140					145					
acc	tgg	aag	caa	gat	gcg	gcc	gct	ttc	gtg	tca	gcc	tgc	acc	gac	cac	595	
Thr	Trp	Lys	Gln	Asp	Ala	Ala	Ala	Phe	Val	Ser	Ala	Cys	Thr	Asp	His		
		150					155					160					
gga	atc	gat	gcg	ttg	gct	gaa	att	tct	cga	tcc	gac	gac	ggc	gcc	ccc	643	
Gly	Ile	Asp	Ala	Leu	Ala	Glu	Ile	Ser	Arg	Ser	Asp	Asp	Gly	Ala	Pro		
				170					175					180			
gtg	tgg	ata	ttt	ttc	gat	acc	cca	atc	tcc	gcg	atg	ctg	gct	cgg	cgc	691	
Val	Trp	Ile	Phe	Phe	Asp	Thr	Pro	Ile	Ser	Ala	Met	Leu	Ala	Arg	Arg		
				185					190					195			
cta	ggt	ttt	gcc	atg	ctc	cgc	caa	gcc	atg	aac	tcc	cgc	cct	gac	atg	739	
Leu	Gly	Phe	Ala	Met	Leu	Arg	Gln	Ala	Met	Asn	Ser	Arg	Pro	Asp	Met		
				200					205					210			
gat	atg	tct	tct	tat	gat	cgc	ttc	ttc	cct	gct	caa	gac	acc	atc	gca	787	
Asp	Met	Ser	Ser	Tyr	Asp	Arg	Phe	Phe	Pro	Ala	Gln	Asp	Thr	Ile	Ala		
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acg	cgc	gca	aac	gga	agc	gca	cgg	ctg	gga	aat	ttg	atc	gcg	ctg	ccc	835	
Thr	Arg	Ala	Asn	Gly	Ser	Ala	Arg	Leu	Gly	Asn	Leu	Ile	Ala	Leu	Pro		
		230					235					240					

ctc aac ggc gac tgt cga gcc cgc aac acc gcc gtc ttc gcc gat tcg	883
Leu Asn Gly Asp Cys Arg Ala Arg Asn Thr Ala Val Phe Ala Asp Ser	
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gaa acg tgg gtt ccc ttc gaa gat cct ttc gca gcg ctc gcg gcc atc	931
Glu Thr Trp Val Pro Phe Glu Asp Pro Phe Ala Ala Leu Ala Ala Ile	
265 270 275	
acg cca cta gcc acc gaa aaa atc gag cag atc ctt gcc acc acg cag	979
Thr Pro Leu Ala Thr Glu Lys Ile Glu Gln Ile Leu Ala Thr Thr Gln	
280 285 290	
gaa aaa ttt ggc ccc gaa ccc gaa cac atc aaa cgc ccc acc cgc gcc	1027
Glu Lys Phe Gly Pro Glu Pro Glu His Ile Lys Arg Pro Thr Arg Ala	
295 300 305	
gaa ctc aaa cag gtt aaa gcc aac ggc gaa acc atc aaa ctc acc atc	1075
Glu Leu Lys Gln Val Lys Ala Asn Gly Glu Thr Ile Lys Leu Thr Ile	
310 315 320 325	
acc aac gag ctg agc gtc ccc acc gaa agg tta ccc gcg gcc gtc atc	1123
Thr Asn Glu Leu Ser Val Pro Thr Glu Arg Leu Pro Ala Ala Val Ile	
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gcg gag att aaa cac cgg gcg gta atc cca aac cct gag ttt tat cgt	1171
Ala Glu Ile Lys His Arg Ala Val Ile Pro Asn Pro Glu Phe Tyr Arg	
345 350 355	
cga caa gcg caa aga ttt tcg acc ttc ggc gtg ccg cgc atc gtc atc	1219
Arg Gln Ala Gln Arg Phe Ser Thr Phe Gly Val Pro Arg Ile Val Ile	
360 365 370	
cgc ttc gcc cag gcc gag cag cgc ttg ctg ctc cca cgc ggg ctt gtc	1267
Arg Phe Ala Gln Ala Glu Gln Arg Leu Leu Leu Pro Arg Gly Leu Val	
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gac gac acc ctc cgg atc ctc acc ctc gcc ggg tac aaa gtc agc gtc	1315
Asp Asp Thr Leu Arg Ile Leu Thr Leu Ala Gly Tyr Lys Val Ser Val	
390 395 400 405	
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Ile Trp Pro Arg Gln Thr Arg Lys Thr Ile Asp Ala Ser Phe Glu Gly	
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Glu Leu Arg Ser Met Gln Gln Glu Gly Ile Asp Ser Leu Lys Gly Gln	
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cgc acc ggc gta ttg gta gca ccg ccg ggc gct gga aaa aca gtg atg	1459
Arg Thr Gly Val Leu Val Ala Pro Pro Gly Ala Gly Lys Thr Val Met	
440 445 450	
gcc tgt gca ctc atc gcg aac aga aaa atc ccc acc gca gtg ata gtc	1507
Ala Cys Ala Leu Ile Ala Asn Arg Lys Ile Pro Thr Ala Val Ile Val	
455 460 465	
aac cgt gca gaa ttg att tcc caa tgg cgg gat cgt ctc gcg caa tac	1555
Asn Arg Ala Glu Leu Ile Ser Gln Trp Arg Asp Arg Leu Ala Gln Tyr	
470 475 480 485	

ctg agc atc gac gca gac tcc atc gga cag atc ggc gcg ggc cga cgc	1603
Leu Ser Ile Asp Ala Asp Ser Ile Gly Gln Ile Gly Ala Gly Arg Arg	
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Lys Thr Thr Gly Ile Ile Asp Leu Ile Thr Val Gln Ser Leu Ser Arg	
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aaa gat tcc gat ccg aaa att ttg gaa caa tac ggc caa atc atc gtc	1699
Lys Asp Ser Asp Pro Lys Ile Leu Glu Gln Tyr Gly Gln Ile Ile Val	
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gac gag tgc cac aac atc gca gcc cca ggc gcc gaa gcc gca ttg aac	1747
Asp Glu Cys His Asn Ile Ala Ala Pro Gly Ala Glu Ala Ala Leu Asn	
535 540 545	
cag gtc aag gcc ccc tac tgg ctg ggt cta acc gcc acg ccg ttt cgt	1795
Gln Val Lys Ala Pro Tyr Trp Leu Gly Leu Thr Ala Thr Pro Phe Arg	
550 555 560 565	
tca gac cac atg gat gaa atc atc acc atg cag tgc ggt cct gtg cgc	1843
Ser Asp His Met Asp Glu Ile Ile Thr Met Gln Cys Gly Pro Val Arg	
570 575 580	
cac cgc atg gaa gtg gca aca gac aat gaa cag cgc ttg att cac atc	1891
His Arg Met Glu Val Ala Thr Asp Asn Glu Gln Arg Leu Ile His Ile	
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cac gaa acc tct ttc gac tct gag gaa acc acc gaa atc cag gat ctc	1939
His Glu Thr Ser Phe Asp Ser Glu Glu Thr Thr Glu Ile Gln Asp Leu	
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tac aat gag ctc gcg gtc gat tct gcc cga aat gcg caa atc act gcc	1987
Tyr Asn Glu Leu Ala Val Asp Ser Ala Arg Asn Ala Gln Ile Thr Ala	
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gaa gtg cac aaa gcg ctt gaa gct ggc gac cga tgt cta gtt ttg gtc	2035
Glu Val His Lys Ala Leu Glu Ala Gly Asp Arg Cys Leu Val Leu Val	
630 635 640 645	
aac cga att gca gcc ctt gaa gca ctg acc agc agt att acc gaa tct	2083
Asn Arg Ile Ala Ala Leu Glu Ala Leu Thr Ser Ser Ile Thr Glu Ser	
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ggc gat cac act gtc tta gtg atg cat ggc cgc caa acc caa gag gag	2131
Gly Asp His Thr Val Leu Val Met His Gly Arg Gln Thr Gln Glu Glu	
665 670 675	
cga gtt cac ctt cgt gcg caa ctt gcc tca ttg agt gaa aag cag gat	2179
Arg Val His Leu Arg Ala Gln Leu Ala Ser Leu Ser Glu Lys Gln Asp	
680 685 690	
ccg ttt gta ctg gtc gcg atg aat aaa gtc gcc ggc gaa ggc ctt gac	2227
Pro Phe Val Leu Val Ala Met Asn Lys Val Ala Gly Glu Gly Leu Asp	
695 700 705	
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Ile Pro Ser Leu Asn Thr Leu Phe Leu Ala Ala Pro Val Ser Phe Lys	
710 715 720 725	
ggg ctg gtg att cag caa atc ggc cga gtt act cgc gca acc ggt gat	2323

Gly Leu Val Ile Gln Gln Ile Gly Arg Val Thr Arg Ala Thr Gly Asp  
730 735 740

caa aac gct cct ccg gtg act gcc acg gtc cat gat ttt gtt gat tcc 2371  
Gln Asn Ala Pro Pro Val Thr Ala Thr Val His Asp Phe Val Asp Ser  
745 750 755

aag att ccg aca ctc aaa cgc atg cac ggt cgc cga ttg cgg gct atg 2419  
Lys Ile Pro Thr Leu Lys Arg Met His Gly Arg Arg Leu Arg Ala Met  
760 765 770

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&lt;210&gt; 76

&lt;211&gt; 783

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 76

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Val Leu Pro Glu Pro Glu Pro Val Lys Val Asp Thr Val Ile Ala Thr  
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Glu Ala Thr Gly Val Asn Ala Ser Ser Gly Pro Glu Ala Lys Ile Ala  
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Leu Phe Met Glu Arg Phe Ser Gly Arg His Asp Val Tyr Ala Arg Arg  
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Trp Thr Ser Arg Lys Thr Gly Lys Ser Gly Trp Ser Pro Ala Thr Arg  
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Gln Gly Phe Tyr Ser Lys Asp Thr Thr Pro Lys Asp Tyr Leu Pro Phe  
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Thr Val Asp Thr Val Asn Ala His Leu Arg Arg Gly Gly Asp His Ile  
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Gly Leu Tyr Val Met Val Pro Ile Asp Thr Cys Lys Leu Leu Ala Cys  
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Ala Cys Thr Asp His Gly Ile Asp Ala Leu Ala Glu Ile Ser Arg Ser  
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Ser Arg Pro Asp Met Asp Met Ser Ser Tyr Asp Arg Phe Phe Pro Ala  
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 Gln Asp Thr Ile Ala Thr Arg Ala Asn Gly Ser Ala Arg Leu Gly Asn  
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 Leu Ile Ala Leu Pro Leu Asn Gly Asp Cys Arg Ala Arg Asn Thr Ala  
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 Val Phe Ala Asp Ser Glu Thr Trp Val Pro Phe Glu Asp Pro Phe Ala  
 260 265 270  
 Ala Leu Ala Ala Ile Thr Pro Leu Ala Thr Glu Lys Ile Glu Gln Ile  
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 Leu Ala Thr Thr Gln Glu Lys Phe Gly Pro Glu Pro Glu His Ile Lys  
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 Arg Pro Thr Arg Ala Glu Leu Lys Gln Val Lys Ala Asn Gly Glu Thr  
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 Ile Lys Leu Thr Ile Thr Asn Glu Leu Ser Val Pro Thr Glu Arg Leu  
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 Pro Ala Ala Val Ile Ala Glu Ile Lys His Arg Ala Val Ile Pro Asn  
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 Pro Glu Phe Tyr Arg Arg Gln Ala Gln Arg Phe Ser Thr Phe Gly Val  
 355 360 365  
 Pro Arg Ile Val Ile Arg Phe Ala Gln Ala Glu Gln Arg Leu Leu Leu  
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 Tyr Lys Val Ser Val Ile Trp Pro Arg Gln Thr Arg Lys Thr Ile Asp  
 405 410 415  
 Ala Ser Phe Glu Gly Glu Leu Arg Ser Met Gln Gln Glu Gly Ile Asp  
 420 425 430  
 Ser Leu Lys Gly Gln Arg Thr Gly Val Leu Val Ala Pro Pro Gly Ala  
 435 440 445  
 Gly Lys Thr Val Met Ala Cys Ala Leu Ile Ala Asn Arg Lys Ile Pro  
 450 455 460  
 Thr Ala Val Ile Val Asn Arg Ala Glu Leu Ile Ser Gln Trp Arg Asp  
 465 470 475 480  
 Arg Leu Ala Gln Tyr Leu Ser Ile Asp Ala Asp Ser Ile Gly Gln Ile  
 485 490 495  
 Gly Ala Gly Arg Arg Lys Thr Thr Gly Ile Ile Asp Leu Ile Thr Val  
 500 505 510  
 Gln Ser Leu Ser Arg Lys Asp Ser Asp Pro Lys Ile Leu Glu Gln Tyr  
 515 520 525  
 Gly Gln Ile Ile Val Asp Glu Cys His Asn Ile Ala Ala Pro Gly Ala

530	535	540
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Ala Thr Pro Phe Arg Ser Asp His Met Asp Glu Ile Ile Thr Met Gln 565 570 575		
Cys Gly Pro Val Arg His Arg Met Glu Val Ala Thr Asp Asn Glu Gln 580 585 590		
Arg Leu Ile His Ile His Glu Thr Ser Phe Asp Ser Glu Glu Thr Thr 595 600 605		
Glu Ile Gln Asp Leu Tyr Asn Glu Leu Ala Val Asp Ser Ala Arg Asn 610 615 620		
Ala Gln Ile Thr Ala Glu Val His Lys Ala Leu Glu Ala Gly Asp Arg 625 630 635 640		
Cys Leu Val Leu Val Asn Arg Ile Ala Ala Leu Glu Ala Leu Thr Ser 645 650 655		
Ser Ile Thr Glu Ser Gly Asp His Thr Val Leu Val Met His Gly Arg 660 665 670		
Gln Thr Gln Glu Glu Arg Val His Leu Arg Ala Gln Leu Ala Ser Leu 675 680 685		
Ser Glu Lys Gln Asp Pro Phe Val Leu Val Ala Met Asn Lys Val Ala 690 695 700		
Gly Glu Gly Leu Asp Ile Pro Ser Leu Asn Thr Leu Phe Leu Ala Ala 705 710 715 720		
Pro Val Ser Phe Lys Gly Leu Val Ile Gln Gln Ile Gly Arg Val Thr 725 730 735		
Arg Ala Thr Gly Asp Gln Asn Ala Pro Pro Val Thr Ala Thr Val His 740 745 750		
Asp Phe Val Asp Ser Lys Ile Pro Thr Leu Lys Arg Met His Gly Arg 755 760 765		
Arg Leu Arg Ala Met Gln Lys Glu Gly Phe Ala Val Ser Glu Pro 770 775 780		

&lt;210&gt; 77

&lt;211&gt; 1812

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1789)

&lt;223&gt; RXA02445

&lt;400&gt; 77

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Leu	Glu	Lys	Asp	Leu	Glu	Arg	Leu	Arg	Lys	Asn	Gly	Lys	Asp	Asp	Glu	
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Thr	Val	Glu	Val	Lys	Ser	Trp	Gly	Arg	Leu	Pro	Leu	Ser	Lys	Gly	Ser	
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Lys	Ser	Phe	Trp	Glu	Ser	Leu	Ser	Ala	Phe	Ala	Asn	Thr	Asn	Gly	Gly	
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Tyr	Ile	Leu	Leu	Gly	Leu	Ser	Glu	Pro	Asp	Phe	Thr	Pro	Val	Glu	Gly	
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Phe	Asp	Ser	Gln	Ala	Ser	Ile	Gln	Phe	Ile	Arg	Ala	Gly	Leu	Asn	Pro	
	70				75					80					85	
caa	gat	cg	gac	gcc	caa	aaa	gtg	gaa	cca	gtg	ccc	cat	cat	gaa	att	403
Gln	Asp	Arg	Asp	Ala	Gln	Lys	Val	Glu	Pro	Val	Pro	His	His	Glu	Ile	
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cat	gaa	atg	act	gtt	gat	ggt	gct	gaa	gtt	gtt	tta	gtt	tca	gtc	tca	451
His	Glu	Met	Thr	Val	Asp	Gly	Ala	Glu	Val	Val	Leu	Val	Ser	Val	Ser	
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Pro	Leu	Ser	Val	Asn	Gly	Pro	Cys	Tyr	Tyr	Leu	Pro	Val	Gly	Ile	Thr	
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Asn	Gly	Ser	Phe	Lys	Arg	Val	Gly	Asp	Glu	Asp	Arg	Lys	Leu	Ser	His	
	135					140					145					
ctt	gaa	att	tac	gag	ctc	caa	aat	agg	ttt	gtt	caa	acc	aaa	aca	gat	595
Leu	Glu	Ile	Tyr	Glu	Leu	Gln	Asn	Arg	Phe	Val	Gln	Thr	Lys	Thr	Asp	
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Arg	Asn	Pro	Val	Pro	Asp	Ser	Ser	Ile	Asp	Asp	Leu	Asn	Asn	Gln	Leu	
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Ala	Ala	Ser	Phe	Lys	Gln	Arg	Leu	Ile	Glu	Ser	Asn	Ser	Arg	Ser	Leu	
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gga	aca	gac	gat	aac	tgg	tta	ctg	cgc	aaa	aat	atc	act	aca	tca	aag	739
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gga	gaa	ctg	acg	att	gct	ggc	tta	ctg	gct	ctc	gga	agc	tat	cct	caa	787
Gly	Glu	Leu	Thr	Ile	Ala	Gly	Leu	Leu	Ala	Leu	Gly	Ser	Tyr	Pro	Gln	
	215					220					225					
cag	ttt	ttc	ccc	cga	gtg	atc	att	gat	gtt	gcc	gta	cat	cca	ggt	ctg	835

Gln	Phe	Phe	Pro	Arg	Val	Ile	Ile	Asp	Val	Ala	Val	His	Pro	Gly	Leu	
230					235					240					245	
cat	aag	tca	cca	atc	ggc	acc	tca	att	cgt	ttt	gaa	gac	cga	aaa	atc	883
His	Lys	Ser	Pro	Ile	Gly	Thr	Ser	Ile	Arg	Phe	Glu	Asp	Arg	Lys	Ile	
				250					255					260		
tgc	gag	gga	aat	ctt	ctc	gag	atg	gtt	caa	gag	gct	atg	tct	gcc	atc	931
Cys	Glu	Gly	Asn	Leu	Leu	Glu	Met	Val	Gln	Glu	Ala	Met	Ser	Ala	Ile	
			265					270					275			
aaa	cga	aac	cta	cgt	gta	cgc	cgc	gtc	gtt	gaa	gga	ctc	tca	ggc	aaa	979
Lys	Arg	Asn	Leu	Arg	Val	Arg	Arg	Val	Val	Glu	Gly	Leu	Ser	Gly	Lys	
		280					285					290				
gat	gtt	cta	gaa	atc	cca	gaa	gaa	gtt	ttg	aga	gag	gct	cta	gca	aac	1027
Asp	Val	Leu	Glu	Ile	Pro	Glu	Glu	Val	Leu	Arg	Glu	Ala	Leu	Ala	Asn	
	295					300					305					
gcc	gta	ctt	cac	cgt	gat	tat	tct	gag	cta	gct	caa	aat	gaa	gca	att	1075
Ala	Val	Leu	His	Arg	Asp	Tyr	Ser	Glu	Leu	Ala	Gln	Asn	Glu	Ala	Ile	
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cat	gta	gac	atc	tat	aag	gat	cga	gtt	gag	atc	acg	agt	cca	ggc	gga	1123
His	Val	Asp	Ile	Tyr	Lys	Asp	Arg	Val	Glu	Ile	Thr	Ser	Pro	Gly	Gly	
				330					335					340		
tta	ccc	aat	ggc	aaa	cgc	cca	gag	tca	ata	ctg	gac	gga	tac	tct	gaa	1171
Leu	Pro	Asn	Gly	Lys	Arg	Pro	Glu	Ser	Ile	Leu	Asp	Gly	Tyr	Ser	Glu	
			345					350					355			
cca	aga	aat	cgt	gtg	ctt	tca	aga	atc	cta	atg	gat	att	cca	tgg	aca	1219
Pro	Arg	Asn	Arg	Val	Leu	Ser	Arg	Ile	Leu	Met	Asp	Ile	Pro	Trp	Thr	
		360					365					370				
cat	gaa	gta	caa	gga	gta	ctt	gct	gaa	agc	aac	ggc	act	ggc	gtt	ccc	1267
His	Glu	Val	Gln	Gly	Val	Leu	Ala	Glu	Ser	Asn	Gly	Thr	Gly	Val	Pro	
	375					380				385						
cga	atg	ttc	aat	ttg	atg	cgt	gaa	gcg	gga	ctt	ccg	gta	ccg	aat	ttt	1315
Arg	Met	Phe	Asn	Leu	Met	Arg	Glu	Ala	Gly	Leu	Pro	Val	Pro	Asn	Phe	
390				395					400						405	
aag	att	gat	att	tct	agc	gtc	act	gtc	gaa	ctc	agc	cgt	cac	ggc	ctt	1363
Lys	Ile	Asp	Ile	Ser	Ser	Val	Thr	Val	Glu	Leu	Ser	Arg	His	Gly	Leu	
				410					415					420		
cta	gat	gcc	caa	aca	agt	gaa	tgg	ctt	gta	gaa	aaa	ctc	gga	tca	gat	1411
Leu	Asp	Ala	Gln	Thr	Ser	Glu	Trp	Leu	Val	Glu	Lys	Leu	Gly	Ser	Asp	
			425					430					435			
ttt	tct	aac	aca	caa	ggc	att	gct	ctt	gtt	ctc	gca	aaa	gaa	ctt	gga	1459
Phe	Ser	Asn	Thr	Gln	Gly	Ile	Ala	Leu	Val	Leu	Ala	Lys	Glu	Leu	Gly	
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gcg	gta	acg	tct	cga	gat	ctc	cgc	aat	caa	act	ggc	cat	gat	tca	gaa	1507
Ala	Val	Thr	Ser	Arg	Asp	Leu	Arg	Asn	Gln	Thr	Gly	His	Asp	Ser	Glu	
	455					460					465					
gac	atg	cgc	agc	tta	ctt	gac	gct	ttg	gtt	gat	cgg	ggc	gtt	cta	aac	1555
Asp	Met	Arg	Ser	Leu	Leu	Asp	Ala	Leu	Val	Asp	Arg	Gly	Val	Leu	Asn	

470	475	480	485	
caa aac tta cag aac caa tat cag ctt gcg aca tcg tct gtg aat gta				1603
Gln Asn Leu Gln Asn Gln Tyr Gln Leu Ala Thr Ser Ser Val Asn Val				
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act caa agc gaa caa gaa gtc tta gat gca atc aat aaa aca act cct				1651
Thr Gln Ser Glu Gln Glu Val Leu Asp Ala Ile Asn Lys Thr Thr Pro				
	505	510	515	
gtc aca att cga gaa att gcc aca aaa aca ggg aaa act gca tcg tct				1699
Val Thr Ile Arg Glu Ile Ala Thr Lys Thr Gly Lys Thr Ala Ser Ser				
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ctt cgg ccg ctg ctt cgt ggc ctt gtt gaa gca ggt ctt gtg gtt gca				1747
Leu Arg Pro Leu Leu Arg Gly Leu Val Glu Ala Gly Leu Val Val Ala				
	535	540	545	
act gct cca cca tca agc cgc aac cga gcg tac ttg aag gct				1789
Thr Ala Pro Pro Ser Ser Arg Asn Arg Ala Tyr Leu Lys Ala				
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Leu Ser Lys Gly Ser Lys Ser Phe Trp Glu Ser Leu Ser Ala Phe Ala				
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Asn Thr Asn Gly Gly Tyr Ile Leu Leu Gly Leu Ser Glu Pro Asp Phe				
	50	55	60	
Thr Pro Val Glu Gly Phe Asp Ser Gln Ala Ser Ile Gln Phe Ile Arg				
	65	70	75	80
Ala Gly Leu Asn Pro Gln Asp Arg Asp Ala Gln Lys Val Glu Pro Val				
	85	90	95	
Pro His His Glu Ile His Glu Met Thr Val Asp Gly Ala Glu Val Val				
	100	105	110	
Leu Val Ser Val Ser Pro Leu Ser Val Asn Gly Pro Cys Tyr Tyr Leu				
	115	120	125	
Pro Val Gly Ile Thr Asn Gly Ser Phe Lys Arg Val Gly Asp Glu Asp				
	130	135	140	
Arg Lys Leu Ser His Leu Glu Ile Tyr Glu Leu Gln Asn Arg Phe Val				
	145	150	155	160

Gln Thr Lys Thr Asp Arg Asn Pro Val Pro Asp Ser Ser Ile Asp Asp  
 165 170 175  
 Leu Asn Asn Gln Leu Ala Ala Ser Phe Lys Gln Arg Leu Ile Glu Ser  
 180 185 190  
 Asn Ser Arg Ser Leu Gly Thr Asp Asp Asn Trp Leu Leu Arg Lys Asn  
 195 200 205  
 Ile Thr Thr Ser Lys Gly Glu Leu Thr Ile Ala Gly Leu Leu Ala Leu  
 210 215 220  
 Gly Ser Tyr Pro Gln Gln Phe Phe Pro Arg Val Ile Ile Asp Val Ala  
 225 230 235 240  
 Val His Pro Gly Leu His Lys Ser Pro Ile Gly Thr Ser Ile Arg Phe  
 245 250 255  
 Glu Asp Arg Lys Ile Cys Glu Gly Asn Leu Leu Glu Met Val Gln Glu  
 260 265 270  
 Ala Met Ser Ala Ile Lys Arg Asn Leu Arg Val Arg Arg Val Val Glu  
 275 280 285  
 Gly Leu Ser Gly Lys Asp Val Leu Glu Ile Pro Glu Glu Val Leu Arg  
 290 295 300  
 Glu Ala Leu Ala Asn Ala Val Leu His Arg Asp Tyr Ser Glu Leu Ala  
 305 310 315 320  
 Gln Asn Glu Ala Ile His Val Asp Ile Tyr Lys Asp Arg Val Glu Ile  
 325 330 335  
 Thr Ser Pro Gly Gly Leu Pro Asn Gly Lys Arg Pro Glu Ser Ile Leu  
 340 345 350  
 Asp Gly Tyr Ser Glu Pro Arg Asn Arg Val Leu Ser Arg Ile Leu Met  
 355 360 365  
 Asp Ile Pro Trp Thr His Glu Val Gln Gly Val Leu Ala Glu Ser Asn  
 370 375 380  
 Gly Thr Gly Val Pro Arg Met Phe Asn Leu Met Arg Glu Ala Gly Leu  
 385 390 395 400  
 Pro Val Pro Asn Phe Lys Ile Asp Ile Ser Ser Val Thr Val Glu Leu  
 405 410 415  
 Ser Arg His Gly Leu Leu Asp Ala Gln Thr Ser Glu Trp Leu Val Glu  
 420 425 430  
 Lys Leu Gly Ser Asp Phe Ser Asn Thr Gln Gly Ile Ala Leu Val Leu  
 435 440 445  
 Ala Lys Glu Leu Gly Ala Val Thr Ser Arg Asp Leu Arg Asn Gln Thr  
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															Met Ser Asp Val Glu	5		
															1			
aga aca gag ttt gaa att ccg gga gga att cca cct cgt cga aac ggt	163																	
Arg Thr Glu Phe Glu Ile Pro Gly Gly Ile Pro Pro Arg Arg Asn Gly																		
															10	15	20	
ggt caa ggc cgt gca gct gat acc aac gta gat gcg aac ctg aag cct	211																	
Gly Gln Gly Arg Ala Ala Asp Thr Asn Val Asp Ala Asn Leu Lys Pro																		
															25	30	35	
gat gaa tac gat gcg gaa gta aca ctt cgt ccg aag tct ttg act gag	259																	
Asp Glu Tyr Asp Ala Glu Val Thr Leu Arg Pro Lys Ser Leu Thr Glu																		
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ttt atc ggc cag ccg aag gtg cgc gat cag ctt agt ttg gtg ctt acc	307																	
Phe Ile Gly Gln Pro Lys Val Arg Asp Gln Leu Ser Leu Val Leu Thr																		
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ggt gcg aaa aac cgt ggt gtg gtt ccc gat cac gtg ttg ttg tct ggc	355																	
Gly Ala Lys Asn Arg Gly Val Val Pro Asp His Val Leu Leu Ser Gly																		
															70	75	80	85
cct cct ggc ctg ggt aag acc acc atg gcg atg att atc gcc cag gag	403																	
Pro Pro Gly Leu Gly Lys Thr Thr Met Ala Met Ile Ile Ala Gln Glu																		
															90	95	100	
ttg ggc acc agt ttg cgt atg acc tca ggc cca gcc ttg gaa cgc gca	451																	
Leu Gly Thr Ser Leu Arg Met Thr Ser Gly Pro Ala Leu Glu Arg Ala																		

105						110						115						
ggc	gat	ctg	gct	gcc	atg	ctg	tcc	aac	ctc	atg	gaa	ggg	gac	gtg	ctg	499		
Gly	Asp	Leu	Ala	Ala	Met	Leu	Ser	Asn	Leu	Met	Glu	Gly	Asp	Val	Leu			
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ttt	att	gat	gag	att	cac	cgc	atc	gca	cgt	cct	gcc	gag	gaa	atg	ctg	547		
Phe	Ile	Asp	Glu	Ile	His	Arg	Ile	Ala	Arg	Pro	Ala	Glu	Glu	Met	Leu			
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tac	atg	gcg	atg	gaa	gat	ttc	cgg	atc	gat	gtc	atc	gtc	ggg	aag	ggg	595		
Tyr	Met	Ala	Met	Glu	Asp	Phe	Arg	Ile	Asp	Val	Ile	Val	Gly	Lys	Gly			
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cct	ggc	gct	acc	tca	atc	ccg	ctg	gag	atc	cca	ccc	ttt	acc	ctc	gtt	643		
Pro	Gly	Ala	Thr	Ser	Ile	Pro	Leu	Glu	Ile	Pro	Pro	Phe	Thr	Leu	Val			
				170					175					180				
ggg	gca	acc	acc	agg	tgc	ggc	atg	ctc	acc	ggc	cca	ctg	cgt	gac	cgt	691		
Gly	Ala	Thr	Thr	Arg	Ser	Gly	Met	Leu	Thr	Gly	Pro	Leu	Arg	Asp	Arg			
			185					190					195					
ttc	ggg	ttt	acc	gcg	cag	atg	gaa	ttc	tac	gat	gtg	cct	gat	ctg	acc	739		
Phe	Gly	Phe	Thr	Ala	Gln	Met	Glu	Phe	Tyr	Asp	Val	Pro	Asp	Leu	Thr			
		200					205					210						
aaa	gtg	gtg	aaa	cga	aca	gct	aag	atc	ctc	gat	gtc	gga	atc	gac	aac	787		
Lys	Val	Val	Lys	Arg	Thr	Ala	Lys	Ile	Leu	Asp	Val	Gly	Ile	Asp	Asn			
	215					220					225							
gat	gcc	gcc	gtg	gaa	att	gcc	tgc	cgg	tct	cgt	ggg	act	cct	cgt	att	835		
Asp	Ala	Ala	Val	Glu	Ile	Ala	Ser	Arg	Ser	Arg	Gly	Thr	Pro	Arg	Ile			
230					235					240					245			
gct	aac	cga	ctg	ctt	cgt	cga	gtc	cgt	gac	ttc	gct	gaa	gtt	cat	gcg	883		
Ala	Asn	Arg	Leu	Leu	Arg	Arg	Val	Arg	Asp	Phe	Ala	Glu	Val	His	Ala			
				250					255					260				
gat	ggg	cac	atc	acg	atg	ggg	gct	gcc	aat	gct	gcg	ctg	att	gta	ttc	931		
Asp	Gly	His	Ile	Thr	Met	Gly	Ala	Ala	Asn	Ala	Ala	Leu	Ile	Val	Phe			
			265					270					275					
gat	gtc	gat	gaa	gtc	gga	ctc	gat	cgc	ctg	gat	agg	gca	gtg	ctt	gat	979		
Asp	Val	Asp	Glu	Val	Gly	Leu	Asp	Arg	Leu	Asp	Arg	Ala	Val	Leu	Asp			
		280					285					290						
gcc	ttg	atc	cgc	gga	cat	ggc	gga	ggc	cct	gtt	ggc	gtg	aac	aca	ctc	1027		
Ala	Leu	Ile	Arg	Gly	His	Gly	Gly	Gly	Pro	Val	Gly	Val	Asn	Thr	Leu			
	295					300					305							
gcg	gtt	gca	gtt	ggg	gaa	gaa	ccc	ggc	act	gtg	gaa	gaa	gta	tgc	gag	1075		
Ala	Val	Ala	Val	Gly	Glu	Glu	Pro	Gly	Thr	Val	Glu	Glu	Val	Cys	Glu			
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ccc	tat	ttg	gtg	cgt	gcc	ggc	atg	att	gca	cga	acc	gga	cgg	gga	cgc	1123		
Pro	Tyr	Leu	Val	Arg	Ala	Gly	Met	Ile	Ala	Arg	Thr	Gly	Arg	Gly	Arg			
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gtg	gca	acc	gca	gct	gca	tgg	aga	cac	ctg	ggg	ctg	gaa	cca	cca	gaa	1171		
Val	Ala	Thr	Ala	Ala	Ala	Trp	Arg	His	Leu	Gly	Leu	Glu	Pro	Pro	Glu			
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 Gly Thr Ile Gly Asp Tyr  
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1212

&lt;210&gt; 80

&lt;211&gt; 363

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 80

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Pro Arg Arg Asn Gly Gly Gln Gly Arg Ala Ala Asp Thr Asn Val Asp  
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Ala Asn Leu Lys Pro Asp Glu Tyr Asp Ala Glu Val Thr Leu Arg Pro  
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Lys Ser Leu Thr Glu Phe Ile Gly Gln Pro Lys Val Arg Asp Gln Leu  
 50 55 60

Ser Leu Val Leu Thr Gly Ala Lys Asn Arg Gly Val Val Pro Asp His  
 65 70 75 80

Val Leu Leu Ser Gly Pro Pro Gly Leu Gly Lys Thr Thr Met Ala Met  
 85 90 95

Ile Ile Ala Gln Glu Leu Gly Thr Ser Leu Arg Met Thr Ser Gly Pro  
 100 105 110

Ala Leu Glu Arg Ala Gly Asp Leu Ala Ala Met Leu Ser Asn Leu Met  
 115 120 125

Glu Gly Asp Val Leu Phe Ile Asp Glu Ile His Arg Ile Ala Arg Pro  
 130 135 140

Ala Glu Glu Met Leu Tyr Met Ala Met Glu Asp Phe Arg Ile Asp Val  
 145 150 155 160

Ile Val Gly Lys Gly Pro Gly Ala Thr Ser Ile Pro Leu Glu Ile Pro  
 165 170 175

Pro Phe Thr Leu Val Gly Ala Thr Thr Arg Ser Gly Met Leu Thr Gly  
 180 185 190

Pro Leu Arg Asp Arg Phe Gly Phe Thr Ala Gln Met Glu Phe Tyr Asp  
 195 200 205

Val Pro Asp Leu Thr Lys Val Val Lys Arg Thr Ala Lys Ile Leu Asp  
 210 215 220

Val Gly Ile Asp Asn Asp Ala Ala Val Glu Ile Ala Ser Arg Ser Arg  
 225 230 235 240

Gly Thr Pro Arg Ile Ala Asn Arg Leu Leu Arg Arg Val Arg Asp Phe  
 245 250 255

Ala Glu Val His Ala Asp Gly His Ile Thr Met Gly Ala Ala Asn Ala

260	265	270
Ala Leu Ile Val Phe Asp Val Asp Glu Val Gly Leu Asp Arg Leu Asp		
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Arg Ala Val Leu Asp Ala Leu Ile Arg Gly His Gly Gly Gly Pro Val		
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Gly Val Asn Thr Leu Ala Val Ala Val Gly Glu Glu Pro Gly Thr Val		
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Glu Glu Val Cys Glu Pro Tyr Leu Val Arg Ala Gly Met Ile Ala Arg		
325	330	335
Thr Gly Arg Gly Arg Val Ala Thr Ala Ala Ala Trp Arg His Leu Gly		
340	345	350
Leu Glu Pro Pro Glu Gly Thr Ile Gly Asp Tyr		
355	360	

&lt;210&gt; 81

&lt;211&gt; 741

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(718)

&lt;223&gt; RXA00928

&lt;400&gt; 81

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	Met Ile Ala Ser Leu	
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cgt ggc act gtt atc aac att ggt ctg agc tct gct gtc att gaa tgc	163
Arg Gly Thr Val Ile Asn Ile Gly Leu Ser Ser Ala Val Ile Glu Cys	
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aat ggc gtg ggc tat gag gtt gtc acc aca ccg aac acc ttg tca cag	211
Asn Gly Val Gly Tyr Glu Val Val Thr Thr Pro Asn Thr Leu Ser Gln	
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Leu Val Arg Gly Glu Glu Ala Leu Val Leu Thr Thr Met Val Val Arg	
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Glu Asp Ala Met Lys Leu Tyr Gly Phe Ile Asp Asn Glu Ser Arg Glu	
55	60
65	

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Met Phe Ser Val Leu Gln Thr Val Ser Gly Leu Gly Pro Arg Leu Ala	
70	75
80	85

ttg gca tgt gaa tcg gtg ttg agc cca ctg gag att tct cag gcg atc	403
Leu Ala Cys Glu Ser Val Leu Ser Pro Leu Glu Ile Ser Gln Ala Ile	
90	95
100	

acc aat gcc gat gcc aaa act ttg cag cgg gtt ccg ggt gtg gga aag 451  
 Thr Asn Ala Asp Ala Lys Thr Leu Gln Arg Val Pro Gly Val Gly Lys  
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cgc atg gca gat cgt ctc atc gtg gag ctt aaa ggc aag gtc gca gct 499  
 Arg Met Ala Asp Arg Leu Ile Val Glu Leu Lys Gly Lys Val Ala Ala  
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ttt gct gcc ggt gtc gtg gat gag gga ggg gag caa att tcc ttg cct 547  
 Phe Ala Ala Gly Val Val Asp Glu Gly Gly Glu Gln Ile Ser Leu Pro  
 135 140 145

aac gcg aac att gct tct gag gtg gtt gtg gag cag gtt tct caa gcg 595  
 Asn Ala Asn Ile Ala Ser Glu Val Val Val Glu Gln Val Ser Gln Ala  
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ctg gtg ggg ttg ggc ttt agc gag aag caa tca gat gat gca gtg agc 643  
 Leu Val Gly Leu Gly Phe Ser Glu Lys Gln Ser Asp Asp Ala Val Ser  
 170 175 180

ttt gtg ctg gcg gcg gat cca tcc ttg gac acc agt ggc gcg ctt cgt 691  
 Phe Val Leu Ala Ala Asp Pro Ser Leu Asp Thr Ser Gly Ala Leu Arg  
 185 190 195

gcc gca ttg gca aaa ctc agc gga aag tagaccctca tgtccgatgt gga 741  
 Ala Ala Leu Ala Lys Leu Ser Gly Lys  
 200 205

&lt;210&gt; 82

&lt;211&gt; 206

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 82

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Ala Val Ile Glu Cys Asn Gly Val Gly Tyr Glu Val Val Thr Thr Pro  
 20 25 30

Asn Thr Leu Ser Gln Leu Val Arg Gly Glu Glu Ala Leu Val Leu Thr  
 35 40 45

Thr Met Val Val Arg Glu Asp Ala Met Lys Leu Tyr Gly Phe Ile Asp  
 50 55 60

Asn Glu Ser Arg Glu Met Phe Ser Val Leu Gln Thr Val Ser Gly Leu  
 65 70 75 80

Gly Pro Arg Leu Ala Leu Ala Cys Glu Ser Val Leu Ser Pro Leu Glu  
 85 90 95

Ile Ser Gln Ala Ile Thr Asn Ala Asp Ala Lys Thr Leu Gln Arg Val  
 100 105 110

Pro Gly Val Gly Lys Arg Met Ala Asp Arg Leu Ile Val Glu Leu Lys  
 115 120 125

Gly Lys Val Ala Ala Phe Ala Ala Gly Val Val Asp Glu Gly Gly Glu

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130              135              140
Gln Ile Ser Leu Pro Asn Ala Asn Ile Ala Ser Glu Val Val Val Glu
145              150              155              160

Gln Val Ser Gln Ala Leu Val Gly Leu Gly Phe Ser Glu Lys Gln Ser
165              170              175

Asp Asp Ala Val Ser Phe Val Leu Ala Ala Asp Pro Ser Leu Asp Thr
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Ser Gly Ala Leu Arg Ala Ala Leu Ala Lys Leu Ser Gly Lys
195              200              205

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<211> 735
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(712)
<223> RXN00172

<400> 83
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Met Phe Gly Ser Ser
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Phe Lys Glu Gln Thr Thr Asn Pro Arg Ser Gln Arg Val Ser Tyr Leu
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Arg Val Ser Ser Thr Asp Gln Asn Leu Ala Arg Gln Arg Glu Ala Val
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Asn His Ser Gly His Ile Asp Arg Glu Phe Thr Asp Glu Leu Ser Gly
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Gly Ala Lys Ser His Arg Pro Gly Leu Glu Asp Cys Ile Asn Tyr Leu
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cgc gag gat gat gtt ctt gtc gtc gca tcc att gac cga ctt gca cgc 355
Arg Glu Asp Asp Val Leu Val Val Ala Ser Ile Asp Arg Leu Ala Arg
70 75 80 85

tcg ctg gtt gat tta cgc gtc atc att gac cgc atc aca gac aaa ggc 403
Ser Leu Val Asp Leu Arg Val Ile Ile Asp Arg Ile Thr Asp Lys Gly
90 95 100

gca tcg gtc att ttt ctc aaa gag aat ttg act ttc gct gca ggc cgc 451
Ala Ser Val Ile Phe Leu Lys Glu Asn Leu Thr Phe Ala Ala Gly Arg
105 110 115

gat gat cct cga gca aac ctc atg ctc ggt att ttg ggc agt ttc gca 499

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 Glu Phe Glu Arg Ser Ile Ile Arg Glu Arg Gln Ala Glu Gly Ile Ala  
 135 140 145  
 ctg gca aaa aag gcc ggc aag tat gca ggt cgc cca aaa gcc ctc gac 595  
 Leu Ala Lys Lys Ala Gly Lys Tyr Ala Gly Arg Pro Lys Ala Leu Asp  
 150 155 160 165  
 aag gaa caa ata caa gaa gca aaa gat atg atc gct caa ggt gaa aca 643  
 Lys Glu Gln Ile Gln Glu Ala Lys Asp Met Ile Ala Gln Gly Glu Thr  
 170 175 180  
 aaa tct gct gtc gcc aag cat ttt ggt att aat cgc tcg acc ttg tac 691  
 Lys Ser Ala Val Ala Lys His Phe Gly Ile Asn Arg Ser Thr Leu Tyr  
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 gaa tat ctc aaa aat cct gac tagattgaga atcaactatg cga 735  
 Glu Tyr Leu Lys Asn Pro Asp  
 200

<210> 84  
 <211> 204  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 84

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 Asp Glu Leu Ser Gly Gly Ala Lys Ser His Arg Pro Gly Leu Glu Asp  
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 Cys Ile Asn Tyr Leu Arg Glu Asp Asp Val Leu Val Val Ala Ser Ile  
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 Ile Thr Asp Lys Gly Ala Ser Val Ile Phe Leu Lys Glu Asn Leu Thr  
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 Phe Ala Ala Gly Arg Asp Asp Pro Arg Ala Asn Leu Met Leu Gly Ile  
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 Ala Glu Gly Ile Ala Leu Ala Lys Lys Ala Gly Lys Tyr Ala Gly Arg  
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Phe Lys Glu Gln Thr Thr Asn Pro Arg Ser Gln Arg Val Ser Tyr Leu						
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Arg Val Ser Ser Thr Asp Gln Asn Leu Ala Arg Gln Arg Glu Ala Val						
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Arg Glu Asp Asp Val Leu Val Val Ala Ser Ile Asp Arg Leu Ala Arg						
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tcg ctg gtt gat tta cgc gtc atc att gac cgc atc aca gac aaa ggc 403						
Ser Leu Val Asp Leu Arg Val Ile Ile Asp Arg Ile Thr Asp Lys Gly						
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Leu  
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Cys Ile Asn Tyr Leu Arg Glu Asp Asp Val Leu Val Val Ala Ser Ile  
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Ile Thr Asp Lys Gly Ala Ser Val Ile Phe Leu Lys Glu Asn Leu Thr  
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Met Ser Thr Val His  
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&lt;211&gt; 391

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 88

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<400> 89

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ccc aac aga att gac tct gac tac ccc aac aaa gat att tgc ggt gcg 643
Pro Asn Arg Ile Asp Ser Asp Tyr Pro Asn Lys Asp Ile Cys Gly Ala
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Val	Ala	Thr	Leu	Asp	Ala	Leu	Asp	Lys	Asn	Thr	Pro	Arg	Glu	Ala	Gln	
470					475					480					485	
ccg	gca	gat	ctg	cat	ttg	gtt	gac	att	gac	cac	gcg	cgt	cct	gtg	ctt	1603
Pro	Ala	Asp	Leu	His	Leu	Val	Asp	Ile	Asp	His	Ala	Arg	Pro	Val	Leu	
				490					495					500		
gat	aac	ccc	tca	ctc	acc	caa	gag	ctc	agt	acg	gtc	gat	gct	gca	gtg	1651
Asp	Asn	Pro	Ser	Leu	Thr	Gln	Glu	Leu	Ser	Thr	Val	Asp	Ala	Ala	Val	
			505					510					515			
gat	gct	gca	cag	ttg	ctt	gtt	ctc	att	gat	cag	ctt	gat	caa	ctg	cag	1699
Asp	Ala	Ala	Gln	Leu	Leu	Val	Leu	Ile	Asp	Gln	Leu	Asp	Gln	Leu	Gln	
		520					525					530				
cca	ttt	gga	cat	ggg	ttt	acc	tat	ccg	cgc	atc	gac	gtg	acg	ttc	agg	1747
Pro	Phe	Gly	His	Gly	Phe	Thr	Tyr	Pro	Arg	Ile	Asp	Val	Thr	Phe	Arg	
	535					540					545					
ccg	gca	gaa	aca	gaa	ttc	aag	gtt	atg	ggg	cag	cac	cat	caa	cat	ctc	1795
Pro	Ala	Glu	Thr	Glu	Phe	Lys	Val	Met	Gly	Gln	His	His	Gln	His	Leu	
550					555					560					565	
aag	gtg	atc	act	cac	tca	ggg	ttg	acc	tta	ttg	tgg	tgg	aat	aag	gct	1843
Lys	Val	Ile	Thr	His	Ser	Gly	Leu	Thr	Leu	Leu	Trp	Trp	Asn	Lys	Ala	
				570					575					580		
cag	cag	ctc	gat	gag	atc	gca	cag	tct	gaa	tta	gtc	acc	atg	tct	gtg	1891
Gln	Gln	Leu	Asp	Glu	Ile	Ala	Gln	Ser	Glu	Leu	Val	Thr	Met	Ser	Val	
			585					590					595			
gag	ctc	gat	gtc	aat	atg	ttc	cgt	ggg	ttt	att	tcc	ccg	caa	ggc	att	1939
Glu	Leu	Asp	Val	Asn	Met	Phe	Arg	Gly	Phe	Ile	Ser	Pro	Gln	Gly	Ile	
		600					605					610				
gtc	tct	gcg	tgc	aca	gtt	atc	tagcttggtt	gcataagcac	caa							1983
Val	Ser	Ala	Cys	Thr	Val	Ile										
		615				620										

&lt;210&gt; 90

&lt;211&gt; 620

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 90

Met	Thr	Val	Thr	Ser	Pro	Ala	Ala	Leu	Ala	Leu	Ser	Asp	Met	Ser	Tyr
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Val Asp Ile Ile Lys Lys Lys Arg Gly Trp Thr Thr Glu Phe Phe His

20					25					30					
Ser	Thr	Ile	Asn	Thr	Gly	Glu	Thr	Thr	Thr	Pro	Leu	Pro	Asp	Ser	Asp
		35					40					45			
Arg	Ala	Thr	Ala	Leu	Ile	His	Asp	His	Ile	Thr	Lys	Ala	Gln	Glu	Ile
	50					55					60				
Thr	Ile	Ile	Thr	Asp	Phe	Asp	Met	Asp	Gly	Ile	Ser	Ala	Gly	Val	Ile
	65					70					75				80
Ala	Tyr	Ala	Gly	Leu	Ala	Glu	Leu	Gly	Ala	Gln	Val	Asn	Met	Val	Val
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Pro	Asp	Tyr	Arg	Gly	Glu	Arg	Asn	Val	Thr	Ala	Ser	Asp	Ile	Asp	Arg
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Ala	Leu	Glu	Leu	Tyr	Pro	Ala	Thr	Ser	Leu	Ile	Ile	Thr	Cys	Asp	Val
		115					120					125			
Gly	Ile	Gly	Ser	His	Glu	Gly	Ile	Ala	Arg	Ala	His	Glu	Arg	Ser	Ile
	130					135					140				
Ala	Val	Leu	Val	Thr	Asp	His	His	Met	Glu	Val	Glu	Pro	Cys	Gln	Ala
	145					150					155				160
Asp	Val	Val	Leu	Asn	Pro	Asn	Arg	Ile	Asp	Ser	Asp	Tyr	Pro	Asn	Lys
				165					170					175	
Asp	Ile	Cys	Gly	Ala	Gln	Val	Ile	Phe	Ala	Thr	Leu	Ser	Asp	Tyr	Ala
			180					185					190		
Arg	Arg	Tyr	Arg	Ala	Asp	Lys	Ile	Ile	Asp	Ile	Asn	Leu	Leu	Ala	Val
		195					200					205			
Phe	Ser	Gly	Ile	Gly	Ala	Leu	Ala	Asp	Val	Met	Pro	Leu	Thr	Arg	Asp
	210					215					220				
Thr	Arg	Pro	Thr	Val	Lys	Gln	Ala	Ile	Ala	Leu	Leu	Arg	Leu	Ala	Ile
	225					230					235				240
Pro	Gln	Val	Ser	Lys	Asn	Arg	Phe	Gly	Gly	Trp	Asp	Thr	Tyr	Ala	Ala
				245					250					255	
Arg	Ser	Val	Asn	Pro	Asp	Thr	Ser	Thr	Leu	Met	His	Ile	Val	Asn	Ala
			260					265					270		
Ser	Gln	His	Asp	His	Arg	Phe	Ile	Ala	Ala	Phe	Gln	Gly	Ile	Ser	Ile
		275					280					285			
Leu	Leu	Gly	Glu	Leu	Ile	Ala	Gln	Lys	Lys	Leu	Val	Asn	Ile	Asp	Asn
	290					295					300				
Ile	Ser	Glu	Ser	Phe	Ile	Gly	Phe	Thr	Leu	Gly	Pro	Met	Phe	Asn	Ala
	305					310					315				320
Thr	Arg	Arg	Val	Gly	Gly	Asp	Met	His	Asp	Ser	Phe	Leu	Val	Phe	Ala
				325					330					335	
Pro	His	Ala	Ala	Leu	Ala	Ser	Gln	Pro	Ser	Met	Asn	Pro	Asn	Arg	His
			340					345					350		

Ala Ala Ile Ser Arg Ile Ile Asp Asn Asn Glu Arg Arg Lys Glu Leu  
           355                                  360                                  365  
 Ser Lys Ser Ser Tyr Ala Ala Val His Ser Ser Asp Gln Pro Tyr Ala  
           370                                  375                                  380  
 Pro Phe Val Trp Leu Ser Glu Ala Pro Ser Gly Ile Leu Gly Leu Ile  
 385                                  390                                  395                                  400  
 Ala Ser Gln Leu Thr Arg Glu Ser Asp Val Pro Ala Ile Val Ile Asn  
                                   405                                  410                                  415  
 Pro Asp Thr Leu Ser Gly Ser Ala Arg Ser Pro Glu Trp Ala Pro Ile  
                                   420                                  425                                  430  
 Ile Thr Gln Val Asn Thr Leu Ser Ala Gln Gly His Gly Gly Ile His  
                                   435                                  440                                  445  
 Ala Ala Gly His Glu Tyr Ala Cys Gly Met Arg Phe Asp Asn His Asp  
           450                                  455                                  460  
 Asp Ile Val Thr Phe Val Ala Thr Leu Asp Ala Leu Asp Lys Asn Thr  
 465                                  470                                  475                                  480  
 Pro Arg Glu Ala Gln Pro Ala Asp Leu His Leu Val Asp Ile Asp His  
                                   485                                  490                                  495  
 Ala Arg Pro Val Leu Asp Asn Pro Ser Leu Thr Gln Glu Leu Ser Thr  
                                   500                                  505                                  510  
 Val Asp Ala Ala Val Asp Ala Ala Gln Leu Leu Val Leu Ile Asp Gln  
           515                                  520                                  525  
 Leu Asp Gln Leu Gln Pro Phe Gly His Gly Phe Thr Tyr Pro Arg Ile  
 530                                  535                                  540  
 Asp Val Thr Phe Arg Pro Ala Glu Thr Glu Phe Lys Val Met Gly Gln  
 545                                  550                                  555                                  560  
 His His Gln His Leu Lys Val Ile Thr His Ser Gly Leu Thr Leu Leu  
                                   565                                  570                                  575  
 Trp Trp Asn Lys Ala Gln Gln Leu Asp Glu Ile Ala Gln Ser Glu Leu  
                                   580                                  585                                  590  
 Val Thr Met Ser Val Glu Leu Asp Val Asn Met Phe Arg Gly Phe Ile  
           595                                  600                                  605  
 Ser Pro Gln Gly Ile Val Ser Ala Cys Thr Val Ile  
           610                                  615                                  620

&lt;210&gt; 91

&lt;211&gt; 786

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(763)

&lt;223&gt; RXA00929

&lt;400&gt; 91

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cacagcgacg aatcagcgac gaatcagtga ggacacgaat atg aac cac gaa ggg 115
                                         Met Asn His Glu Gly
                                         1 5

ctt cgg gta atg ggc att gac cca ggt ctt acc cgt tgt ggc tta tct 163
Leu Arg Val Met Gly Ile Asp Pro Gly Leu Thr Arg Cys Gly Leu Ser
                        10                      15                      20

gtg gtt caa gca ggt cgt ggt cgt acc gtg tat cca gtg tcg gtg ggc 211
Val Val Gln Ala Gly Arg Gly Arg Thr Val Tyr Pro Val Ser Val Gly
                        25                      30                      35

gtg gtg cgc acc cca cca gat gcg gag ttg gcg gag cgg ttg ctt cgg 259
Val Val Arg Thr Pro Pro Asp Ala Glu Leu Ala Glu Arg Leu Leu Arg
                        40                      45                      50

ctc agc aaa gca gtg ggt gag tgg atg gat gag tac acc cca gat gtc 307
Leu Ser Lys Ala Val Gly Glu Trp Met Asp Glu Tyr Thr Pro Asp Val
                        55                      60                      65

att gct att gag cgt gtc ttt gag cgc gga aat gtt tcc acc gtg atg 355
Ile Ala Ile Glu Arg Val Phe Glu Arg Gly Asn Val Ser Thr Val Met
                        70                      75                      80                      85

aac act gcg cat gcg gtg ggt gtg ttg atc ttg gct gct gct gaa cgc 403
Asn Thr Ala His Ala Val Gly Val Leu Ile Leu Ala Ala Ala Glu Arg
                        90                      95                      100

gga ttg cca gtt cac atg tac acc ccc agt gag gtg aaa aag gct atc 451
Gly Leu Pro Val His Met Tyr Thr Pro Ser Glu Val Lys Lys Ala Ile
                        105                      110                      115

tcc ggt aat ggt cgc gct gat aag aaa cag atg acg gtc atg atc act 499
Ser Gly Asn Gly Arg Ala Asp Lys Lys Gln Met Thr Val Met Ile Thr
                        120                      125                      130

cga att ctg ggc ctt ggt gag cca ccc aaa cct gct gac gcc gct gat 547
Arg Ile Leu Gly Leu Gly Glu Pro Pro Lys Pro Ala Asp Ala Ala Asp
                        135                      140                      145

gct tta tcg ttg gcg gtg tgt cac tgc tgg cgg gcg cca atg ctt atg 595
Ala Leu Ser Leu Ala Val Cys His Cys Trp Arg Ala Pro Met Leu Met
                        150                      155                      160                      165

cgg gcg caa tcg cag tac tcc gag caa gag ttg gaa aag cga cgg cgt 643
Arg Ala Gln Ser Gln Tyr Ser Glu Gln Glu Leu Glu Lys Arg Arg Arg
                        170                      175                      180

gtg cag caa gga aaa ttg ggt aaa gcg aaa tca act tac aat gcg gaa 691
Val Gln Gln Gly Lys Leu Gly Lys Ala Lys Ser Thr Tyr Asn Ala Glu
                        185                      190                      195

caa gct caa tcc cat gca tcc gat cct gct aaa gcg gct cat ccc agt 739
Gln Ala Gln Ser His Ala Ser Asp Pro Ala Lys Ala His Pro Ser
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786

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 <211> 221  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 92  
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 Pro Val Ser Val Gly Val Val Arg Thr Pro Pro Asp Ala Glu Leu Ala  
 35 40 45  
 Glu Arg Leu Leu Arg Leu Ser Lys Ala Val Gly Glu Trp Met Asp Glu  
 50 55 60  
 Tyr Thr Pro Asp Val Ile Ala Ile Glu Arg Val Phe Glu Arg Gly Asn  
 65 70 75 80  
 Val Ser Thr Val Met Asn Thr Ala His Ala Val Gly Val Leu Ile Leu  
 85 90 95  
 Ala Ala Ala Glu Arg Gly Leu Pro Val His Met Tyr Thr Pro Ser Glu  
 100 105 110  
 Val Lys Lys Ala Ile Ser Gly Asn Gly Arg Ala Asp Lys Lys Gln Met  
 115 120 125  
 Thr Val Met Ile Thr Arg Ile Leu Gly Leu Gly Glu Pro Pro Lys Pro  
 130 135 140  
 Ala Asp Ala Ala Asp Ala Leu Ser Leu Ala Val Cys His Cys Trp Arg  
 145 150 155 160  
 Ala Pro Met Leu Met Arg Ala Gln Ser Gln Tyr Ser Glu Gln Glu Leu  
 165 170 175  
 Glu Lys Arg Arg Arg Val Gln Gln Gly Lys Leu Gly Lys Ala Lys Ser  
 180 185 190  
 Thr Tyr Asn Ala Glu Gln Ala Gln Ser His Ala Ser Asp Pro Ala Lys  
 195 200 205  
 Ala Ala His Pro Ser Gln Phe Gln Arg Thr Asp Thr Asn  
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<210> 93  
 <211> 423  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS

&lt;222&gt; (101)..(400)

&lt;223&gt; RXA02251

&lt;400&gt; 93

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                                         Val Ala Asp Pro Thr
                                         1 5
act tat cgc ccg gct cca gga aca att cca acg gag ccg ggt gtt tat 163
Thr Tyr Arg Pro Ala Pro Gly Thr Ile Pro Thr Glu Pro Gly Val Tyr
                        10 15 20
aaa ttc agg gac gaa aac cgc cgc gtg atc tac gtg ggc aag gcc aaa 211
Lys Phe Arg Asp Glu Asn Arg Arg Val Ile Tyr Val Gly Lys Ala Lys
                        25 30 35
aac ttg cgt tcg cgg ttg tcg aac tat ttc cag gat gtc acc caa ctg 259
Asn Leu Arg Ser Arg Leu Ser Asn Tyr Phe Gln Asp Val Thr Gln Leu
                        40 45 50
cat ccg cgc acc cgc caa atg gtg ttc gca gcg tcg tct gtg gag tgg 307
His Pro Arg Thr Arg Gln Met Val Phe Ala Ala Ser Ser Val Glu Trp
                        55 60 65
acc gtg gtg tcc agc gaa gtc gag gcg ctg cag ctg gaa tac acc tgg 355
Thr Val Val Ser Ser Glu Val Glu Ala Leu Gln Leu Glu Tyr Thr Trp
                        70 75 80 85
att aaa cgc ttt gat ccg cgg ttc aaa cgt aaa ata ccg cga cga 400
Ile Lys Arg Phe Asp Pro Arg Phe Lys Arg Lys Ile Pro Arg Arg
                        90 95 100
taaaacctat cccatgctgg cag 423

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&lt;210&gt; 94

&lt;211&gt; 100

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 94

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Val Ala Asp Pro Thr Thr Tyr Arg Pro Ala Pro Gly Thr Ile Pro Thr
  1 5 10 15
Glu Pro Gly Val Tyr Lys Phe Arg Asp Glu Asn Arg Arg Val Ile Tyr
  20 25 30
Val Gly Lys Ala Lys Asn Leu Arg Ser Arg Leu Ser Asn Tyr Phe Gln
  35 40 45
Asp Val Thr Gln Leu His Pro Arg Thr Arg Gln Met Val Phe Ala Ala
  50 55 60
Ser Ser Val Glu Trp Thr Val Val Ser Ser Glu Val Glu Ala Leu Gln
  65 70 75 80
Leu Glu Tyr Thr Trp Ile Lys Arg Phe Asp Pro Arg Phe Lys Arg Lys
  85 90 95

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Ile Pro Arg Arg  
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<210> 95

<211> 1947

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1924)

<223> RXA02252

<400> 95

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gtcgaggcgc tgcagctgga atacacctgg attaaacgct ttg atc cgc ggt tca 115
                                   Leu Ile Arg Gly Ser
                                   1 5

aac gta aaa tac cgc gac gat aaa acc tat ccc atg ctg gca gta tcc 163
Asn Val Lys Tyr Arg Asp Asp Lys Thr Tyr Pro Met Leu Ala Val Ser
                                   10 15 20

aca ggg gag agg ttc ccg cgc gcg ttc ttc ttc cga ggt ccg cgc cgc 211
Thr Gly Glu Arg Phe Pro Arg Ala Phe Phe Phe Arg Gly Pro Arg Arg
                                   25 30 35

aaa ggt gtg cgc tat ttc gga ccg tat tcc cac gcg tgg gca gtg cgg 259
Lys Gly Val Arg Tyr Phe Gly Pro Tyr Ser His Ala Trp Ala Val Arg
                                   40 45 50

gaa acc ctt gat ctt ctc acc cgc gtt ttc ccc atg cgc acc tgt tca 307
Glu Thr Leu Asp Leu Leu Thr Arg Val Phe Pro Met Arg Thr Cys Ser
                                   55 60 65

aag ggt gtg ttt aac cgc cac gaa agc ctc ggc cgg ccg tgt ttg ttg 355
Lys Gly Val Phe Asn Arg His Glu Ser Leu Gly Arg Pro Cys Leu Leu
                                   70 75 80 85

ggc tat atc gat aaa tgt gcg gcc ccg tgc gtg ggc cgc gtg agc gaa 403
Gly Tyr Ile Asp Lys Cys Ala Ala Pro Cys Val Gly Arg Val Ser Glu
                                   90 95 100

gag gaa cac cgc gaa atc gtt gac ggt ttc acc tct ttc atg gct ggt 451
Glu Glu His Arg Glu Ile Val Asp Gly Phe Thr Ser Phe Met Ala Gly
                                   105 110 115

cac acc gac aaa gtc act cgc aaa ctc aac gcc gac atg atg gct gcg 499
His Thr Asp Lys Val Thr Arg Lys Leu Asn Ala Asp Met Met Ala Ala
                                   120 125 130

gcc gag gaa ctc gat ttc gag cgc gcg gcc cgc ctg cgc gat gat ctg 547
Ala Glu Glu Leu Asp Phe Glu Arg Ala Ala Arg Leu Arg Asp Asp Leu
                                   135 140 145

gaa gcc att gac aag gtc atg gaa aaa cag gcc gtc gtc ctt ggc gat 595
Glu Ala Ile Asp Lys Val Met Glu Lys Gln Ala Val Val Leu Gly Asp
                                   150 155 160 165

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ggc acc gac gcc gac atc atc gca ttc gcc acc gat cag cta gaa gcc	643
Gly Thr Asp Ala Asp Ile Ile Ala Phe Ala Thr Asp Gln Leu Glu Ala	
170 175 180	
gcc gtg caa gtc ttc aac atc cga ggt ggc cga atc cgc ggc cag cgc	691
Ala Val Gln Val Phe Asn Ile Arg Gly Gly Arg Ile Arg Gly Gln Arg	
185 190 195	
ggc tgg gtt gtg gaa aag ccc ggc gac tac gcc gga ttg ctt gtc gac	739
Gly Trp Val Val Glu Lys Pro Gly Asp Tyr Ala Gly Leu Leu Val Asp	
200 205 210	
gct acg acc caa cct gag ggt gat gcc ccg gaa aca gat ccc gca ctg	787
Ala Thr Thr Gln Pro Glu Gly Asp Ala Pro Glu Thr Asp Pro Ala Leu	
215 220 225	
cca ttt ttg atg caa gat ttc ctc gtt cag ttt tat ggc gac gcc gtc	835
Pro Phe Leu Met Gln Asp Phe Leu Val Gln Phe Tyr Gly Asp Ala Val	
230 235 240 245	
gag cgt gct gaa act gag gct aag gaa gat gct gcg gtg atc gag cga	883
Glu Arg Ala Glu Thr Glu Ala Lys Glu Asp Ala Ala Val Ile Glu Arg	
250 255 260	
cgt ggc gtc gat aag cat tct ttt gaa gag gca gcc cca gtg acg cgc	931
Arg Gly Val Asp Lys His Ser Phe Glu Glu Ala Ala Pro Val Thr Arg	
265 270 275	
gct tcg gtc gtg ccc cgt gaa atc ctc gtg caa gtt gcg ccc aat gaa	979
Ala Ser Val Val Pro Arg Glu Ile Leu Val Gln Val Ala Pro Asn Glu	
280 285 290	
gct gag caa acc ctg aaa gta ctg gag gaa ttg cgc ggt gct ggc gtt	1027
Ala Glu Gln Thr Leu Lys Val Leu Glu Glu Leu Arg Gly Ala Gly Val	
295 300 305	
gat gcc cgc gtg cca cag cgc ggt gac aag cgt gcg ctc atg gaa act	1075
Asp Ala Arg Val Pro Gln Arg Gly Asp Lys Arg Ala Leu Met Glu Thr	
310 315 320 325	
gtg gag cgc aac gcc aaa gag ctg ctg aaa caa cac aag ctt aag cgt	1123
Val Glu Arg Asn Ala Lys Glu Leu Leu Lys Gln His Lys Leu Lys Arg	
330 335 340	
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Val Gly Asp Leu Thr Ala Arg Ser Ala Ala Leu Gln Glu Leu Gln Glu	
345 350 355	
gcg ctg gac atg gag cag gct ccg ctg cgc atc gaa tgt acc gat att	1219
Ala Leu Asp Met Glu Gln Ala Pro Leu Arg Ile Glu Cys Thr Asp Ile	
360 365 370	
tcc cat att cag ggc acc gat gtg gtg gca tcc ctg gtg gtt ttt gaa	1267
Ser His Ile Gln Gly Thr Asp Val Val Ala Ser Leu Val Val Phe Glu	
375 380 385	
gat ggt ttg cct cga aaa tcg gac tac cga cgc tat cga gtc aaa gaa	1315
Asp Gly Leu Pro Arg Lys Ser Asp Tyr Arg Arg Tyr Arg Val Lys Glu	
390 395 400 405	
gcc gca ggc gat gga cat tcc aac gac gtg gca tcc att gcg gaa atc	1363

Ala	Ala	Gly	Asp	Gly	His	Ser	Asn	Asp	Val	Ala	Ser	Ile	Ala	Glu	Ile		
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acc	agg	cgc	cgc	ttc	ctg	cgc	cac	aac	caa	gac	aaa	ctt	gct	gtt	ccc	1411	
Thr	Arg	Arg	Arg	Phe	Leu	Arg	His	Asn	Gln	Asp	Lys	Leu	Ala	Val	Pro		
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Glu	Ala	Glu	Glu	Phe	Asp	Gly	Ser	Thr	Phe	Ser	Asp	Glu	Lys	Val	Glu		
		440					445					450					
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Glu	Met	Ser	Thr	Asp	Ala	Arg	Arg	Phe	Ala	Tyr	Pro	Pro	Gln	Ile	Phe		
	455					460					465						
atc	gtc	gat	ggg	ggg	gcc	cgc	cag	gta	gct	gca	gcc	caa	gaa	gtc	ttt	1555	
Ile	Val	Asp	Gly	Gly	Ala	Pro	Gln	Val	Ala	Ala	Ala	Gln	Glu	Val	Phe		
470					475				480						485		
gat	gaa	tta	ggc	atc	gtt	gac	gtg	gtg	ctc	att	ggc	cta	gcc	aag	cgc	1603	
Asp	Glu	Leu	Gly	Ile	Val	Asp	Val	Val	Leu	Ile	Gly	Leu	Ala	Lys	Arg		
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Leu	Glu	Glu	Ile	Trp	Leu	Pro	Gly	Asp	Pro	Asp	Pro	Val	Ile	Leu	Pro		
			505					510					515				
aga	aac	tcc	caa	gca	ctg	ttt	ttg	ctc	cag	caa	atc	cgt	gac	gaa	gcc	1699	
Arg	Asn	Ser	Gln	Ala	Leu	Phe	Leu	Leu	Gln	Gln	Ile	Arg	Asp	Glu	Ala		
		520					525					530					
cac	cgc	ttt	gcc	atc	acc	tac	cac	cgc	cag	caa	cga	tcc	aag	cgc	atg	1747	
His	Arg	Phe	Ala	Ile	Thr	Tyr	His	Arg	Gln	Gln	Arg	Ser	Lys	Arg	Met		
	535					540					545						
cgt	gtt	tcc	gag	cta	gat	agc	atc	aag	ggc	ctt	ggc	cag	agc	cgt	cgc	1795	
Arg	Val	Ser	Glu	Leu	Asp	Ser	Ile	Lys	Gly	Leu	Gly	Gln	Ser	Arg	Arg		
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act	gaa	cta	gtc	aag	cac	ttt	gga	tcc	gtg	gca	aaa	ctg	aaa	gag	gca	1843	
Thr	Glu	Leu	Val	Lys	His	Phe	Gly	Ser	Val	Ala	Lys	Leu	Lys	Glu	Ala		
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agc	gtt	gag	gac	att	tcc	caa	gtg	aaa	ggc	ttc	ggc	ccg	aaa	ctt	gcg	1891	
Ser	Val	Glu	Asp	Ile	Ser	Gln	Val	Lys	Gly	Phe	Gly	Pro	Lys	Leu	Ala		
			585					590					595				
gag	gct	gtc	tat	gaa	ggg	ctt	cac	gcg	tca	aaa	taagtagatc	gctaggatgt	1944				
Glu	Ala	Val	Tyr	Glu	Gly	Leu	His	Ala	Ser	Lys							
		600					605										
aac																1947	

&lt;210&gt; 96

&lt;211&gt; 608

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 96

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Ile	Arg	Gly	Gln
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Gly	Leu	Leu	Val
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Thr	Asp	Pro	Ala
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Tyr	Gly	Asp	Ala
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Tyr	Gly	Asp	Ala
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Ala	Pro	Val	Thr
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Val	Ala	Pro	Asn
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Val	Ala	Pro	Asn
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Arg	Gly	Ala	Gly
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Arg	Gly	Ala	Gly
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Ala	Leu	Met	Glu
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Ala	Leu	Met	Glu
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His Lys Leu Lys Arg Val Gly Asp Leu Thr Ala Arg Ser Ala Ala Leu  
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 Gln Glu Leu Gln Glu Ala Leu Asp Met Glu Gln Ala Pro Leu Arg Ile  
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 Glu Cys Thr Asp Ile Ser His Ile Gln Gly Thr Asp Val Val Ala Ser  
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 Tyr Arg Val Lys Glu Ala Ala Gly Asp Gly His Ser Asn Asp Val Ala  
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 Lys Leu Ala Val Pro Glu Ala Glu Glu Phe Asp Gly Ser Thr Phe Ser  
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 Asp Glu Lys Val Glu Glu Met Ser Thr Asp Ala Arg Arg Phe Ala Tyr  
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 Pro Pro Gln Ile Phe Ile Val Asp Gly Gly Ala Pro Gln Val Ala Ala  
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 485 490 495  
 Gly Leu Ala Lys Arg Leu Glu Glu Ile Trp Leu Pro Gly Asp Pro Asp  
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 Pro Val Ile Leu Pro Arg Asn Ser Gln Ala Leu Phe Leu Leu Gln Gln  
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 Ile Arg Asp Glu Ala His Arg Phe Ala Ile Thr Tyr His Arg Gln Gln  
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 Arg Ser Lys Arg Met Arg Val Ser Glu Leu Asp Ser Ile Lys Gly Leu  
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 Gly Gln Ser Arg Arg Thr Glu Leu Val Lys His Phe Gly Ser Val Ala  
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Glu His Asn Leu Lys Gly Val Asp Ile Asp Leu Pro Arg Asp Ser Met  
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Val Val Phe Thr Gly Leu Ser Gly Ser Gly Lys Ser Ser Leu Ala Phe  
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Asp Thr Ile Phe Ala Glu Gly Gln Arg Arg Tyr Val Glu Ser Leu Ser  
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agt tac gcc cgc atg ttc ttg ggg cag atg gac aag ccg gac gtg gat    307  
Ser Tyr Ala Arg Met Phe Leu Gly Gln Met Asp Lys Pro Asp Val Asp  
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 Asn Arg Asn Pro Arg Ser Thr Val Gly Thr Ile Thr Glu Val Tyr Asp  
 90 95 100

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Tyr	Leu	Arg	Leu	Leu	Tyr	Ala	Arg	Ala	Gly	Thr	Ala	His	Cys	Pro	Val	
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 Cys Asp Ala Arg Val Glu Arg Gln Thr Pro Gln Gln Met Val Asp Gln  
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Ile Leu Gly Met Glu Glu Gly Leu Lys Phe Gln Ile Leu Ala Pro Val  
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Val Arg Thr Arg Lys Gly Glu Phe Val Asp Leu Phe Ala Asp Leu Ala  
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Ser	Gln	Gly	Tyr	Ser	Arg	Val	Arg	Val	Asp	Gly	Glu	Val	His	Gln	Leu	
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Ser Asp Pro Pro Lys Leu Glu Lys Gln Ile Lys His Asp Ile Asp Val	
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	195

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Val Val Asp Arg Leu Gln Val Lys Ala Ser Gln Lys Gln Arg Leu Thr  
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Asp Ser Met Glu Thr Ala Leu Arg Leu Ala Asp Gly Val Ala Val Leu	
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Glu Phe Val Gly Leu Glu Asp Asp Pro Asn Arg Leu Arg Arg Phe	
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Ser Glu Lys Met Ser Cys Pro Asn Gly His Ala Leu Thr Val Asp Glu	
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ctg gag cct cgt gct ttt tcc ttc aac tct cct tat ggc gcg tgt cct	931
Leu Glu Pro Arg Ala Phe Ser Phe Asn Ser Pro Tyr Gly Ala Cys Pro	
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gcc tgt gat ggc ttg ggt gtg cgc acc gaa gtt gat att gat ctg atc	979
Ala Cys Asp Gly Leu Gly Val Arg Thr Glu Val Asp Ile Asp Leu Ile	
280 285 290	
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Ile Pro Asp Pro Asp Ala Pro Ala Thr Lys Ala Val Gln Pro Trp Asn	
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Ser Ser Pro Asn His Ser Tyr Phe Glu Lys Leu Ile Glu Gly Leu Ala	
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Lys Ala Leu Gly Phe Asp Pro Glu Thr Pro Tyr Ser Glu Leu Thr Ala	
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Ala Gln Lys Lys Ala Leu Val Tyr Gly Ser Lys Glu Glu Val Ser Val	
345 350 355	
cga tac aag aac cgc tac gga cgc gtg cgt tct tgg act gcg cct ttt	1219
Arg Tyr Lys Asn Arg Tyr Gly Arg Val Arg Ser Trp Thr Ala Pro Phe	
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Glu Gly Val Met Gly Tyr Phe Asp Arg Lys Leu Glu Gln Thr Asp Ser	
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Pro Thr Cys Lys Gly Ala Arg Leu Lys Pro Glu Ile Leu Ala Val Arg	
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425 430 435	
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Leu Ser Val His Glu Ala Phe Glu Phe Leu Asp Asn Leu Thr Leu Gly	
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Arg	Leu	Lys	Phe	Leu	Leu	Asp	Val	Gly	Leu	Ser	Tyr	Leu	Thr	Leu	Asp		
470					475					480					485		
cgc	gcc	gca	ggc	acc	ctg	tct	ggg	ggg	gaa	gcg	cag	cgt	atc	cgc	ctg	1603	
Arg	Ala	Ala	Gly	Thr	Leu	Ser	Gly	Gly	Glu	Ala	Gln	Arg	Ile	Arg	Leu		
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gct	act	caa	att	ggg	tcc	ggg	ctg	gct	ggg	gtg	ctc	tac	gtc	ttg	gat	1651	
Ala	Thr	Gln	Ile	Gly	Ser	Gly	Leu	Ala	Gly	Val	Leu	Tyr	Val	Leu	Asp		
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Glu	Pro	Ser	Ile	Gly	Leu	His	Gln	Arg	Asp	Asn	Gln	Arg	Leu	Ile	Thr		
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acc	ctt	gag	cat	ctc	cga	gat	atc	gga	aac	acg	ctc	att	gtt	gtg	gaa	1747	
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His	Asp	Glu	Asp	Thr	Ile	Arg	Arg	Ala	Asp	Trp	Leu	Val	Asp	Ile	Gly		
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cct	cga	gct	ggg	gaa	ttt	ggg	ggc	gaa	gtg	gtc	tac	caa	ggg	gag	cgc	1843	
Pro	Arg	Ala	Gly	Glu	Phe	Gly	Gly	Glu	Val	Val	Tyr	Gln	Gly	Glu	Pro		
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Ile	Asp	Val	Lys	Ile	Pro	Leu	Gly	Val	Leu	Cys	Cys	Ile	Thr	Gly	Val		
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tgc	gga	tct	ggg	aaa	tcc	acg	ctg	gtc	aat	cag	att	ttg	gcc	aag	gtt	2083	
Ser	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Val	Asn	Gln	Ile	Leu	Ala	Lys	Val		
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ctg	gcc	aac	aaa	ctc	aac	cgc	gca	cgc	caa	gtg	cct	ggg	cgc	gca	aag	2131	
Leu	Ala	Asn	Lys	Leu	Asn	Arg	Ala	Arg	Gln	Val	Pro	Gly	Arg	Ala	Lys		
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cgg	gtg	gaa	ggc	ctc	gag	cac	ttg	gat	aag	ttg	gtc	caa	gtg	gat	cag	2179	
Arg	Val	Glu	Gly	Leu	Glu	His	Leu	Asp	Lys	Leu	Val	Gln	Val	Asp	Gln		
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tgc	cca	att	ggg	cgt	act	cca	cgt	tca	aac	cca	gcg	acg	tac	acg	ggg	2227	
Ser	Pro	Ile	Gly	Arg	Thr	Pro	Arg	Ser	Asn	Pro	Ala	Thr	Tyr	Thr	Gly		

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Val Phe Asp Lys Val Arg Asn Leu Phe Ala Glu Thr Thr Glu Ala Lys			
710	715	720	725
gtc cgc ggt tac aag cct ggc cgc ttc tcc ttc aat att aag ggt gga	2323		
Val Arg Gly Tyr Lys Pro Gly Arg Phe Ser Phe Asn Ile Lys Gly Gly			
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cgc tgc gaa gca tgt cag ggc gat ggc acg ctg aag atc gaa atg aac	2371		
Arg Cys Glu Ala Cys Gln Gly Asp Gly Thr Leu Lys Ile Glu Met Asn			
	745	750	755
ttc ctg ccc gac gtg tat gtt ccg tgt gaa gtc tgt gat ggt cag cgc	2419		
Phe Leu Pro Asp Val Tyr Val Pro Cys Glu Val Cys Asp Gly Gln Arg			
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tac aac cgc gag acc ctc gag gtg aag tac aag ggc aaa aac atc gct	2467		
Tyr Asn Arg Glu Thr Leu Glu Val Lys Tyr Lys Gly Lys Asn Ile Ala			
	775	780	785
gaa gta ttg ggc atg ccg atc tct gag gct gcg gac ttc ttt gag ccc	2515		
Glu Val Leu Gly Met Pro Ile Ser Glu Ala Ala Asp Phe Phe Glu Pro			
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atc acc tca att cac cga tac cta gca acg ctg gtt gat gtc ggc ctt	2563		
Ile Thr Ser Ile His Arg Tyr Leu Ala Thr Leu Val Asp Val Gly Leu			
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ggc tat gtc cgt ttg ggc cag gca gca aca acc ttg tct ggt ggt gaa	2611		
Gly Tyr Val Arg Leu Gly Gln Ala Ala Thr Thr Leu Ser Gly Gly Glu			
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gcc cag cgt gtg aaa ctt gcc gct gag ctg cag aag cgt tcc aac ggt	2659		
Ala Gln Arg Val Lys Leu Ala Ala Glu Leu Gln Lys Arg Ser Asn Gly			
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cgc acc gtt tac atc ctc gat gag cca act act ggt ttg cac ttt gaa	2707		
Arg Thr Val Tyr Ile Leu Asp Glu Pro Thr Thr Gly Leu His Phe Glu			
	855	860	865
gat att cgc aaa ctc atg atg gtg atc gaa ggc ctg gtg gac aag ggt	2755		
Asp Ile Arg Lys Leu Met Met Val Ile Glu Gly Leu Val Asp Lys Gly			
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aac tcc gtg atc atc atc gag cac aac ctc gac gtg atc aag gct gcc	2803		
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Ala	His	Cys	Pro	Val	Cys	Asp	Ala	Arg	Val	Glu	Arg	Gln	Thr	Pro	Gln
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Gln	Met	Val	Asp	Gln	Ile	Leu	Gly	Met	Glu	Glu	Gly	Leu	Lys	Phe	Gln
	130					135					140				
Ile	Leu	Ala	Pro	Val	Val	Arg	Thr	Arg	Lys	Gly	Glu	Phe	Val	Asp	Leu
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Phe	Ala	Asp	Leu	Ala	Ser	Gln	Gly	Tyr	Ser	Arg	Val	Arg	Val	Asp	Gly
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Glu	Val	His	Gln	Leu	Ser	Asp	Pro	Pro	Lys	Leu	Glu	Lys	Gln	Ile	Lys
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His	Asp	Ile	Asp	Val	Val	Val	Asp	Arg	Leu	Gln	Val	Lys	Ala	Ser	Gln
	195						200					205			
Lys	Gln	Arg	Leu	Thr	Asp	Ser	Met	Glu	Thr	Ala	Leu	Arg	Leu	Ala	Asp
	210					215					220				
Gly	Val	Ala	Val	Leu	Glu	Phe	Val	Gly	Leu	Glu	Glu	Asp	Asp	Pro	Asn
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Arg	Leu	Arg	Arg	Phe	Ser	Glu	Lys	Met	Ser	Cys	Pro	Asn	Gly	His	Ala
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Leu	Thr	Val	Asp	Glu	Leu	Glu	Pro	Arg	Ala	Phe	Ser	Phe	Asn	Ser	Pro
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Tyr	Gly	Ala	Cys	Pro	Ala	Cys	Asp	Gly	Leu	Gly	Val	Arg	Thr	Glu	Val
	275						280					285			

Asp Ile Asp Leu Ile Ile Pro Asp Pro Asp Ala Pro Ala Thr Lys Ala  
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 Val Gln Pro Trp Asn Ser Ser Pro Asn His Ser Tyr Phe Glu Lys Leu  
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 Ile Glu Gly Leu Ala Lys Ala Leu Gly Phe Asp Pro Glu Thr Pro Tyr  
 325 330 335  
 Ser Glu Leu Thr Ala Ala Gln Lys Lys Ala Leu Val Tyr Gly Ser Lys  
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 Glu Glu Val Ser Val Arg Tyr Lys Asn Arg Tyr Gly Arg Val Arg Ser  
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 Glu Gln Thr Asp Ser Glu Thr Gln Lys Asp Arg Leu Leu Gly Tyr Thr  
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 Arg Glu Val Pro Cys Pro Thr Cys Lys Gly Ala Arg Leu Lys Pro Glu  
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 Ile Leu Ala Val Arg Leu Asp Ser Gly Ser His Gly Ala Leu Ser Ile  
 420 425 430  
 Ala Gly Leu Thr Ala Leu Ser Val His Glu Ala Phe Glu Phe Leu Asp  
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 Asn Leu Thr Leu Gly Lys Arg Glu Glu Met Ile Ala Gly Ala Val Leu  
 450 455 460  
 Lys Glu Ile His Ala Arg Leu Lys Phe Leu Leu Asp Val Gly Leu Ser  
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 Tyr Leu Thr Leu Asp Arg Ala Ala Gly Thr Leu Ser Gly Gly Glu Ala  
 485 490 495  
 Gln Arg Ile Arg Leu Ala Thr Gln Ile Gly Ser Gly Leu Ala Gly Val  
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Arg Glu Ile Asp Lys Glu Arg Gln Leu Lys Val Val Gly Ala Arg Glu  
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 Asn Asn Leu Gln Gly Ile Asp Val Lys Ile Pro Leu Gly Val Leu Cys  
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 Cys Ile Thr Gly Val Ser Gly Ser Gly Lys Ser Thr Leu Val Asn Gln  
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 Val Gln Val Asp Gln Ser Pro Ile Gly Arg Thr Pro Arg Ser Asn Pro  
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 Ala Thr Tyr Thr Gly Val Phe Asp Lys Val Arg Asn Leu Phe Ala Glu  
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 Thr Thr Glu Ala Lys Val Arg Gly Tyr Lys Pro Gly Arg Phe Ser Phe  
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 Asn Ile Lys Gly Gly Arg Cys Glu Ala Cys Gln Gly Asp Gly Thr Leu  
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 Cys Asp Gly Gln Arg Tyr Asn Arg Glu Thr Leu Glu Val Lys Tyr Lys  
 770 775 780  
 Gly Lys Asn Ile Ala Glu Val Leu Gly Met Pro Ile Ser Glu Ala Ala  
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 Val Asp Val Gly Leu Gly Tyr Val Arg Leu Gly Gln Ala Ala Thr Thr  
 820 825 830  
 Leu Ser Gly Gly Glu Ala Gln Arg Val Lys Leu Ala Ala Glu Leu Gln  
 835 840 845  
 Lys Arg Ser Asn Gly Arg Thr Val Tyr Ile Leu Asp Glu Pro Thr Thr  
 850 855 860  
 Gly Leu His Phe Glu Asp Ile Arg Lys Leu Met Met Val Ile Glu Gly  
 865 870 875 880  
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 Val Ile Lys Ala Ala Asp Trp Ile Val Asp Met Gly Pro Glu Gly Gly  
 900 905 910  
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 Ile Thr Glu Val Tyr Asp Tyr Leu Arg Leu Leu Tyr Ala Arg Ala Gly  
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 Thr Ala His Cys Pro Val Cys Asp Ala Arg Val Glu Arg Gln Thr Pro  
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 Gln Gln Met Val Asp Gln Ile Leu Gly Met Glu Glu Gly Leu Lys Phe  
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 Gln Ile Leu Ala Pro Val Val Arg Thr Arg Lys Gly Glu Phe Val Asp  
 85 90 95  
 ctt ttc gca gat ctt gca tcc caa ggt tat tcc cgc gtg cgg gtt gat 336  
 Leu Phe Ala Asp Leu Ala Ser Gln Gly Tyr Ser Arg Val Arg Val Asp  
 100 105 110  
 ggg gaa gtg cac cag ctc tcg gat cct cca aag cta gaa aag cag atc 384  
 Gly Glu Val His Gln Leu Ser Asp Pro Pro Lys Leu Glu Lys Gln Ile  
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 Lys His Asp Ile Asp Val Val Val Asp Arg Leu Gln Val Lys Ala Ser  
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 Gln Lys Gln Arg Leu Thr Asp Ser Met Glu Thr Ala Leu Arg Leu Ala  
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 Asp Gly Val Ala Val Leu Glu Phe Val Gly Leu Glu Glu Asp Asp Pro  
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 Asn Arg Leu Arg Arg Phe Ser Glu Lys Met Ser Cys Pro Asn Gly His  
 180 185 190

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Ala Leu Thr Val Asp Glu Leu Glu Pro Arg Ala Phe Ser Phe Asn Ser	
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Pro Tyr Gly Ala Cys Pro Ala Cys Asp Gly Leu Gly Val Arg Thr Glu	
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Val Asp Ile Asp Leu Ile Ile Pro Asp Pro Asp Ala Pro Ala Thr Lys	
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Ala Val Gln Pro Trp Asn Ser Ser Pro Asn His Ser Tyr Phe Glu Lys	
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ctc att gaa ggc ctg gcg aaa gcc ctc gga ttt gat ccg gaa act ccg	816
Leu Ile Glu Gly Leu Ala Lys Ala Leu Gly Phe Asp Pro Glu Thr Pro	
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Tyr Ser Glu Leu Thr Ala Ala Gln Lys Lys Ala Leu Val Tyr Gly Ser	
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Lys Glu Glu Val Ser Val Arg Tyr Lys Asn Arg Tyr Gly Arg Val Arg	
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Ser Trp Thr Ala Pro Phe Glu Gly Val Met Gly Tyr Phe Asp Arg Lys	
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Asp Asn Leu Thr Leu Gly Lys Arg Glu Glu Met Ile Ala Gly Ala Val	
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Ser Tyr Leu Thr Leu Asp Arg Ala Ala Gly Thr Leu Ser Gly Gly Glu	
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Val Leu Tyr Val Leu Asp Glu Pro Ser Ile Gly Leu His Gln Arg Asp	
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Asn Gln Arg Leu Ile Thr Thr Leu Glu His Leu Arg Asp Ile Gly Asn	
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Thr Leu Ile Val Val Glu His Asp Glu Asp Thr Ile Arg Arg Ala Asp	
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Trp Leu Val Asp Ile Gly Pro Arg Ala Gly Glu Phe Gly Gly Glu Val	
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Val Tyr Gln Gly Glu Pro Lys Gly Ile Leu Asp Cys Glu Glu Ser Leu	
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Thr Gly Ala Tyr Leu Ser Gly Arg Arg Thr Leu Gly Val Pro Asp Thr	
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Glu Asn Asn Leu Gln Gly Ile Asp Val Lys Ile Pro Leu Gly Val Leu	
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Cys Cys Ile Thr Gly Val Ser Gly Ser Gly Lys Ser Thr Leu Val Asn	
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Gln Ile Leu Ala Lys Val Leu Ala Asn Lys Leu Asn Arg Ala Arg Gln	
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Val Pro Gly Arg Ala Lys Arg Val Glu Gly Leu Glu His Leu Asp Lys	
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Leu Val Gln Val Asp Gln Ser Pro Ile Gly Arg Thr Pro Arg Ser Asn	
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Pro Ala Thr Tyr Thr Gly Val Phe Asp Lys Val Arg Asn Leu Phe Ala	
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Glu Thr Thr Glu Ala Lys Val Arg Gly Tyr Lys Pro Gly Arg Phe Ser	
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Leu	Lys	Ile	Glu	Met	Asn	Phe	Leu	Pro	Asp	Val	Tyr	Val	Pro	Cys	Glu	
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Val	Cys	Asp	Gly	Gln	Arg	Tyr	Asn	Arg	Glu	Thr	Leu	Glu	Val	Lys	Tyr	
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Thr	Leu	Ser	Gly	Gly	Glu	Ala	Gln	Arg	Val	Lys	Leu	Ala	Ala	Glu	Leu	
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Gln	Lys	Arg	Ser	Asn	Gly	Arg	Thr	Val	Tyr	Ile	Leu	Asp	Glu	Pro	Thr	
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Thr	Gly	Leu	His	Phe	Glu	Asp	Ile	Arg	Lys	Leu	Met	Met	Val	Ile	Glu	
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Gly	Leu	Val	Asp	Lys	Gly	Asn	Ser	Val	Ile	Ile	Ile	Glu	His	Asn	Leu	
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Gly	Ser	Gly	Gly	Gly	Thr	Val	Val	Ala	Glu	Gly	Thr	Pro	Glu	Gln	Val	
	850					855					860					
gct	gaa	gtt	gcg	ggg	tcc	tac	acc	ggc	caa	ttc	ctt	aaa	gag	ttg	ttg	2640
Ala	Glu	Val	Ala	Gly	Ser	Tyr	Thr	Gly	Gln	Phe	Leu	Lys	Glu	Leu	Leu	
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taggagaaga	tgaggggctt	tca														2663

&lt;210&gt; 100

&lt;211&gt; 880

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 100

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Ile Thr Glu Val Tyr Asp Tyr Leu Arg Leu Leu Tyr Ala Arg Ala Gly	35	40	45
Thr Ala His Cys Pro Val Cys Asp Ala Arg Val Glu Arg Gln Thr Pro	50	55	60
Gln Gln Met Val Asp Gln Ile Leu Gly Met Glu Glu Gly Leu Lys Phe	65	70	75
Gln Ile Leu Ala Pro Val Val Arg Thr Arg Lys Gly Glu Phe Val Asp	85	90	95
Leu Phe Ala Asp Leu Ala Ser Gln Gly Tyr Ser Arg Val Arg Val Asp	100	105	110
Gly Glu Val His Gln Leu Ser Asp Pro Pro Lys Leu Glu Lys Gln Ile	115	120	125
Lys His Asp Ile Asp Val Val Val Asp Arg Leu Gln Val Lys Ala Ser	130	135	140
Gln Lys Gln Arg Leu Thr Asp Ser Met Glu Thr Ala Leu Arg Leu Ala	145	150	155
Asp Gly Val Ala Val Leu Glu Phe Val Gly Leu Glu Glu Asp Asp Pro	165	170	175
Asn Arg Leu Arg Arg Phe Ser Glu Lys Met Ser Cys Pro Asn Gly His	180	185	190
Ala Leu Thr Val Asp Glu Leu Glu Pro Arg Ala Phe Ser Phe Asn Ser	195	200	205
Pro Tyr Gly Ala Cys Pro Ala Cys Asp Gly Leu Gly Val Arg Thr Glu	210	215	220
Val Asp Ile Asp Leu Ile Ile Pro Asp Pro Asp Ala Pro Ala Thr Lys	225	230	235
Ala Val Gln Pro Trp Asn Ser Ser Pro Asn His Ser Tyr Phe Glu Lys	245	250	255
Leu Ile Glu Gly Leu Ala Lys Ala Leu Gly Phe Asp Pro Glu Thr Pro	260	265	270
Tyr Ser Glu Leu Thr Ala Ala Gln Lys Lys Ala Leu Val Tyr Gly Ser	275	280	285
Lys Glu Glu Val Ser Val Arg Tyr Lys Asn Arg Tyr Gly Arg Val Arg	290	295	300
Ser Trp Thr Ala Pro Phe Glu Gly Val Met Gly Tyr Phe Asp Arg Lys	305	310	315
Leu Glu Gln Thr Asp Ser Glu Thr Gln Lys Asp Arg Leu Leu Gly Tyr	325	330	335

Thr Arg Glu Val Pro Cys Pro Thr Cys Lys Gly Ala Arg Leu Lys Pro  
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 Glu Ile Leu Ala Val Arg Leu Asp Ser Gly Ser His Gly Ala Leu Ser  
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 Ile Ala Gly Leu Thr Ala Leu Ser Val His Glu Ala Phe Glu Phe Leu  
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 Ser Tyr Leu Thr Leu Asp Arg Ala Ala Gly Thr Leu Ser Gly Gly Glu  
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 Thr Leu Ile Val Val Glu His Asp Glu Asp Thr Ile Arg Arg Ala Asp  
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 Val Tyr Gln Gly Glu Pro Lys Gly Ile Leu Asp Cys Glu Glu Ser Leu  
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 Cys Cys Ile Thr Gly Val Ser Gly Ser Gly Lys Ser Thr Leu Val Asn  
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 Gln Ile Leu Ala Lys Val Leu Ala Asn Lys Leu Asn Arg Ala Arg Gln  
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 Val Pro Gly Arg Ala Lys Arg Val Glu Gly Leu Glu His Leu Asp Lys  
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 Pro Ala Thr Tyr Thr Gly Val Phe Asp Lys Val Arg Asn Leu Phe Ala  
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Glu Thr Thr Glu Ala Lys Val Arg Gly Tyr Lys Pro Gly Arg Phe Ser  
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 Phe Asn Ile Lys Gly Gly Arg Cys Glu Ala Cys Gln Gly Asp Gly Thr  
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 Lys Gly Lys Asn Ile Ala Glu Val Leu Gly Met Pro Ile Ser Glu Ala  
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 Ala Asp Phe Phe Glu Pro Ile Thr Ser Ile His Arg Tyr Leu Ala Thr  
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 Thr Leu Ser Gly Gly Glu Ala Gln Arg Val Lys Leu Ala Ala Glu Leu  
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 Gln Lys Arg Ser Asn Gly Arg Thr Val Tyr Ile Leu Asp Glu Pro Thr  
 785 790 795 800  
 Thr Gly Leu His Phe Glu Asp Ile Arg Lys Leu Met Met Val Ile Glu  
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 Asp Val Ile Lys Ala Ala Asp Trp Ile Val Asp Met Gly Pro Glu Gly  
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 Met Met Pro Tyr Ile  
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Glu	Lys	Val	Pro	Ala	Phe	Arg	Val	Leu	Arg	Glu	Lys	Arg	Met	Leu	Asp	
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Phe	Arg	Ala	Pro	Ile	Thr	Val	Ile	Thr	Gly	Glu	Asn	Gly	Val	Gly	Lys	
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Ser	Thr	Leu	Leu	Glu	Ala	Ile	Ala	Ile	Asn	Ala	Gly	Phe	Asp	Thr	Ala	
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Gly	Gly	Glu	His	Thr	Gly	Lys	Phe	Lys	Pro	Ser	Asp	Asn	Pro	Leu	Gln	
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Thr	Val	Ala	Lys	Ala	His	Lys	Gly	Lys	Glu	Pro	Met	Arg	Gly	Tyr	Phe	
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Leu	Arg	Ala	Glu	Thr	His	Phe	Asn	Val	Ala	Ser	Gly	Tyr	Arg	Asp	Glu	
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Ala	Pro	Gly	Trp	Val	Asn	Leu	His	His	Met	Ser	His	Gly	Glu	Ser	Val	
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Asp	Glu	Pro	Glu	Ala	Gly	Leu	Ser	Phe	Ile	Arg	Gln	Met	Ala	Ile	Leu	
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Ala	Glu	Leu	Asn	Phe	Leu	Ala	Glu	Ser	Gly	Ala	Gln	Ile	Ile	Ile	Val	
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Thr	His	Ser	Pro	Val	Leu	Met	Ala	Ile	Pro	Gly	Ala	Glu	Ile	Trp	Glu	
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ttt	agt	gca	tcg	ggg	gaa	ctg	cat	cga	ggg	ttt	gat	ttt	gag	gtg	aca	739
Phe	Ser	Ala	Ser	Gly	Glu	Leu	His	Arg	Gly	Phe	Asp	Phe	Glu	Val	Thr	
				200					205					210		
acg	gcg	ttt	cga	gcg	cta	cgt	gac	ttc	ttt	gag	gat	ccg	gaa	gaa	att	787
Thr	Ala	Phe	Arg	Ala	Leu	Arg	Asp	Phe	Phe	Glu	Asp	Pro	Glu	Glu	Ile	
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gct	gag	tac	atg	atg	gac	gtc	atg	atg	gac	aac	aag	ggg	gag	tcc		832
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 <212> PRT  
 <213> Corynebacterium glutamicum

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 Asn Gly Val Gly Lys Ser Thr Leu Leu Glu Ala Ile Ala Ile Asn Ala  
             50                    55                    60  
 Gly Phe Asp Thr Ala Gly Gly Glu His Thr Gly Lys Phe Lys Pro Ser  
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 Asp Asn Pro Leu Gln Thr Val Ala Lys Ala His Lys Gly Lys Glu Pro  
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 Met Arg Gly Tyr Phe Leu Arg Ala Glu Thr His Phe Asn Val Ala Ser  
                     100                    105                    110  
 Gly Tyr Arg Asp Glu Ala Pro Gly Trp Val Asn Leu His His Met Ser  
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 His Gly Glu Ser Val Met His Ile Val Gln Asn Ala Phe Val Gly Lys  
             130                    135                    140  
 Gly Leu Tyr Leu Met Asp Glu Pro Glu Ala Gly Leu Ser Phe Ile Arg  
             145                    150                    155                    160  
 Gln Met Ala Ile Leu Ala Glu Leu Asn Phe Leu Ala Glu Ser Gly Ala  
                     165                    170                    175  
 Gln Ile Ile Ile Val Thr His Ser Pro Val Leu Met Ala Ile Pro Gly  
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 Ala Glu Ile Trp Glu Phe Ser Ala Ser Gly Glu Leu His Arg Gly Phe  
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 Asp Phe Glu Val Thr Thr Ala Phe Arg Ala Leu Arg Asp Phe Phe Glu  
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&lt;222&gt; (101)..(2197)

&lt;223&gt; RXA02731

&lt;400&gt; 103

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Glu His Pro Val Leu Ser His Ser Glu His Arg Pro Val Gly Glu Ile
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gag cgt agc gat gac aaa ttt gtt gtc gtt agt gaa ttt gag cct gcg 211
Glu Arg Ser Asp Asp Lys Phe Val Val Val Ser Glu Phe Glu Pro Ala
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ggg gac cag cct gcg gct att aaa gag ctc gat gag cgc ttg gat cgc 259
Gly Asp Gln Pro Ala Ala Ile Lys Glu Leu Asp Glu Arg Leu Asp Arg
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Gly Glu Arg Asp Val Val Leu Met Gly Ala Thr Gly Thr Gly Lys Ser
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gcg act gcg gcg tgg ttg atc gaa aag cag cag cgc ccc gct ttg gtg 355
Ala Thr Ala Ala Trp Leu Ile Glu Lys Gln Gln Arg Pro Ala Leu Val
                        70                        75                        80                        85

atg gcg ccg aat aag acg ctg gct gcg cag ttg gct aat gaa ttg cgg 403
Met Ala Pro Asn Lys Thr Leu Ala Ala Gln Leu Ala Asn Glu Leu Arg
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Gln Leu Leu Pro Asn Asn Ala Val Glu Tyr Phe Val Ser Tyr Tyr Asp
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Tyr Tyr Gln Pro Glu Ala Tyr Ile Ala Gln Thr Asp Thr Tyr Ile Glu
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Lys Asp Ser Ser Ile Asn Glu Asp Val Glu Arg Leu Arg His Ser Ala
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Thr Ser Ser Leu Leu Ser Arg Arg Asp Val Val Val Val Ser Ser Val
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tcg tgt att tat ggc ttg ggc act cca cag tct tat ctt gac cgt tcc 643
Ser Cys Ile Tyr Gly Leu Gly Thr Pro Gln Ser Tyr Leu Asp Arg Ser
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gtt gtg ttg aac gtg ggg gag gag atc gac cgc gat cgc ttt ttg cgc 691
Val Val Leu Asn Val Gly Glu Glu Ile Asp Arg Asp Arg Phe Leu Arg
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cta ttg gta gat att caa tac gaa cgc aat gat gtg ggc ttt act cgt 739

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Gly	Ala	Phe	Arg	Val	Lys	Gly	Asp	Thr	Val	Asp	Ile	Ile	Pro	Ala	Tyr	
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Glu	Glu	Leu	Ala	Val	Arg	Ile	Glu	Phe	Phe	Gly	Asp	Glu	Ile	Asp	Ala	
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Leu	Tyr	Tyr	Ile	His	Pro	Leu	Thr	Gly	Asp	Thr	Ile	Arg	Gln	Val	Asn	
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Glu	Ile	Arg	Ile	Phe	Pro	Ala	Thr	His	Tyr	Val	Ala	Gly	Pro	Glu	Arg	
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Ser	Gly	Ile	Glu	Asn	Tyr	Ser	Arg	His	Ile	Asp	Gly	Arg	Gly	Glu	Gly	
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Thr	Ala	Pro	Ala	Thr	Leu	Ile	Asp	Tyr	Phe	Pro	Glu	Asp	Phe	Leu	Thr	
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Ile	Ile	Asp	Glu	Ser	His	Val	Thr	Val	Pro	Gln	Ile	Gly	Gly	Met	Phe	
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Glu	Gly	Asp	Met	Ser	Arg	Lys	Arg	Asn	Leu	Val	Glu	Phe	Gly	Phe	Arg	
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Thr	Gly	Leu	Val	Asp	Pro	Lys	Val	Thr	Val	Lys	Pro	Thr	Lys	Gly	Gln	

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gat tac ctg ctg gaa aac ggc atc cgc gtg cgc tac ctg cac tca gat Asp Tyr Leu Leu Glu Asn Gly Ile Arg Val Arg Tyr Leu His Ser Asp 490 495 500			1603
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gaa tac gat gtg ttg gta ggt att aac ctg ctg cgt gag ggc ctt gac Glu Tyr Asp Val Leu Val Gly Ile Asn Leu Leu Arg Glu Gly Leu Asp 520 525 530			1699
ctg cca gaa gtc tct ctg gtt gcg att ctc gac gcc gac aag gaa ggc Leu Pro Glu Val Ser Leu Val Ala Ile Leu Asp Ala Asp Lys Glu Gly 535 540 545			1747
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2220

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 <213> Corynebacterium glutamicum

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 35 40 45  
 Glu Arg Leu Asp Arg Gly Glu Arg Asp Val Val Leu Met Gly Ala Thr  
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 Gly Thr Gly Lys Ser Ala Thr Ala Ala Trp Leu Ile Glu Lys Gln Gln  
 65 70 75 80  
 Arg Pro Ala Leu Val Met Ala Pro Asn Lys Thr Leu Ala Ala Gln Leu  
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 Ala Asn Glu Leu Arg Gln Leu Leu Pro Asn Asn Ala Val Glu Tyr Phe  
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 Val Ser Tyr Tyr Asp Tyr Tyr Gln Pro Glu Ala Tyr Ile Ala Gln Thr  
 115 120 125  
 Asp Thr Tyr Ile Glu Lys Asp Ser Ser Ile Asn Glu Asp Val Glu Arg  
 130 135 140  
 Leu Arg His Ser Ala Thr Ser Ser Leu Leu Ser Arg Arg Asp Val Val  
 145 150 155 160  
 Val Val Ser Ser Val Ser Cys Ile Tyr Gly Leu Gly Thr Pro Gln Ser  
 165 170 175  
 Tyr Leu Asp Arg Ser Val Val Leu Asn Val Gly Glu Glu Ile Asp Arg  
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 Asp Arg Phe Leu Arg Leu Leu Val Asp Ile Gln Tyr Glu Arg Asn Asp  
 195 200 205  
 Val Gly Phe Thr Arg Gly Ala Phe Arg Val Lys Gly Asp Thr Val Asp  
 210 215 220  
 Ile Ile Pro Ala Tyr Glu Glu Leu Ala Val Arg Ile Glu Phe Phe Gly  
 225 230 235 240  
 Asp Glu Ile Asp Ala Leu Tyr Tyr Ile His Pro Leu Thr Gly Asp Thr  
 245 250 255  
 Ile Arg Gln Val Asn Glu Ile Arg Ile Phe Pro Ala Thr His Tyr Val

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Gly	Arg	Gly	Glu	Gly	Thr	Ala	Pro	Ala	Thr	Leu	Ile	Asp	Tyr	Phe	Pro				
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Glu	Asp	Phe	Leu	Thr	Ile	Ile	Asp	Glu	Ser	His	Val	Thr	Val	Pro	Gln				
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Glu	Phe	Gly	Phe	Arg	Leu	Pro	Ser	Ala	Met	Asp	Asn	Arg	Pro	Leu	Thr				
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Trp	Glu	Glu	Phe	Asp	Glu	Arg	Arg	Gly	Gln	Thr	Val	Phe	Met	Ser	Ala				
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Thr	Pro	Gly	Lys	Phe	Glu	Ile	Ala	Ala	Ala	Asp	Gly	Glu	Phe	Val	Glu				
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Gln	Val	Ile	Arg	Pro	Thr	Gly	Leu	Val	Asp	Pro	Lys	Val	Thr	Val	Lys				
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Pro	Thr	Lys	Gly	Gln	Ile	Asp	Asp	Leu	Ile	His	Glu	Ile	Arg	Gln	Arg				
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Tyr	Leu	His	Ser	Asp	Ile	Asp	Thr	Leu	Gln	Arg	Val	Glu	Leu	Leu	Arg				
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Gln	Leu	Arg	Leu	Gly	Glu	Tyr	Asp	Val	Leu	Val	Gly	Ile	Asn	Leu	Leu				
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Arg	Glu	Gly	Leu	Asp	Leu	Pro	Glu	Val	Ser	Leu	Val	Ala	Ile	Leu	Asp				
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Ala	Asp	Lys	Glu	Gly	Phe	Leu	Arg	Ser	Thr	Thr	Ser	Leu	Ile	Gln	Thr				
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Asp	Lys	Ile	Thr	Asp	Ser	Met	Gln	Tyr	Ala	Ile	Glu	Glu	Thr	Asp	Arg				
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Arg Arg Glu Lys Gln Val Ala Tyr Asn Lys Glu His Gly Ile Asp Pro  
 595 600 605

Gln Pro Leu Arg Lys Lys Ile Ala Asp Ile Leu Asp Gln Val Tyr Asp  
 610 615 620

Asn Ser Ala Asp Gly Ala Gly Pro Ser Ala Ser Gly Asp Ala Ala Val  
 625 630 635 640

Val Ala Lys Pro Asp Val Ser Ser Met Pro Ala Lys Glu Val Gln Lys  
 645 650 655

Leu Ile Asp Asp Leu Ser Ala Gln Met Ala Ala Ala Ala Arg Glu Leu  
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Lys Phe Glu Leu Ala Gly Arg Leu Arg Asp Glu Ile Phe Glu Leu Lys  
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Lys Glu Leu Arg Gly Ile Lys Asp Ala Gly Ile  
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 <223> RXA00998

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 Met Thr Ser Arg Asp  
 1 5

gat caa ccc caa gat ctg ctt tcg ctt gca gaa ctt gcc gcc acc aga 163  
 Asp Gln Pro Gln Asp Leu Leu Ser Leu Ala Glu Leu Ala Ala Thr Arg  
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gct tta acc aca gac gaa ctt gaa gca ctc aac aac gcc aat tat ggc 211  
 Ala Leu Thr Thr Asp Glu Leu Glu Ala Leu Asn Asn Ala Asn Tyr Gly  
 25 30 35

ctc gac cgc aat ctg ggg ctg cgc tac acc acc atc gag ccc ggc cgg 259  
 Leu Asp Arg Asn Leu Gly Leu Arg Tyr Thr Thr Ile Glu Pro Gly Arg  
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gtg gtc agc gaa ctt cac gtg gca tcc aag cac ctg caa gtg gtg ggc 307  
 Val Val Ser Glu Leu His Val Ala Ser Lys His Leu Gln Val Val Gly  
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ttg gtc aac ggt ggt gtc tac gcc gcc atc gcc gaa tcc act gga tca 355  
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&lt;221&gt; CDS

&lt;222&gt; (101)..(559)

&lt;223&gt; RXN02386

&lt;400&gt; 107

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Glu	Asn	Tyr	Gln	Thr	Pro	Ala	Pro	Ser	Ser	Gln	Val	Val	Val	Ser	Val	
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gtg	ggg	cac	gtg	gct	aaa	ccc	ggc	ctg	gtc	acg	ctc	gct	gag	ggc	tcg	211
Val	Gly	His	Val	Ala	Lys	Pro	Gly	Leu	Val	Thr	Leu	Ala	Glu	Gly	Ser	
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Arg	Val	Ala	Asp	Ala	Leu	Ala	Ile	Ala	Gly	Ala	Leu	Pro	Asp	Ala	Asp	
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ctg	acg	gcg	ctc	aac	ttg	gcg	caa	ttg	ctt	gtc	gac	ggc	acc	cag	atc	307
Leu	Thr	Ala	Leu	Asn	Leu	Ala	Gln	Leu	Leu	Val	Asp	Gly	Thr	Gln	Ile	
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cat	gtt	tta	gct	atc	ggc	gag	gta	caa	cct	att	tcg	gtt	gat	gct	gct	355
His	Val	Leu	Ala	Ile	Gly	Glu	Val	Gln	Pro	Ile	Ser	Val	Asp	Ala	Ala	
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Asp	Leu	Val	Thr	Leu	Pro	Gly	Val	Gly	Glu	Lys	Thr	Ala	Gln	Ala	Ile	
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Leu	Gln	Val	Lys	Gly	Ile	Gly	Pro	Ser	Lys	Phe	Glu	Gln	Ile	Ser	Gly	
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Leu	Val	Ser	Pro				
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&lt;210&gt; 108

&lt;211&gt; 153

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 108

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Leu Pro Asp Ala Asp Leu Thr Ala Leu Asn Leu Ala Gln Leu Leu Val	50	55	60
Asp Gly Thr Gln Ile His Val Leu Ala Ile Gly Glu Val Gln Pro Ile	65	70	75
Ser Val Asp Ala Ala Ala Thr Ser Ala Ser Gly Leu Ile Ser Leu Asn	85	90	95
Thr Ala Thr Val Ala Asp Leu Val Thr Leu Pro Gly Val Gly Glu Lys	100	105	110
Thr Ala Gln Ala Ile Ile Asp Phe Arg Glu Ser Asn Gly Gly Phe Ser	115	120	125
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 Val Ser Val Val Gly  
 1 5  
 cac gtg gct aaa ccc ggc ctg gtc acg ctc gct gag ggc tcg cgg gtg 163  
 His Val Ala Lys Pro Gly Leu Val Thr Leu Ala Glu Gly Ser Arg Val  
 10 15 20  
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 Ala Asp Ala Leu Ala Ile Ala Gly Ala Leu Pro Asp Ala Asp Leu Thr  
 25 30 35  
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 Ala Leu Asn Leu Ala Gln Leu Leu Val Asp Gly Thr Gln Ile His Val  
 40 45 50  
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 Leu Ala Ile Gly Glu Val Gln Pro Ile Ser Val Asp Ala Ala Ala Thr

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Ser Ala Ser Gly Leu Ile Ser Leu Asn Thr Ala Thr Val Ala Asp Leu			
70	75	80	85
gtg acg ctg cct ggg gtg ggg gag aag aca gcg cag gcg atc att gac			403
Val Thr Leu Pro Gly Val Gly Glu Lys Thr Ala Gln Ala Ile Ile Asp			
	90	95	100
ttt cgg gag agc aac ggt ggg ttt agc acc gtg gag gat tta ctg cag			451
Phe Arg Glu Ser Asn Gly Gly Phe Ser Thr Val Glu Asp Leu Leu Gln			
	105	110	115
gtc aag ggg att ggg ccc tca aag ttt gag cag atc tct gga ttg gtg			499
Val Lys Gly Ile Gly Pro Ser Lys Phe Glu Gln Ile Ser Gly Leu Val			
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Ser Pro			
135			

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 35 40 45  
 Thr Gln Ile His Val Leu Ala Ile Gly Glu Val Gln Pro Ile Ser Val  
 50 55 60  
 Asp Ala Ala Ala Thr Ser Ala Ser Gly Leu Ile Ser Leu Asn Thr Ala  
 65 70 75 80  
 Thr Val Ala Asp Leu Val Thr Leu Pro Gly Val Gly Glu Lys Thr Ala  
 85 90 95  
 Gln Ala Ile Ile Asp Phe Arg Glu Ser Asn Gly Gly Phe Ser Thr Val  
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 Ile Ser Gly Leu Val Ser Pro  
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<210> 111  
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&lt;221&gt; CDS

&lt;222&gt; (101)..(1762)

&lt;223&gt; RXN02388

&lt;400&gt; 111

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				Met	Ile	Glu	Val	Arg	
				1				5	

ttg	ggt	ccc	gtg	gcg	gct	gtg	atg	tgg	atg	gct	gtc	gct	gcg	ttg	att	163
Leu	Val	Pro	Val	Ala	Ala	Val	Met	Trp	Met	Ala	Val	Ala	Ala	Leu	Ile	
			10					15						20		

atc	aat	ggt	tcg	tgg	gtg	ttg	tcg	gtg	ggg	att	gtt	ggc	atc	gcg	atc	211
Ile	Asn	Gly	Ser	Trp	Val	Leu	Ser	Val	Gly	Ile	Val	Gly	Ile	Ala	Ile	
			25					30					35			

att	gct	gct	tgt	gtg	ttt	aaa	cac	tgg	ggt	caa	gct	gtg	gtg	ata	gct	259
Ile	Ala	Ala	Cys	Val	Phe	Lys	His	Trp	Gly	Gln	Ala	Val	Val	Ile	Ala	
		40					45					50				

gca	ctg	ggc	gtt	ggt	gcc	gta	gtg	atg	gct	gcg	ttg	aga	atc	agc	agc	307
Ala	Leu	Gly	Val	Gly	Ala	Val	Val	Met	Ala	Ala	Leu	Arg	Ile	Ser	Ser	
	55					60					65					

gcg	aag	gca	ttt	gaa	gca	ccg	caa	acc	tgg	gtg	ggt	acc	gca	gaa	acc	355
Ala	Lys	Ala	Phe	Glu	Ala	Pro	Gln	Thr	Trp	Val	Gly	Thr	Ala	Glu	Thr	
	70				75					80					85	

atc	aag	ttt	tta	gac	agc	ggt	gat	caa	cta	atc	ggt	ttg	aga	gta	gaa	403
Ile	Lys	Phe	Leu	Asp	Ser	Gly	Asp	Gln	Leu	Ile	Gly	Leu	Arg	Val	Glu	
			90						95					100		

ggc	tat	cca	gcg	ccg	att	cca	gtg	ttt	tac	tct	ggt	agc	gac	acc	att	451
Gly	Tyr	Pro	Ala	Pro	Ile	Pro	Val	Phe	Tyr	Ser	Gly	Ser	Asp	Thr	Ile	
			105					110					115			

gag	aaa	gcc	tct	ctc	att	gca	gtg	tcc	ggt	cgg	att	aaa	cca	gat	agt	499
Glu	Lys	Ala	Ser	Leu	Ile	Ala	Val	Ser	Gly	Arg	Ile	Lys	Pro	Asp	Ser	
		120					125						130			

ttc	cct	ggg	gtg	ggt	gat	ctg	acc	att	tcc	act	gaa	gac	att	gat	cag	547
Phe	Pro	Gly	Val	Gly	Asp	Leu	Thr	Ile	Ser	Thr	Glu	Asp	Ile	Asp	Gln	
		135				140						145				

ttg	gaa	ccg	acc	act	ggt	tat	agc	gca	tgg	gtg	aac	cag	gtg	cgt	gac	595
Leu	Glu	Pro	Thr	Thr	Gly	Tyr	Ser	Ala	Trp	Val	Asn	Gln	Val	Arg	Asp	
	150				155					160				165		

ggg	ttt	tcc	caa	gcc	gtg	gaa	gaa	acc	gtg	ggg	gag	tct	tcc	cgt	gga	643
Gly	Phe	Ser	Gln	Ala	Val	Glu	Glu	Thr	Val	Gly	Glu	Ser	Ser	Arg	Gly	
			170						175					180		

ctg	att	cca	ggc	atg	gtg	ttg	ggg	gat	acg	cgg	ttg	cag	ggg	tca	att	691
Leu	Ile	Pro	Gly	Met	Val	Leu	Gly	Asp	Thr	Arg	Leu	Gln	Gly	Ser	Ile	
			185					190					195			

gaa gcc caa acc tat att gat acg ggg ttg tct cac ctg tca gct gtt	739
Glu Ala Gln Thr Tyr Ile Asp Thr Gly Leu Ser His Leu Ser Ala Val	
200 205 210	
agt gga agc aat gta gcc att gtg gtg tcc tct gtg gtg gtg ttg tcg	787
Ser Gly Ser Asn Val Ala Ile Val Val Ser Ser Val Val Val Leu Ser	
215 220 225	
tat ttt ctc acc gct ggg cca cgc atc agg gtg gtg gcg tca ttg ctg	835
Tyr Phe Leu Thr Ala Gly Pro Arg Ile Arg Val Val Ala Ser Leu Leu	
230 235 240 245	
tcc tta gtt att ttt gtc tcc ctc gtg ggg ttt gaa cca agt gtg ctt	883
Ser Leu Val Ile Phe Val Ser Leu Val Gly Phe Glu Pro Ser Val Leu	
250 255 260	
cgt gct tcg gtc aca ggc atc gtg ggg ctt ctg gca atc atc aac tct	931
Arg Ala Ser Val Thr Gly Ile Val Gly Leu Leu Ala Ile Ile Asn Ser	
265 270 275	
tct cgg atg gag ccg atg cat ggg ttg agt ctt tcg gtg att tgc tta	979
Ser Arg Met Glu Pro Met His Gly Leu Ser Leu Ser Val Ile Cys Leu	
280 285 290	
ctg ttt tat gat tcc aac ctg gcg gtg cat tac gga ttc tta ctc tcg	1027
Leu Phe Tyr Asp Ser Asn Leu Ala Val His Tyr Gly Phe Leu Leu Ser	
295 300 305	
tgt gca gca act gct ggc att gtg atg ctt caa cca ctg ctg tac cgt	1075
Cys Ala Ala Thr Ala Gly Ile Val Met Leu Gln Pro Leu Leu Tyr Arg	
310 315 320 325	
gcc atc ggt cca cca ctg gcg gtg tgg aaa gta cca gac atc gtg gtg	1123
Ala Ile Gly Pro Pro Leu Ala Val Trp Lys Val Pro Asp Ile Val Val	
330 335 340	
cgc gct ttc gcg gtg tcc att gcc gct gat ctg gtg acc atc ccg att	1171
Arg Ala Phe Ala Val Ser Ile Ala Ala Asp Leu Val Thr Ile Pro Ile	
345 350 355	
atc gct ctg atg gct cgc caa ata tcc ctc gtg gca gtg ctg gcc aac	1219
Ile Ala Leu Met Ala Arg Gln Ile Ser Leu Val Ala Val Leu Ala Asn	
360 365 370	
gtg ttg gtt gaa tta gct gtt cca ccc atc acg ttg ctt ggg ttg att	1267
Val Leu Val Glu Leu Ala Val Pro Pro Ile Thr Leu Leu Gly Leu Ile	
375 380 385	
gcc gtg ctg gca agc ctt ctt ccc tgg cca gtg gaa tac cca ctc ttg	1315
Ala Val Leu Ala Ser Leu Leu Pro Trp Pro Val Glu Tyr Pro Leu Leu	
390 395 400 405	
aaa atc att gag ccc ttc acc tgg tgg att cat cac gtg gcc aag tgg	1363
Lys Ile Ile Glu Pro Phe Thr Trp Trp Ile His His Val Ala Lys Trp	
410 415 420	
tgc caa caa tta ccc aat tcg acg ctg gaa ata agt gct ggt tgg gca	1411
Cys Gln Gln Leu Pro Asn Ser Thr Leu Glu Ile Ser Ala Gly Trp Ala	
425 430 435	
ggg att gcc tgg gcg tgt atg gca gcg gtg tgg gtg gtg gtg att atc	1459

Gly Ile Ala Trp Ala Cys Met Ala Ala Val Trp Val Val Val Ile Ile  
 440 445 450

tac aaa gga tat gtg cgc acc ctt gca gtg tgt tgt gtc tgc ttc ttt 1507  
 Tyr Lys Gly Tyr Val Arg Thr Leu Ala Val Cys Cys Val Cys Phe Phe  
 455 460 465

ctt ttc ggc gcg tgg aat aac aga ctg cca gcc caa ata gat ccg aca 1555  
 Leu Phe Gly Ala Trp Asn Asn Arg Leu Pro Ala Gln Ile Asp Pro Thr  
 470 475 480 485

gag ctg cgg ttt gtc atc atc gcc gat gat tct gag ctc act gat gtg 1603  
 Glu Leu Arg Phe Val Ile Ile Ala Asp Asp Ser Glu Leu Thr Asp Val  
 490 495 500

ccc gaa cat gca gaa ttg atc atc gtg gaa gac ccc cac ggc agc atg 1651  
 Pro Glu His Ala Glu Leu Ile Ile Val Glu Asp Pro His Gly Ser Met  
 505 510 515

tcc gat cgc ccc atc gtc acc aga gaa gga atc cct gtg ctg tat cca 1699  
 Ser Asp Arg Pro Ile Val Thr Arg Glu Gly Ile Pro Val Leu Tyr Pro  
 520 525 530

tac cgc gat ggg gag gtc agc ctt cat att gat ggc acc cag cat gca 1747  
 Tyr Arg Asp Gly Glu Val Ser Leu His Ile Asp Gly Thr Gln His Ala  
 535 540 545

gcg gac ggg aga ttt taacgacact tgtggcacga tgg 1785  
 Ala Asp Gly Arg Phe  
 550

&lt;210&gt; 112

&lt;211&gt; 554

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 112

Met Ile Glu Val Arg Leu Val Pro Val Ala Ala Val Met Trp Met Ala  
 1 5 10 15

Val Ala Ala Leu Ile Ile Asn Gly Ser Trp Val Leu Ser Val Gly Ile  
 20 25 30

Val Gly Ile Ala Ile Ile Ala Ala Cys Val Phe Lys His Trp Gly Gln  
 35 40 45

Ala Val Val Ile Ala Ala Leu Gly Val Gly Ala Val Val Met Ala Ala  
 50 55 60

Leu Arg Ile Ser Ser Ala Lys Ala Phe Glu Ala Pro Gln Thr Trp Val  
 65 70 75 80

Gly Thr Ala Glu Thr Ile Lys Phe Leu Asp Ser Gly Asp Gln Leu Ile  
 85 90 95

Gly Leu Arg Val Glu Gly Tyr Pro Ala Pro Ile Pro Val Phe Tyr Ser  
 100 105 110

Gly Ser Asp Thr Ile Glu Lys Ala Ser Leu Ile Ala Val Ser Gly Arg  
 115 120 125

Ile	Lys	Pro	Asp	Ser	Phe	Pro	Gly	Val	Gly	Asp	Leu	Thr	Ile	Ser	Thr	130	135	140	
Glu	Asp	Ile	Asp	Gln	Leu	Glu	Pro	Thr	Thr	Gly	Tyr	Ser	Ala	Trp	Val	145	150	155	160
Asn	Gln	Val	Arg	Asp	Gly	Phe	Ser	Gln	Ala	Val	Glu	Glu	Thr	Val	Gly	165	170	175	
Glu	Ser	Ser	Arg	Gly	Leu	Ile	Pro	Gly	Met	Val	Leu	Gly	Asp	Thr	Arg	180	185	190	
Leu	Gln	Gly	Ser	Ile	Glu	Ala	Gln	Thr	Tyr	Ile	Asp	Thr	Gly	Leu	Ser	195	200	205	
His	Leu	Ser	Ala	Val	Ser	Gly	Ser	Asn	Val	Ala	Ile	Val	Val	Ser	Ser	210	215	220	
Val	Val	Val	Leu	Ser	Tyr	Phe	Leu	Thr	Ala	Gly	Pro	Arg	Ile	Arg	Val	225	230	235	240
Val	Ala	Ser	Leu	Leu	Ser	Leu	Val	Ile	Phe	Val	Ser	Leu	Val	Gly	Phe	245	250	255	
Glu	Pro	Ser	Val	Leu	Arg	Ala	Ser	Val	Thr	Gly	Ile	Val	Gly	Leu	Leu	260	265	270	
Ala	Ile	Ile	Asn	Ser	Ser	Arg	Met	Glu	Pro	Met	His	Gly	Leu	Ser	Leu	275	280	285	
Ser	Val	Ile	Cys	Leu	Leu	Phe	Tyr	Asp	Ser	Asn	Leu	Ala	Val	His	Tyr	290	295	300	
Gly	Phe	Leu	Leu	Ser	Cys	Ala	Ala	Thr	Ala	Gly	Ile	Val	Met	Leu	Gln	305	310	315	320
Pro	Leu	Leu	Tyr	Arg	Ala	Ile	Gly	Pro	Pro	Leu	Ala	Val	Trp	Lys	Val	325	330	335	
Pro	Asp	Ile	Val	Val	Arg	Ala	Phe	Ala	Val	Ser	Ile	Ala	Ala	Asp	Leu	340	345	350	
Val	Thr	Ile	Pro	Ile	Ile	Ala	Leu	Met	Ala	Arg	Gln	Ile	Ser	Leu	Val	355	360	365	
Ala	Val	Leu	Ala	Asn	Val	Leu	Val	Glu	Leu	Ala	Val	Pro	Pro	Ile	Thr	370	375	380	
Leu	Leu	Gly	Leu	Ile	Ala	Val	Leu	Ala	Ser	Leu	Leu	Pro	Trp	Pro	Val	385	390	395	400
Glu	Tyr	Pro	Leu	Leu	Lys	Ile	Ile	Glu	Pro	Phe	Thr	Trp	Trp	Ile	His	405	410	415	
His	Val	Ala	Lys	Trp	Cys	Gln	Gln	Leu	Pro	Asn	Ser	Thr	Leu	Glu	Ile	420	425	430	
Ser	Ala	Gly	Trp	Ala	Gly	Ile	Ala	Trp	Ala	Cys	Met	Ala	Ala	Val	Trp	435	440	445	

Val Val Val Ile Ile Tyr Lys Gly Tyr Val Arg Thr Leu Ala Val Cys  
 450 455 460

Cys Val Cys Phe Phe Leu Phe Gly Ala Trp Asn Asn Arg Leu Pro Ala  
 465 470 475 480

Gln Ile Asp Pro Thr Glu Leu Arg Phe Val Ile Ile Ala Asp Asp Ser  
 485 490 495

Glu Leu Thr Asp Val Pro Glu His Ala Glu Leu Ile Ile Val Glu Asp  
 500 505 510

Pro His Gly Ser Met Ser Asp Arg Pro Ile Val Thr Arg Glu Gly Ile  
 515 520 525

Pro Val Leu Tyr Pro Tyr Arg Asp Gly Glu Val Ser Leu His Ile Asp  
 530 535 540

Gly Thr Gln His Ala Ala Asp Gly Arg Phe  
 545 550

<210> 113  
 <211> 871  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(871)  
 <223> FRXA02385

<400> 113  
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ggccctcaaa gtttgagcag atctctggat tgggtgtcccc atg att gag gtg cgt 115  
 Met Ile Glu Val Arg  
 1 5

ttg gtt ccc gtg gcg gct gtg atg tgg atg gct gtc gct gcg ttg att 163  
 Leu Val Pro Val Ala Ala Val Met Trp Met Ala Val Ala Ala Leu Ile  
 10 15 20

atc aat ggt tcg tgg gtg ttg tcg gtg ggg att gtt ggc atc gcg atc 211  
 Ile Asn Gly Ser Trp Val Leu Ser Val Gly Ile Val Gly Ile Ala Ile  
 25 30 35

att gct gct tgt gtg ttt aaa cac tgg ggt caa gct gtg gtg ata gct 259  
 Ile Ala Ala Cys Val Phe Lys His Trp Gly Gln Ala Val Val Ile Ala  
 40 45 50

gca ctg ggc gtt ggt gcc gta gtg atg gct gcg ttg aga atc agc agc 307  
 Ala Leu Gly Val Gly Ala Val Val Met Ala Ala Leu Arg Ile Ser Ser  
 55 60 65

gcg aag gca ttt gaa gca ccg caa acc tgg gtg ggt acc gca gaa acc 355  
 Ala Lys Ala Phe Glu Ala Pro Gln Thr Trp Val Gly Thr Ala Glu Thr  
 70 75 80 85

atc aag ttt tta gac agc ggt gat caa cta atc ggt ttg aga gta gaa 403  
 Ile Lys Phe Leu Asp Ser Gly Asp Gln Leu Ile Gly Leu Arg Val Glu

90										95					100					
ggc	tat	cca	gcg	ccg	att	cca	gtg	ttt	tac	tct	ggt	agc	gac	acc	att	451				
Gly	Tyr	Pro	Ala	Pro	Ile	Pro	Val	Phe	Tyr	Ser	Gly	Ser	Asp	Thr	Ile					
			105					110					115							
gag	aaa	gcc	tct	ctc	att	gca	gtg	tcc	ggt	cgg	att	aaa	cca	gat	agt	499				
Glu	Lys	Ala	Ser	Leu	Ile	Ala	Val	Ser	Gly	Arg	Ile	Lys	Pro	Asp	Ser					
		120					125					130								
ttc	cct	ggg	gtg	ggt	gat	ctg	acc	att	tcc	act	gaa	gac	att	gat	cag	547				
Phe	Pro	Gly	Val	Gly	Asp	Leu	Thr	Ile	Ser	Thr	Glu	Asp	Ile	Asp	Gln					
	135					140					145									
ttg	gaa	ccg	acc	act	ggt	tat	agc	gca	tgg	gtg	aac	cag	gtg	cgt	gac	595				
Leu	Glu	Pro	Thr	Thr	Gly	Tyr	Ser	Ala	Trp	Val	Asn	Gln	Val	Arg	Asp					
150					155				160						165					
ggg	ttt	tcc	caa	gcc	gtg	gaa	gaa	acc	gtg	ggg	gag	tct	tcc	cgt	gga	643				
Gly	Phe	Ser	Gln	Ala	Val	Glu	Glu	Thr	Val	Gly	Glu	Ser	Ser	Arg	Gly					
			170					175						180						
ctg	att	cca	ggc	atg	gtg	ttg	ggg	gat	acg	cgg	ttg	cag	ggg	tca	att	691				
Leu	Ile	Pro	Gly	Met	Val	Leu	Gly	Asp	Thr	Arg	Leu	Gln	Gly	Ser	Ile					
			185					190					195							
gaa	gcc	caa	acc	tat	att	gat	acg	ggg	ttg	tct	cac	ctg	tca	gct	gtt	739				
Glu	Ala	Gln	Thr	Tyr	Ile	Asp	Thr	Gly	Leu	Ser	His	Leu	Ser	Ala	Val					
		200					205					210								
agt	gga	agc	aat	gta	gcc	att	gtg	gtg	tcc	tct	gtg	gtg	gtg	ttg	tcg	787				
Ser	Gly	Ser	Asn	Val	Ala	Ile	Val	Val	Ser	Ser	Val	Val	Val	Leu	Ser					
	215					220					225									
tat	ttt	ctc	acc	gct	ggg	cca	cgc	atc	agg	gtg	gtg	gcg	tca	ttg	ctg	835				
Tyr	Phe	Leu	Thr	Ala	Gly	Pro	Arg	Ile	Arg	Val	Val	Ala	Ser	Leu	Leu					
230					235				240						245					
tcc	tta	ggt	att	ttt	gtc	tcc	ctc	gtg	ggg	ttt	gaa					871				
Ser	Leu	Gly	Ile	Phe	Val	Ser	Leu	Val	Gly	Phe	Glu									
				250					255											

&lt;210&gt; 114

&lt;211&gt; 257

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 114

Met	Ile	Glu	Val	Arg	Leu	Val	Pro	Val	Ala	Ala	Val	Met	Trp	Met	Ala
1				5					10					15	

Val	Ala	Ala	Leu	Ile	Ile	Asn	Gly	Ser	Trp	Val	Leu	Ser	Val	Gly	Ile
			20					25					30		

Val	Gly	Ile	Ala	Ile	Ile	Ala	Ala	Cys	Val	Phe	Lys	His	Trp	Gly	Gln
	35						40					45			

Ala	Val	Val	Ile	Ala	Ala	Leu	Gly	Val	Gly	Ala	Val	Val	Met	Ala	Ala
	50					55					60				

Leu Arg Ile Ser Ser Ala Lys Ala Phe Glu Ala Pro Gln Thr Trp Val  
 65 70 75 80  
 Gly Thr Ala Glu Thr Ile Lys Phe Leu Asp Ser Gly Asp Gln Leu Ile  
 85 90 95  
 Gly Leu Arg Val Glu Gly Tyr Pro Ala Pro Ile Pro Val Phe Tyr Ser  
 100 105 110  
 Gly Ser Asp Thr Ile Glu Lys Ala Ser Leu Ile Ala Val Ser Gly Arg  
 115 120 125  
 Ile Lys Pro Asp Ser Phe Pro Gly Val Gly Asp Leu Thr Ile Ser Thr  
 130 135 140  
 Glu Asp Ile Asp Gln Leu Glu Pro Thr Thr Gly Tyr Ser Ala Trp Val  
 145 150 155 160  
 Asn Gln Val Arg Asp Gly Phe Ser Gln Ala Val Glu Glu Thr Val Gly  
 165 170 175  
 Glu Ser Ser Arg Gly Leu Ile Pro Gly Met Val Leu Gly Asp Thr Arg  
 180 185 190  
 Leu Gln Gly Ser Ile Glu Ala Gln Thr Tyr Ile Asp Thr Gly Leu Ser  
 195 200 205  
 His Leu Ser Ala Val Ser Gly Ser Asn Val Ala Ile Val Val Ser Ser  
 210 215 220  
 Val Val Val Leu Ser Tyr Phe Leu Thr Ala Gly Pro Arg Ile Arg Val  
 225 230 235 240  
 Val Ala Ser Leu Leu Ser Leu Gly Ile Phe Val Ser Leu Val Gly Phe  
 245 250 255  
 Glu

<210> 115  
 <211> 869  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(846)  
 <223> FRXA02388

<400> 115  
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 tcg gtg att tgc tta ctg ttt tat gat tcc aac ctg gcg gtg cat tac 96  
 Ser Val Ile Cys Leu Leu Phe Tyr Asp Ser Asn Leu Ala Val His Tyr  
 20 25 30  
 gga ttc tta ctc tcg tgt gca gca act gct ggc att gtg atg ctt caa 144  
 Gly Phe Leu Leu Ser Cys Ala Ala Thr Ala Gly Ile Val Met Leu Gln

35								40				45								
cca	ctg	ctg	tac	cgt	gcc	atc	ggg	cca	cca	ctg	gcg	gtg	tgg	aaa	gta	192				
Pro	Leu	Leu	Tyr	Arg	Ala	Ile	Gly	Pro	Pro	Leu	Ala	Val	Trp	Lys	Val					
50				55				60												
cca	gac	atc	gtg	gtg	cgc	gct	ttc	gcg	gtg	tcc	att	gcc	gct	gat	ctg	240				
Pro	Asp	Ile	Val	Val	Arg	Ala	Phe	Ala	Val	Ser	Ile	Ala	Ala	Asp	Leu	80				
				70				75												
gtg	acc	atc	cgc	att	atc	gct	ctg	atg	gct	cgc	caa	ata	tcc	ctc	gtg	288				
Val	Thr	Ile	Pro	Ile	Ile	Ala	Leu	Met	Ala	Arg	Gln	Ile	Ser	Leu	Val					
				85				90				95								
gca	gtg	ctg	gcc	aac	gtg	ttg	gtt	gaa	tta	gct	gtt	cca	ccc	atc	acg	336				
Ala	Val	Leu	Ala	Asn	Val	Leu	Val	Glu	Leu	Ala	Val	Pro	Pro	Ile	Thr					
				100				105				110								
ttg	ctt	ggg	ttg	att	gcc	gtg	ctg	gca	agc	ctt	ctt	ccc	tgg	cca	gtg	384				
Leu	Leu	Gly	Leu	Ile	Ala	Val	Leu	Ala	Ser	Leu	Leu	Pro	Trp	Pro	Val					
				115				120				125								
gaa	tac	cca	ctc	ttg	aaa	atc	att	gag	ccc	ttc	acc	tgg	tgg	att	cat	432				
Glu	Tyr	Pro	Leu	Leu	Lys	Ile	Ile	Glu	Pro	Phe	Thr	Trp	Trp	Ile	His					
				130				135				140								
cac	gtg	gcc	aag	tgg	tgc	caa	caa	tta	ccc	aat	tgc	acg	ctg	gaa	ata	480				
His	Val	Ala	Lys	Trp	Cys	Gln	Gln	Leu	Pro	Asn	Ser	Thr	Leu	Glu	Ile					
				145				150				155				160				
agt	gct	ggg	tgg	gca	ggg	att	gcc	tgg	gcg	tgt	atg	gca	gcg	gtg	tgg	528				
Ser	Ala	Gly	Trp	Ala	Gly	Ile	Ala	Trp	Ala	Cys	Met	Ala	Ala	Val	Trp					
				165				170				175								
gtg	gtg	gtg	att	atc	tac	aaa	gga	tat	gtg	cgc	acc	ctt	gca	gtg	tgt	576				
Val	Val	Val	Ile	Ile	Tyr	Lys	Gly	Tyr	Val	Arg	Thr	Leu	Ala	Val	Cys					
				180				185				190								
tgt	gtc	tgc	ttc	ttt	ctt	ttc	ggc	gcg	tgg	aat	aac	aga	ctg	cca	gcc	624				
Cys	Val	Cys	Phe	Phe	Leu	Phe	Gly	Ala	Trp	Asn	Asn	Arg	Leu	Pro	Ala					
				195				200				205								
caa	ata	gat	cgc	aca	gag	ctg	cgc	ttt	gtc	atc	atc	gcc	gat	gat	tct	672				
Gln	Ile	Asp	Pro	Thr	Glu	Leu	Arg	Phe	Val	Ile	Ile	Ala	Asp	Asp	Ser					
				210				215				220								
gag	ctc	act	gat	gtg	ccc	gaa	cat	gca	gaa	ttg	atc	atc	gtg	gaa	gac	720				
Glu	Leu	Thr	Asp	Val	Pro	Glu	His	Ala	Glu	Leu	Ile	Ile	Val	Glu	Asp					
				225				230				235				240				
ccc	cac	ggc	agc	atg	tcc	gat	cgc	ccc	atc	gtc	acc	aga	gaa	gga	atc	768				
Pro	His	Gly	Ser	Met	Ser	Asp	Arg	Pro	Ile	Val	Thr	Arg	Glu	Gly	Ile					
				245				250				255								
cct	gtg	ctg	tat	cca	tac	cgc	gat	ggg	gag	gtc	agc	ctt	cat	att	gat	816				
Pro	Val	Leu	Tyr	Pro	Tyr	Arg	Asp	Gly	Glu	Val	Ser	Leu	His	Ile	Asp					

&lt;210&gt; 116

&lt;211&gt; 282

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 116

Ala Ile Ile Asn Ser Ser Arg Met Glu Pro Met His Gly Leu Ser Leu  
 1 5 10 15

Ser Val Ile Cys Leu Leu Phe Tyr Asp Ser Asn Leu Ala Val His Tyr  
 20 25 30

Gly Phe Leu Leu Ser Cys Ala Ala Thr Ala Gly Ile Val Met Leu Gln  
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Pro Leu Leu Tyr Arg Ala Ile Gly Pro Pro Leu Ala Val Trp Lys Val  
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Pro Asp Ile Val Val Arg Ala Phe Ala Val Ser Ile Ala Ala Asp Leu  
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Val Thr Ile Pro Ile Ile Ala Leu Met Ala Arg Gln Ile Ser Leu Val  
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Ala Val Leu Ala Asn Val Leu Val Glu Leu Ala Val Pro Pro Ile Thr  
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Leu Leu Gly Leu Ile Ala Val Leu Ala Ser Leu Leu Pro Trp Pro Val  
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Glu Tyr Pro Leu Leu Lys Ile Ile Glu Pro Phe Thr Trp Trp Ile His  
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His Val Ala Lys Trp Cys Gln Gln Leu Pro Asn Ser Thr Leu Glu Ile  
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Ser Ala Gly Trp Ala Gly Ile Ala Trp Ala Cys Met Ala Ala Val Trp  
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Val Val Val Ile Ile Tyr Lys Gly Tyr Val Arg Thr Leu Ala Val Cys  
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Cys Val Cys Phe Phe Leu Phe Gly Ala Trp Asn Asn Arg Leu Pro Ala  
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Gln Ile Asp Pro Thr Glu Leu Arg Phe Val Ile Ile Ala Asp Asp Ser  
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Glu Leu Thr Asp Val Pro Glu His Ala Glu Leu Ile Ile Val Glu Asp  
 225 230 235 240

Pro His Gly Ser Met Ser Asp Arg Pro Ile Val Thr Arg Glu Gly Ile  
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Pro Val Leu Tyr Pro Tyr Arg Asp Gly Glu Val Ser Leu His Ile Asp  
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Gly Thr Gln His Ala Ala Asp Gly Arg Phe  
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<223> RXA01975
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Leu Ser His His Thr 5																
cac ctc aat aac tac atc acg agc ttg agt gat aac gct gat ctc cgt 163																
His Leu Asn Asn Tyr Ile Thr Ser Leu Ser Asp Asn Ala Asp Leu Arg 20																
gaa aaa gtc acc gca acc gta gac gct ttc cgc cat acc gtc atg gat 211																
Glu Lys Val Thr Ala Thr Val Asp Ala Phe Arg His Thr Val Met Asp 35																
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Asp Phe Asp Tyr Ile Ser Asp Gln Gln Val Leu Leu Tyr Gly Asp Val 50																
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Gln Ser Gly Lys Thr Ser His Met Leu Gly Ile Ile Ala Asp Cys Leu 65																
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Ser Leu Thr Pro Arg Lys Ser Ile Val Val Val Gly Lys Ile Pro Ala 130																
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Gly His Pro Val Leu Ile Ile Asp Asp Glu Ala Asp Ala Thr Ser Leu 165																
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Asn Thr Lys Val Asn Gln Ser Asp Val Ser Thr Ile Asn His Gln Leu																

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Thr	Ser	Ile	Arg	Asp	Leu	Ala	Thr	Gly	Cys	Ile	Tyr	Leu	Gln	Val	Thr	
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Gln	Leu	Phe	Phe	Ser	Glu	Leu	Asn	Asn	Pro	Tyr	Leu	Arg	Leu	Phe	Ala	
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Tyr	Leu	Leu	Thr	Ala	Ala	Leu	Phe	Lys	Leu	Arg	Gly	Glu	Ser	Leu	Cys	
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Thr	Met	Leu	Ile	His	Pro	Ser	His	Thr	Ala	Ser	Ser	His	Arg	Asp	Phe	
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Gln	Thr	Asp	Ser	Asn	Leu	Pro	Pro	Leu	Arg	Lys	Ile	Leu	Asn	Ile	Leu	
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Gly	Gly	Met	Glu	Asp	Asp	Phe	Ser	Ile	His	Ile	Val	Asn	Ser	Asp	Asn	
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Pro	Thr	Val	Glu	Glu	Asp	Trp	Ala	Asp	Gly	Tyr	Asn	Ile	Ile	Val	Gly	
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Phe	Tyr	Val	Arg	Glu	Ser	Lys	Arg	Pro	Gln	Ala	Asp	Thr	Leu	Trp	Gln	
390					395					400					405	
cac	gcc	cgc	atg	ttt	ggc	tac	aaa	cgc	cac	aaa	gac	acc	atg	cgt	gtg	1363
His	Ala	Arg	Met	Phe	Gly	Tyr	Lys	Arg	His	Lys	Asp	Thr	Met	Arg	Val	
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Phe Met Pro Ala Thr Ile Ala Gln Thr Phe Gln Glu Val Tyr Leu Gly	
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Asn Glu Ala Ile Lys Asn Gln Leu Asp His Gly Thr His Ile Asn Asp	
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att cgg gtc att tta ggt gat ggc gtc gca cct act cgt gcc aat gtt	1507
Ile Arg Val Ile Leu Gly Asp Gly Val Ala Pro Thr Arg Ala Asn Val	
455 460 465	
ctc gac aaa cgc aaa gtt gga aac ctc agc ggt ggc gtc aac tac ttt	1555
Leu Asp Lys Arg Lys Val Gly Asn Leu Ser Gly Gly Val Asn Tyr Phe	
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Ala Ala Asp Pro Arg Ile Lys Asn Val Glu Ala Leu Asp Lys Lys Leu	
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Leu Ala Tyr Leu Asp Lys His Gly Glu Asp Ser Thr Ile Gly Met Arg	
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gcg ata atc acc att ctc aac gcc ttt act gta gac ccc aac gat ctc	1699
Ala Ile Ile Thr Ile Leu Asn Ala Phe Thr Val Asp Pro Asn Asp Leu	
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Asp Leu Ala Thr Phe Lys Ala Ala Leu Leu Asp Phe Glu Arg Asn Gln	
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Pro His Leu Thr Ala Arg Met Val Leu Arg Thr Asn Arg Lys Val Asn	
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&lt;210&gt; 118

&lt;211&gt; 632

&lt;212&gt; PRT

<213> Corynebacterium glutamicum

<400> 118

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Leu	Tyr	Gly	Asp	Val	Gln	Ser	Gly	Lys	Thr	Ser	His	Met	Leu	Gly	Ile	50		55		60		
Ile	Ala	Asp	Cys	Leu	Asp	Ser	Thr	Phe	His	Thr	Ile	Val	Ile	Leu	Thr	65		70		75		80
Ser	Pro	Asn	Thr	Arg	Leu	Val	Gln	Gln	Thr	Tyr	Asp	Arg	Val	Ala	Gln		85		90		95	
Ala	Phe	Pro	Asp	Thr	Leu	Val	Cys	Asp	Arg	Asp	Gly	Tyr	Asn	Asp	Phe		100		105		110	
Arg	Ala	Asn	Gln	Lys	Ser	Leu	Thr	Pro	Arg	Lys	Ser	Ile	Val	Val	Val	115		120		125		
Gly	Lys	Ile	Pro	Ala	Val	Leu	Gly	Asn	Trp	Leu	Arg	Val	Phe	Asn	Asp	130		135		140		
Ser	Gly	Ala	Leu	Ser	Gly	His	Pro	Val	Leu	Ile	Ile	Asp	Asp	Glu	Ala	145		150		155		160
Asp	Ala	Thr	Ser	Leu	Asn	Thr	Lys	Val	Asn	Gln	Ser	Asp	Val	Ser	Thr		165		170		175	
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Tyr	Leu	Gln	Val	Thr	Gly	Thr	Pro	Gln	Ala	Val	Leu	Leu	Gln	Ser	Asp	195		200		205		
Asp	Ser	Asn	Trp	Ala	Ala	Glu	His	Val	Leu	His	Phe	Ala	Pro	Gly	Glu	210		215		220		
Ser	Tyr	Ile	Gly	Gly	Gln	Leu	Phe	Phe	Ser	Glu	Leu	Asn	Asn	Pro	Tyr	225		230		235		240
Leu	Arg	Leu	Phe	Ala	Asn	Thr	Gln	Phe	Asp	Glu	Asp	Ser	Arg	Phe	Ser		245		250		255	
Asp	Ala	Ile	Tyr	Thr	Tyr	Leu	Leu	Thr	Ala	Ala	Leu	Phe	Lys	Leu	Arg	260		265		270		
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Ser	His	Arg	Asp	Phe	Ala	Gln	Glu	Ala	Arg	Leu	Gln	Leu	Thr	Phe	Ala	290		295		300		
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Tyr	Glu	Gln	Leu	Ala	Gln	Thr	Asp	Ser	Asn	Leu	Pro	Pro	Leu	Arg	Lys			
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Phe	Glu	Arg	Asn	Gln	Pro	His	Leu	Thr	Ala	Arg	Met	Val	Leu	Arg	Thr			
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Gln	Ala	Leu	Ser	Arg	Ala	Glu	Val	Ala	His	Pro	Leu	Leu	Ile	Leu	Tyr			
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Arg	Ile	Glu	Gly	Val	Asn	Asp	Ala	Ala	Ala	Gln	Arg	Gly	Glu	Pro	Thr			
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Trp	Ser	Ser	Asp	Pro	Ile	Trp	Val	Pro	Asn	Ile	Lys	Leu	Pro	Gly	Gln			
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Met	Phe	Tyr	Pro	Val	Trp	Phe	Asp	Glu	Ser	Thr	Gly	Arg	Leu	Ser	His					
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Pro	Thr	Arg	Ala	Ala	Pro	Arg	Arg	Ser	Ile	Leu	Asp	Tyr	Ala	Leu	His					
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Pro	His	Leu																		
		280																		

&lt;210&gt; 120

&lt;211&gt; 280

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 120

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Pro	Phe	His	Thr	Val	Val	Asn	Ala	Glu	Asn	Tyr	His	Ala	Leu	Glu	Met
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Leu	Thr	Tyr	Thr	His	Arg	His	Ser	Ile	Asp	Ala	Ile	Tyr	Ile	Asp	Pro
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Pro	Tyr	Asn	Thr	Gly	Ala	Arg	Asp	Trp	Lys	Tyr	Asp	Asn	Asp	Tyr	Val
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Ala	Ser	Asp	Asp	Asp	Tyr	Arg	His	Ser	Lys	Trp	Leu	Ala	Phe	Met	Glu
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Arg	Arg	Leu	Lys	Ile	Cys	Arg	Glu	Leu	Met	Arg	Ser	Asp	Ala	Thr	Leu
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Val	Ala	Pro	Ile	Asp	Glu	His	Glu	Val	Asn	Arg	Leu	Gly	Val	Leu	Leu
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 130 135 140  
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 Arg Pro Arg Trp Lys Gly Leu Leu Arg Ser Gly Asp Asp Ser Leu Arg  
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 Ala Asp Arg Lys Asp Met Phe Tyr Pro Val Trp Phe Asp Glu Ser Thr  
 210 215 220  
 Gly Arg Leu Ser His Ala Gly Glu Ala Leu Pro Leu Asp Glu Thr Pro  
 225 230 235 240  
 Asp Phe Ser Pro Gln Asp Gly Leu Thr Pro Ile Trp Pro Ile Arg Arg  
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 Asp Met Lys Glu Gly Pro Thr Arg Ala Ala Pro Arg Arg Ser Ile Leu  
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 Asp Tyr Ala Leu His Pro His Leu  
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&lt;210&gt; 121

&lt;211&gt; 441

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(418)

&lt;223&gt; RXA02236

&lt;400&gt; 121

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 Leu Thr Asp Glu Gln Arg Lys Ala Ala Leu Ala Lys Ala Ala Glu Ala  
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 Arg Lys Ala Arg Ala Glu Leu Lys Glu Asn Leu Lys Arg Gly Asn Thr  
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 aac ctc agg gaa gtt ctg gac aag gct gag tct gac gag atc atc ggc 259  
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Val Leu Ile Val Gly
1 5
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 Ile Arg Arg Asp Thr Gly Phe Asp Phe Lys His Pro Ala Pro Thr His  
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ggc cct cgc ggt gac atg ccg tat aag act gcc ggc gaa gcg ctc aaa 211  
 Gly Pro Arg Gly Asp Met Pro Tyr Lys Thr Ala Gly Glu Ala Leu Lys  
                     25                    30                    35

ggc gtg aag gat gtc ccc aca aac aac aac cac atg aag atc atg cct 259  
 Gly Val Lys Asp Val Pro Thr Asn Asn Asn His Met Lys Ile Met Pro  
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 Arg Thr Val Glu Val Leu Lys Arg Ile Pro Glu Gly Glu Asn Phe Thr  
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gtt tac cgt cgc ttg cac cgt gat gag cca tcc aaa acc ctt atc gcc 403  
 Val Tyr Arg Arg Leu His Arg Asp Glu Pro Ser Lys Thr Leu Ile Ala  
                     90                    95                    100

ggt ggc ggc ggg ggt aca tgg gga tac cat tat gaa aaa aat cga gca 451  
 Gly Gly Gly Gly Gly Thr Trp Gly Tyr His Tyr Glu Lys Asn Arg Ala  
                     105                    110                    115

ttg acc aac cgc gag cgg gct aga att caa tcg ttc ccc gat gac ttt 499  
 Leu Thr Asn Arg Glu Arg Ala Arg Ile Gln Ser Phe Pro Asp Asp Phe  
                     120                    125                    130

gag ttt ttg gga tca aac acc gaa gtc cgc cgc caa atc ggt aat gct 547  
 Glu Phe Leu Gly Ser Asn Thr Glu Val Arg Arg Gln Ile Gly Asn Ala  
                     135                    140                    145

gtt cct cct gta ggt atg cac gct gtg ggt gag cga ctg atg aac ctg 595  
 Val Pro Pro Val Gly Met His Ala Val Gly Glu Arg Leu Met Asn Leu  
                     150                    155                    160                    165

tac acc ggg aat tac act ccc gtc gat cta gag gaa cag cac gcg tac 643  
 Tyr Thr Gly Asn Tyr Thr Pro Val Asp Leu Glu Glu Gln His Ala Tyr  
                     170                    175                    180

ctg cag acg ctc tcc att aag gaa cgt ctc gcg ctg gct gat cag gaa 691  
 Leu Gln Thr Leu Ser Ile Lys Glu Arg Leu Ala Leu Ala Asp Gln Glu  
                     185                    190                    195

gct gat taagtagata tatgaagccc acc 720  
 Ala Asp

&lt;210&gt; 124

&lt;211&gt; 199

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 124

Val Leu Ile Val Gly Ile Arg Arg Asp Thr Gly Phe Asp Phe Lys His  
                     1                    5                    10                    15

cat cga ttt ttt gat gat tcc gca gtc tat tat ccc tgc ttc gtc ccg 211  
His Arg Phe Phe Asp Asp Ser Ala Val Tyr Tyr Pro Cys Phe Val Pro

25										30					35					
ctt	gac	cga	gcc	atc	ggc	gaa	cac	ttt	gat	cgt	cag	aac	aaa	ccg	atg	259				
Leu	Asp	Arg	Ala	Ile	Gly	Glu	His	Phe	Asp	Arg	Gln	Asn	Lys	Pro	Met					
		40					45					50								
tcc	aga	ttc	atc	gga	acg	ctc	att	ctg	ccg	tta	gcc	aaa	ctg	gaa	gaa	307				
Ser	Arg	Phe	Ile	Gly	Thr	Leu	Ile	Leu	Pro	Leu	Ala	Lys	Leu	Glu	Glu					
	55					60					65									
gcc	gcc	caa	tac	acc	ggc	gat	gaa	gtc	ctt	cgc	gtg	tcg	gca	gta	atc	355				
Ala	Ala	Gln	Tyr	Thr	Gly	Asp	Glu	Val	Leu	Arg	Val	Ser	Ala	Val	Ile					
70					75					80					85					
agt	act	gat	ggg	ctc	gct	gat	ctg	cga	agg	gat	ttt	tac	gaa	ctc	ccc	403				
Ser	Thr	Asp	Gly	Leu	Ala	Asp	Leu	Arg	Arg	Asp	Phe	Tyr	Glu	Leu	Pro					
				90					95					100						
aac	atc	gac	atc	gcc	tcg	gtg	gaa	atc	aag	ctg	gtc	ggc	gca	gcc	ctc	451				
Asn	Ile	Asp	Ile	Ala	Ser	Val	Glu	Ile	Lys	Leu	Val	Gly	Ala	Ala	Leu					
			105					110					115							
acc	aac	acc	gct	tgg	ttg	gga	gat	gtg	gaa	aaa	ctc	atc	caa	caa	cat	499				
Thr	Asn	Thr	Ala	Trp	Leu	Gly	Asp	Val	Glu	Lys	Leu	Ile	Gln	Gln	His					
		120					125					130								
cgc	aac	act	ttc	gta	tgg	gtt	gag	att	ccg	aca	gcc	ctg	gtc	acc	gca	547				
Arg	Asn	Thr	Phe	Val	Trp	Val	Glu	Ile	Pro	Thr	Ala	Leu	Val	Thr	Ala					
	135					140					145									
gat	att	gtc	cga	aaa	ctc	cgc	cac	atg	gga	gct	ggc	ctg	aaa	tac	aga	595				
Asp	Ile	Val	Arg	Lys	Leu	Arg	His	Met	Gly	Ala	Gly	Leu	Lys	Tyr	Arg					
150					155					160					165					
act	gga	ggt	gat	agg	gaa	gag	ctc	ttc	ccc	tca	ccg	cag	gac	ttg	gtc	643				
Thr	Gly	Gly	Asp	Arg	Glu	Glu	Leu	Phe	Pro	Ser	Pro	Gln	Asp	Leu	Val					
				170					175					180						
act	gtg	ctg	cgc	acc	gcc	atc	gat	gct	gca	ttg	ccg	ttt	aaa	ctc	act	691				
Thr	Val	Leu	Arg	Thr	Ala	Ile	Asp	Ala	Ala	Leu	Pro	Phe	Lys	Leu	Thr					
			185				190						195							
gca	ggc	ctg	cat	cgt	gct	ctc	agg	tat	cgt	gac	gag	aaa	acc	ggc	cga	739				
Ala	Gly	Leu	His	Arg	Ala	Leu	Arg	Tyr	Arg	Asp	Glu	Lys	Thr	Gly	Arg					
		200					205					210								
ctt	cac	ttc	gga	ttc	ctc	aac	att	gca	gcc	gcc	gtg	gcg	aca	ctt	cgt	787				
Leu	His	Phe	Gly	Phe	Leu	Asn	Ile	Ala	Ala	Ala	Val	Ala	Thr	Leu	Arg					
		215				220					225									
gct	gga	aaa	ggc	gag	gca	gag	gca	ctg	aag	atc	ctt	gaa	ggc	gat	gat	835				
Ala	Gly	Lys	Gly	Glu	Ala	Glu	Ala	Leu	Lys	Ile	Leu	Glu	Gly	Asp	Asp					
230					235					240					245					
gcc	gct	ccg	ctt	att	cac	gca	cta	caa	agc	ggc	gaa	aac	tgg	cgg	gat	883				
Ala	Ala	Pro	Leu	Ile	His	Ala	Leu	Gln	Ser	Gly	Glu	Asn	Trp	Arg	Asp					
				250					255					260						
tcc	ttc	cgc	agc	ttc	agt	acc	tgc	aat	gtt	gtt	gaa	cca	ctc	aac	act	931				
Ser	Phe	Arg	Ser	Phe	Ser	Thr	Cys	Asn	Val	Val	Glu	Pro	Leu	Asn	Thr					
			265					270					275							

973

996

<210> 126

<211> 291

<212> PRT

<213> Corynebacterium glutamicum

<400> 126

Val Gln Lys Trp Gly Leu Ser Phe Val Glu Arg Ile Val Ile Val Asn  
1 5 10 15

Asn Val Gln Gln Phe His Arg Phe Phe Asp Asp Ser Ala Val Tyr Tyr  
20 25 30

Pro Cys Phe Val Pro Leu Asp Arg Ala Ile Gly Glu His Phe Asp Arg  
35 40 45

Gln Asn Lys Pro Met Ser Arg Phe Ile Gly Thr Leu Ile Leu Pro Leu  
50 55 60

Ala Lys Leu Glu Glu Ala Ala Gln Tyr Thr Gly Asp Glu Val Leu Arg  
65 70 75 80

Val Ser Ala Val Ile Ser Thr Asp Gly Leu Ala Asp Leu Arg Arg Asp  
85 90 95

Phe Tyr Glu Leu Pro Asn Ile Asp Ile Ala Ser Val Glu Ile Lys Leu  
100 105 110

Val Gly Ala Ala Leu Thr Asn Thr Ala Trp Leu Gly Asp Val Glu Lys  
115 120 125

Leu Ile Gln Gln His Arg Asn Thr Phe Val Trp Val Glu Ile Pro Thr  
130 135 140

Ala Leu Val Thr Ala Asp Ile Val Arg Lys Leu Arg His Met Gly Ala  
145 150 155 160

Gly Leu Lys Tyr Arg Thr Gly Gly Asp Arg Glu Glu Leu Phe Pro Ser  
165 170 175

Pro Gln Asp Leu Val Thr Val Leu Arg Thr Ala Ile Asp Ala Ala Leu  
180 185 190

Pro Phe Lys Leu Thr Ala Gly Leu His Arg Ala Leu Arg Tyr Arg Asp  
195 200 205

Glu Lys Thr Gly Arg Leu His Phe Gly Phe Leu Asn Ile Ala Ala Ala  
210 215 220

Val Ala Thr Leu Arg Ala Gly Lys Gly Glu Ala Glu Ala Leu Lys Ile  
225 230 235 240

Leu Glu Gly Asp Asp Ala Ala Pro Leu Ile His Ala Leu Gln Ser Gly  
245 250 255

Glu Asn Trp Arg Asp Ser Phe Arg Ser Phe Ser Thr Cys Asn Val Val  
                   260                                  265                                  270

Glu Pro Leu Asn Thr Leu Ile Asp Leu Asp Val Leu Ala Glu Gly Asp  
                   275                                  280                                  285

Val His Pro  
           290

<210> 127

<211> 729

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(706)

<223> RXN02988

<400> 127

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acggtaaaca cgcacaagat aaaacattgc gagatttttc atg agt aca aaa ccc 115  
   Met Ser Thr Lys Pro  
   1                                  5

act att gtg tcc aca ttt tct ggt tgc ggt ggc ctc gat ctt ggc ctc 163  
   Thr Ile Val Ser Thr Phe Ser Gly Cys Gly Gly Leu Asp Leu Gly Leu  
                                   10                                  15                                  20

caa gag gtc gga ttc gac ccc att tgg gcc aac gac ttc tca gaa gaa 211  
   Gln Glu Val Gly Phe Asp Pro Ile Trp Ala Asn Asp Phe Ser Glu Glu  
                                   25                                  30                                  35

gca gtc caa acc tat aag cac aac atc ggt gac cac att gtt cac ggc 259  
   Ala Val Gln Thr Tyr Lys His Asn Ile Gly Asp His Ile Val His Gly  
                                   40                                  45                                  50

gac atc act gaa att gat ccg ttt act gat gac acc atc cct gac ggc 307  
   Asp Ile Thr Glu Ile Asp Pro Phe Thr Asp Asp Thr Ile Pro Asp Gly  
                                   55                                  60                                  65

gat ctc gtc acc ggc ggc ttc ccg tgc cag gac ttc tcc atg atc tgg 355  
   Asp Leu Val Thr Gly Gly Phe Pro Cys Gln Asp Phe Ser Met Ile Trp  
                                   70                                  75                                  80                                  85

aag cgt cct gga ctc gac ggc aag cgt ggc acc ctg tac caa aac ttc 403  
   Lys Arg Pro Gly Leu Asp Gly Lys Arg Gly Thr Leu Tyr Gln Asn Phe  
                                   90                                  95                                  100

cgt gac ttt gtt gca gca aag aag cct aaa gcc ttt atc gca gaa aac 451  
   Arg Asp Phe Val Ala Ala Lys Lys Pro Lys Ala Phe Ile Ala Glu Asn  
                                   105                                  110                                  115

gtg aag ggc cta ctc act gct aac cag cac aag gct att aag acc ata 499  
   Val Lys Gly Leu Leu Thr Ala Asn Gln His Lys Ala Ile Lys Thr Ile  
                                   120                                  125                                  130

ttg aag acc tcg aag ctg ttg agc ctg gct aca tcg tca agc ctc gcc 547

Leu Lys Thr Ser Lys Leu Leu Ser Leu Ala Thr Ser Ser Ser Leu Ala  
 135 140 145  
 tgt aca act tcg ctg aat acg gtg tcc cac aat tcc gcg aac gtg tgc 595  
 Cys Thr Thr Ser Leu Asn Thr Val Ser His Asn Ser Ala Asn Val Cys  
 150 155 160 165  
 tca ttg ttg gca ttc gcc gtg aca ccg gct ttg att tca agc acc cag 643  
 Ser Leu Leu Ala Phe Ala Val Thr Pro Ala Leu Ile Ser Ser Thr Gln  
 170 175 180  
 ctc cta ccc atg gcc ctc gcg gtg aca tgc cgt ata aga ctg ccg gcg 691  
 Leu Leu Pro Met Ala Leu Ala Val Thr Cys Arg Ile Arg Leu Pro Ala  
 185 190 195  
 aag cgc tca aag gcg tgaaggatgt cccacaaac aac 729  
 Lys Arg Ser Lys Ala  
 200

&lt;210&gt; 128

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 128

Met Ser Thr Lys Pro Thr Ile Val Ser Thr Phe Ser Gly Cys Gly Gly  
 1 5 10 15  
 Leu Asp Leu Gly Leu Gln Glu Val Gly Phe Asp Pro Ile Trp Ala Asn  
 20 25 30  
 Asp Phe Ser Glu Glu Ala Val Gln Thr Tyr Lys His Asn Ile Gly Asp  
 35 40 45  
 His Ile Val His Gly Asp Ile Thr Glu Ile Asp Pro Phe Thr Asp Asp  
 50 55 60  
 Thr Ile Pro Asp Gly Asp Leu Val Thr Gly Gly Phe Pro Cys Gln Asp  
 65 70 75 80  
 Phe Ser Met Ile Trp Lys Arg Pro Gly Leu Asp Gly Lys Arg Gly Thr  
 85 90 95  
 Leu Tyr Gln Asn Phe Arg Asp Phe Val Ala Ala Lys Lys Pro Lys Ala  
 100 105 110  
 Phe Ile Ala Glu Asn Val Lys Gly Leu Leu Thr Ala Asn Gln His Lys  
 115 120 125  
 Ala Ile Lys Thr Ile Leu Lys Thr Ser Lys Leu Leu Ser Leu Ala Thr  
 130 135 140  
 Ser Ser Ser Leu Ala Cys Thr Thr Ser Leu Asn Thr Val Ser His Asn  
 145 150 155 160  
 Ser Ala Asn Val Cys Ser Leu Leu Ala Phe Ala Val Thr Pro Ala Leu  
 165 170 175  
 Ile Ser Ser Thr Gln Leu Leu Pro Met Ala Leu Ala Val Thr Cys Arg  
 180 185 190

Ile Arg Leu Pro Ala Lys Arg Ser Lys Ala  
 195 200

<210> 129

<211> 588

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(565)

<223> RXN00127

<400> 129

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gaagccgccca acattggcgc ggcttgattt agatttaccg gtg tgg acg ttg tgc 115  
 Val Trp Thr Leu Ser  
 1 5

ccg tat gac ggc ccg cat cgc aac gtg ctc att gcg ctg aag gag cac 163  
 Pro Tyr Asp Gly Pro His Arg Asn Val Leu Ile Ala Leu Lys Glu His  
 10 15 20

ggc cgt gca gac ctt gtg gcg ttt gtg ggc gcg gtg gtg ggg gcg tgc 211  
 Gly Arg Ala Asp Leu Val Ala Phe Val Gly Ala Val Val Gly Ala Ser  
 25 30 35

ata agc tat ctg gcg gct cag ggg gaa att gag cac gac atc acg ctg 259  
 Ile Ser Tyr Leu Ala Ala Gln Gly Glu Ile Glu His Asp Ile Thr Leu  
 40 45 50

gtt ccg gcg ccc acc cgc gcc acc tcg cga cgc cgg cgg ggc ggc gat 307  
 Val Pro Ala Pro Thr Arg Ala Thr Ser Arg Arg Arg Arg Gly Gly Asp  
 55 60 65

ccg gtt gag cgg gtg tgc aat gca tca cgc tta tcg acg ttt ccc tgc 355  
 Pro Val Glu Arg Val Cys Asn Ala Ser Arg Leu Ser Thr Phe Pro Cys  
 70 75 80 85

ctt caa atc tca tcc cgc aca cca gac tcc gtc ggt caa act gcg caa 403  
 Leu Gln Ile Ser Ser Arg Thr Pro Asp Ser Val Gly Gln Thr Ala Gln  
 90 95 100

cag cga aga ctc aat atg cga gtg gag tta gtc cga caa cct cgg ggt 451  
 Gln Arg Arg Leu Asn Met Arg Val Glu Leu Val Arg Gln Pro Arg Gly  
 105 110 115

tct gtc ttg atc atc gac gat gtg gta aca acg ggg gca act att tcc 499  
 Ser Val Leu Ile Ile Asp Asp Val Val Thr Thr Gly Ala Thr Ile Ser  
 120 125 130

gca tct gca aac gtt ctt cgc gca gcg ggt gtg cag gtc aga gga gct 547  
 Ala Ser Ala Asn Val Leu Arg Ala Ala Gly Val Gln Val Arg Gly Ala  
 135 140 145

tta act tat tgc caa gcg tgatcttggga tataaaaggg gcc 588  
 Leu Thr Tyr Cys Gln Ala  
 150 155

<210> 130  
 <211> 155  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 130  
 Val Trp Thr Leu Ser Pro Tyr Asp Gly Pro His Arg Asn Val Leu Ile  
   1                  5                  10                  15  
 Ala Leu Lys Glu His Gly Arg Ala Asp Leu Val Ala Phe Val Gly Ala  
                   20                  25                  30  
 Val Val Gly Ala Ser Ile Ser Tyr Leu Ala Ala Gln Gly Glu Ile Glu  
           35                  40                  45  
 His Asp Ile Thr Leu Val Pro Ala Pro Thr Arg Ala Thr Ser Arg Arg  
       50                  55                  60  
 Arg Arg Gly Gly Asp Pro Val Glu Arg Val Cys Asn Ala Ser Arg Leu  
   65                  70                  75                  80  
 Ser Thr Phe Pro Cys Leu Gln Ile Ser Ser Arg Thr Pro Asp Ser Val  
                   85                  90                  95  
 Gly Gln Thr Ala Gln Gln Arg Arg Leu Asn Met Arg Val Glu Leu Val  
                   100                  105                  110  
 Arg Gln Pro Arg Gly Ser Val Leu Ile Ile Asp Asp Val Val Thr Thr  
           115                  120                  125  
 Gly Ala Thr Ile Ser Ala Ser Ala Asn Val Leu Arg Ala Ala Gly Val  
   130                  135                  140  
 Gln Val Arg Gly Ala Leu Thr Tyr Cys Gln Ala  
 145                  150                  155

<210> 131  
 <211> 864  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(841)  
 <223> RXN02938

<400> 131  
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 atcgaatgacc tcgaaaccgc tgtggcaggg gcgctgcaga atg cgt aac tac cct 115  
   Met Arg Asn Tyr Pro  
   1                  5  
 gat tta ccg cat gat ttc cca ggt caa aac aca gag ctc acc ccc gca 163  
 Asp Leu Pro His Asp Phe Pro Gly Gln Asn Thr Glu Leu Thr Pro Ala  
                   10                  15                  20  
 aag gca ccc gtg tgg atg cac cga ctc tta gac cgc atc cac acc ggc 211

Lys	Ala	Pro	Val	Trp	Met	His	Arg	Leu	Leu	Asp	Arg	Ile	His	Thr	Gly	
			25					30					35			
cgc	atg	gcc	aac	ccg	ctg	gac	ggt	gcg	gaa	acg	ctc	ggc	gac	aca	gac	259
Arg	Met	Ala	Asn	Pro	Leu	Asp	Gly	Ala	Glu	Thr	Leu	Gly	Asp	Thr	Asp	
		40					45					50				
tcc	gaa	aag	cgc	gct	gcc	gtg	ctc	atg	cta	ttt	tct	ggc	tcg	gaa	acc	307
Ser	Glu	Lys	Arg	Ala	Ala	Val	Leu	Met	Leu	Phe	Ser	Gly	Ser	Glu	Thr	
	55					60					65					
tcc	ttt	gac	ctg	ccc	aat	gac	gcc	tcc	gtg	ctg	ctg	acg	cac	cgc	acc	355
Ser	Phe	Asp	Leu	Pro	Asn	Asp	Ala	Ser	Val	Leu	Leu	Thr	His	Arg	Thr	
70					75				80						85	
ccg	acg	atg	cgt	tcc	cat	gca	ggt	cag	att	gcc	ttt	ccc	ggt	ggc	cga	403
Pro	Thr	Met	Arg	Ser	His	Ala	Gly	Gln	Ile	Ala	Phe	Pro	Gly	Gly	Arg	
				90				95						100		
atc	gac	ccc	acc	gat	act	aac	gcc	gtg	gac	tgc	gcc	ttc	cgc	gag	gcc	451
Ile	Asp	Pro	Thr	Asp	Thr	Asn	Ala	Val	Asp	Cys	Ala	Phe	Arg	Glu	Ala	
			105					110					115			
tgg	gaa	gaa	acc	ggg	ctg	gat	cgc	cgc	acc	gca	acc	cca	tta	gcc	cag	499
Trp	Glu	Glu	Thr	Gly	Leu	Asp	Arg	Arg	Thr	Ala	Thr	Pro	Leu	Ala	Gln	
	120						125					130				
ctc	aac	gag	gtg	cac	atc	cgt	gcc	acc	gga	tac	ccc	gtc	tac	cca	atc	547
Leu	Asn	Glu	Val	His	Ile	Arg	Ala	Thr	Gly	Tyr	Pro	Val	Tyr	Pro	Ile	
	135					140					145					
ctt	gga	cac	tgg	cac	acc	cca	tca	ccc	gtc	gcc	gtg	gcc	agc	cca	cac	595
Leu	Gly	His	Trp	His	Thr	Pro	Ser	Pro	Val	Ala	Val	Ala	Ser	Pro	His	
150					155				160						165	
gaa	acc	gac	gaa	gtt	ttg	gac	gcc	cca	ctc	tac	gac	ctc	atc	gac	ccc	643
Glu	Thr	Asp	Glu	Val	Leu	Asp	Ala	Pro	Leu	Tyr	Asp	Leu	Ile	Asp	Pro	
				170				175						180		
aaa	aac	cgc	ctc	atg	gtc	ggc	tgg	cgc	gaa	tgg	cac	gga	cca	gcg	ttt	691
Lys	Asn	Arg	Leu	Met	Val	Gly	Trp	Arg	Glu	Trp	His	Gly	Pro	Ala	Phe	
			185				190						195			
cga	atc	aac	gac	tac	atc	atc	tgg	gga	ttc	acc	ggc	gga	cta	ctc	tcc	739
Arg	Ile	Asn	Asp	Tyr	Ile	Ile	Trp	Gly	Phe	Thr	Gly	Gly	Leu	Leu	Ser	
		200					205					210				
gcg	atc	ctc	gac	acc	gcc	ggc	tgg	gcc	acc	gaa	tgg	gac	acc	gac	cgc	787
Ala	Ile	Leu	Asp	Thr	Ala	Gly	Trp	Ala	Thr	Glu	Trp	Asp	Thr	Asp	Arg	
	215					220					225					
atc	ttc	gac	ctg	gaa	aat	aca	ttg	tca	aca	tct	cgc	aac	aat	gag	cgt	835
Ile	Phe	Asp	Leu	Glu	Asn	Thr	Leu	Ser	Thr	Ser	Arg	Asn	Asn	Glu	Arg	
230					235					240					245	
atg	cgt	taggctgacg	ggctccggtg	gcc												864
Met	Arg															

&lt;210&gt; 132

<211> 247  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 132

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Met Arg Asn Tyr Pro Asp Leu Pro His Asp Phe Pro Gly Gln Asn Thr
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Glu Leu Thr Pro Ala Lys Ala Pro Val Trp Met His Arg Leu Leu Asp
          20          25          30
Arg Ile His Thr Gly Arg Met Ala Asn Pro Leu Asp Gly Ala Glu Thr
          35          40          45
Leu Gly Asp Thr Asp Ser Glu Lys Arg Ala Ala Val Leu Met Leu Phe
          50          55          60
Ser Gly Ser Glu Thr Ser Phe Asp Leu Pro Asn Asp Ala Ser Val Leu
          65          70          75          80
Leu Thr His Arg Thr Pro Thr Met Arg Ser His Ala Gly Gln Ile Ala
          85          90          95
Phe Pro Gly Gly Arg Ile Asp Pro Thr Asp Thr Asn Ala Val Asp Cys
          100         105         110
Ala Phe Arg Glu Ala Trp Glu Glu Thr Gly Leu Asp Arg Arg Thr Ala
          115         120         125
Thr Pro Leu Ala Gln Leu Asn Glu Val His Ile Arg Ala Thr Gly Tyr
          130         135         140
Pro Val Tyr Pro Ile Leu Gly His Trp His Thr Pro Ser Pro Val Ala
          145         150         155         160
Val Ala Ser Pro His Glu Thr Asp Glu Val Leu Asp Ala Pro Leu Tyr
          165         170         175
Asp Leu Ile Asp Pro Lys Asn Arg Leu Met Val Gly Trp Arg Glu Trp
          180         185         190
His Gly Pro Ala Phe Arg Ile Asn Asp Tyr Ile Ile Trp Gly Phe Thr
          195         200         205
Gly Gly Leu Leu Ser Ala Ile Leu Asp Thr Ala Gly Trp Ala Thr Glu
          210         215         220
Trp Asp Thr Asp Arg Ile Phe Asp Leu Glu Asn Thr Leu Ser Thr Ser
          225         230         235         240
Arg Asn Asn Glu Arg Met Arg
          245

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<210> 133  
 <211> 597  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS

&lt;222&gt; (83)..(574)

&lt;223&gt; RXN03102

&lt;400&gt; 133

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cgtggtcacg ggtctgcagt acctgtggga ttcacgaaag tccgcagaaa gctagaccat 60
gtcggagaat ctggcggggc ga gtg gtg gag ctg ttg aaa tcg cgc ggt gaa 112
                        Val Val Glu Leu Leu Lys Ser Arg Gly Glu
                        1                        5                        10

acg ctg gcg ttt tgt gaa tcc ctc acc gcc ggc ctt gcc agt gcg acg 160
Thr Leu Ala Phe Cys Glu Ser Leu Thr Ala Gly Leu Ala Ser Ala Thr
                        15                        20                        25

atc gca gag atc ccc ggc gcc tca gtg gta ctt aaa ggc ggg ctg gtc 208
Ile Ala Glu Ile Pro Gly Ala Ser Val Val Leu Lys Gly Gly Leu Val
                        30                        35                        40

acc tat gcc acc gag ctt aag gtt gcg ctt gcc ggt gtg ccg cag gag 256
Thr Tyr Ala Thr Glu Leu Lys Val Ala Leu Ala Gly Val Pro Gln Glu
                        45                        50                        55

ctt atc gac gcg cac ggc gtt gtt tcc ccg cag tgc gcc cgt gcg atg 304
Leu Ile Asp Ala His Gly Val Val Ser Pro Gln Cys Ala Arg Ala Met
                        60                        65                        70

gca acg ggg gcc gca cac aga tgc cag gca gat tgg gcg gtt tcg ctc 352
Ala Thr Gly Ala Ala His Arg Cys Gln Ala Asp Trp Ala Val Ser Leu
                        75                        80                        85                        90

acg ggc gtt gct ggc ccc agc aaa caa gat ggt cat ccg gtg ggg gaa 400
Thr Gly Val Ala Gly Pro Ser Lys Gln Asp Gly His Pro Val Gly Glu
                        95                        100                        105

gtg tgg atc gga gtg gct ggt cct gcg cat ttt ggg gcg tcg gga aca 448
Val Trp Ile Gly Val Ala Gly Pro Ala His Phe Gly Ala Ser Gly Thr
                        110                        115                        120

att gac gcg tat cgt gcg ttt gaa agt gaa caa cag gta ata ttg gct 496
Ile Asp Ala Tyr Arg Ala Phe Glu Ser Glu Gln Gln Val Ile Leu Ala
                        125                        130                        135

gaa ttg gga cgg cat cat att aga gag tct gct gtg cag caa agc ttt 544
Glu Leu Gly Arg His His Ile Arg Glu Ser Ala Val Gln Gln Ser Phe
                        140                        145                        150

cgc ctg ctg att gac cat att gag tcg cag tgactcaagt ttccaggtaa act 597
Arg Leu Leu Ile Asp His Ile Glu Ser Gln
155                        160

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&lt;210&gt; 134

&lt;211&gt; 164

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 134

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Val Val Glu Leu Leu Lys Ser Arg Gly Glu Thr Leu Ala Phe Cys Glu
  1                        5                        10                        15

Ser Leu Thr Ala Gly Leu Ala Ser Ala Thr Ile Ala Glu Ile Pro Gly

```

20					25					30					
Ala	Ser	Val	Val	Leu	Lys	Gly	Gly	Leu	Val	Thr	Tyr	Ala	Thr	Glu	Leu
	35					40						45			
Lys	Val	Ala	Leu	Ala	Gly	Val	Pro	Gln	Glu	Leu	Ile	Asp	Ala	His	Gly
	50					55					60				
Val	Val	Ser	Pro	Gln	Cys	Ala	Arg	Ala	Met	Ala	Thr	Gly	Ala	Ala	His
	65					70					75				80
Arg	Cys	Gln	Ala	Asp	Trp	Ala	Val	Ser	Leu	Thr	Gly	Val	Ala	Gly	Pro
				85					90					95	
Ser	Lys	Gln	Asp	Gly	His	Pro	Val	Gly	Glu	Val	Trp	Ile	Gly	Val	Ala
			100					105					110		
Gly	Pro	Ala	His	Phe	Gly	Ala	Ser	Gly	Thr	Ile	Asp	Ala	Tyr	Arg	Ala
		115					120					125			
Phe	Glu	Ser	Glu	Gln	Gln	Val	Ile	Leu	Ala	Glu	Leu	Gly	Arg	His	His
	130					135					140				
Ile	Arg	Glu	Ser	Ala	Val	Gln	Gln	Ser	Phe	Arg	Leu	Leu	Ile	Asp	His
	145					150					155				160
Ile	Glu	Ser	Gln												

&lt;210&gt; 135

&lt;211&gt; 933

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(910)

&lt;223&gt; RXN03118

&lt;400&gt; 135

acactcccgt cgatctagag gaacagcacg cgtacctgca gacgctctcc attaaggaac 60

gtctcgcgct ggctgatcag gaagctgatt aagtagatat atg aag ccc acc gtt 115  
 Met Lys Pro Thr Val  
 1 5

aat gtt gtg ttc aat gcg cat cac ccc aaa gat acg cag ccg ttg gat 163  
 Asn Val Val Phe Asn Ala His His Pro Lys Asp Thr Gln Pro Leu Asp  
 10 15 20

aag ttc ttc gat aaa gaa ctt aaa gac aca cat cat ctc gat ata acg 211  
 Lys Phe Phe Asp Lys Glu Leu Lys Asp Thr His His Leu Asp Ile Thr  
 25 30 35

gtg ggt tat atc agt gag aaa tca cta caa tat ttg ctt ctt att gca 259  
 Val Gly Tyr Ile Ser Glu Lys Ser Leu Gln Tyr Leu Leu Leu Ile Ala  
 40 45 50

ggc act tac ccc gac ctc acc att aca ctt acc tgt gga atg cac gct 307  
 Gly Thr Tyr Pro Asp Leu Thr Ile Thr Leu Thr Cys Gly Met His Ala

55	60	65	
cgt gaa ggc atg act gct gcc caa ctg cat cat gcg cga gtg ctc cat			355
Arg Glu Gly Met Thr Ala Ala Gln Leu His His Ala Arg Val Leu His			
70	75	80	85
gac tac tta agc gac cat gat cga ggc ggg gtg ttc gtt att ccc cga			403
Asp Tyr Leu Ser Asp His Asp Arg Gly Gly Val Phe Val Ile Pro Arg			
	90	95	100
ttg cgt tat cac ggg aaa atc tat ctt ttc cac aag aac cag cac aca			451
Leu Arg Tyr His Gly Lys Ile Tyr Leu Phe His Lys Asn Gln His Thr			
	105	110	115
gat cct att gct tat atc ggt agc gct aac ctc tca gcc atc gtt cct			499
Asp Pro Ile Ala Tyr Ile Gly Ser Ala Asn Leu Ser Ala Ile Val Pro			
	120	125	130
ggg tac acc tct aca ttc gag ccc ggc gtc atc tta gac ccc gca cct			547
Gly Tyr Thr Ser Thr Phe Glu Pro Gly Val Ile Leu Asp Pro Ala Pro			
	135	140	145
gaa gat ctc gtg ctt cat ctc aac cgt gat gtc gta ccc cta tgt gtc			595
Glu Asp Leu Val Leu His Leu Asn Arg Asp Val Val Pro Leu Cys Val			
	150	155	160
ccc att gac acc gcg cat gtc ccc atc att aaa gat caa gaa tcc ccg			643
Pro Ile Asp Thr Ala His Val Pro Ile Ile Lys Asp Gln Glu Ser Pro			
	170	175	180
atg aag cac gtc gct gaa gca aca gct gtg tcc acc tct gat gtt gtt			691
Met Lys His Val Ala Glu Ala Thr Ala Val Ser Thr Ser Asp Val Val			
	185	190	195
gcc atc atg tcc agc cca ttt act tat agt ttt gac ctt aaa ctc aaa			739
Ala Ile Met Ser Ser Pro Phe Thr Tyr Ser Phe Asp Leu Lys Leu Lys			
	200	205	210
gcc act gcc agc agc aac ctc aat gct cat aac tca ggc ggt ggc gcg			787
Ala Thr Ala Ser Ser Asn Leu Asn Ala His Asn Ser Gly Gly Gly Ala			
	215	220	225
cgc aaa cag aaa aac ggt agc ttc ctt gca cgc aat tgg tat gag ggc			835
Arg Lys Gln Lys Asn Gly Ser Phe Leu Ala Arg Asn Trp Tyr Glu Gly			
	230	235	240
gaa atc att gtc ggt gtc gag aca aca aga ctc cca ggt tac cca caa			883
Glu Ile Ile Val Gly Val Glu Thr Thr Arg Leu Pro Gly Tyr Pro Gln			
	250	255	260
aac aaa tcc gaa ttc act gcg ggt cac tgatgacggc tggtcatttg ttt			933
Asn Lys Ser Glu Phe Thr Ala Gly His			
	265	270	

&lt;210&gt; 136

&lt;211&gt; 270

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 136

Met Lys Pro Thr Val Asn Val Val Phe Asn Ala His His Pro Lys Asp  
 1 5 10 15  
 Thr Gln Pro Leu Asp Lys Phe Phe Asp Lys Glu Leu Lys Asp Thr His  
 20 25 30  
 His Leu Asp Ile Thr Val Gly Tyr Ile Ser Glu Lys Ser Leu Gln Tyr  
 35 40 45  
 Leu Leu Leu Ile Ala Gly Thr Tyr Pro Asp Leu Thr Ile Thr Leu Thr  
 50 55 60  
 Cys Gly Met His Ala Arg Glu Gly Met Thr Ala Ala Gln Leu His His  
 65 70 75 80  
 Ala Arg Val Leu His Asp Tyr Leu Ser Asp His Asp Arg Gly Gly Val  
 85 90 95  
 Phe Val Ile Pro Arg Leu Arg Tyr His Gly Lys Ile Tyr Leu Phe His  
 100 105 110  
 Lys Asn Gln His Thr Asp Pro Ile Ala Tyr Ile Gly Ser Ala Asn Leu  
 115 120 125  
 Ser Ala Ile Val Pro Gly Tyr Thr Ser Thr Phe Glu Pro Gly Val Ile  
 130 135 140  
 Leu Asp Pro Ala Pro Glu Asp Leu Val Leu His Leu Asn Arg Asp Val  
 145 150 155 160  
 Val Pro Leu Cys Val Pro Ile Asp Thr Ala His Val Pro Ile Ile Lys  
 165 170 175  
 Asp Gln Glu Ser Pro Met Lys His Val Ala Glu Ala Thr Ala Val Ser  
 180 185 190  
 Thr Ser Asp Val Val Ala Ile Met Ser Ser Pro Phe Thr Tyr Ser Phe  
 195 200 205  
 Asp Leu Lys Leu Lys Ala Thr Ala Ser Ser Asn Leu Asn Ala His Asn  
 210 215 220  
 Ser Gly Gly Gly Ala Arg Lys Gln Lys Asn Gly Ser Phe Leu Ala Arg  
 225 230 235 240  
 Asn Trp Tyr Glu Gly Glu Ile Ile Val Gly Val Glu Thr Thr Arg Leu  
 245 250 255  
 Pro Gly Tyr Pro Gln Asn Lys Ser Glu Phe Thr Ala Gly His  
 260 265 270

<210> 137

<211> 1263

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1240)

<223> RXN02989

&lt;400&gt; 137

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aggggtcact gctgcagtcg tgttttagtc agtgctgaag tgatgcaacc gtaggaattt 60

tcgtccacat caacgtcaat aaaactaaga ggaattaaaa atg gct ccc aag aag 115
                                         Met Ala Pro Lys Lys
                                         1           5

aca gca aca aag gca act gcc gcc aag ggg aat gat cgt cag aag gca 163
Thr Ala Thr Lys Ala Thr Ala Ala Lys Gly Asn Asp Arg Gln Lys Ala
                        10                        15                        20

ctt gat gcc gca cta gcc ctg att gag aag gat ttc ggt aaa ggc gct 211
Leu Asp Ala Ala Leu Ala Leu Ile Glu Lys Asp Phe Gly Lys Gly Ala
                        25                        30                        35

gtc atg cgt ctg ggt gat gag aat cgt ccg cca atc cag acc atc tca 259
Val Met Arg Leu Gly Asp Glu Asn Arg Pro Pro Ile Gln Thr Ile Ser
                        40                        45                        50

tct ggt aac acc gcg att gat att gcc ttg ggt atc ggt gga ttc cca 307
Ser Gly Asn Thr Ala Ile Asp Ile Ala Leu Gly Ile Gly Gly Phe Pro
                        55                        60                        65

cgt ggt cga atc gtt gag gtg tat ggc cca gaa tca tca ggt aaa acc 355
Arg Gly Arg Ile Val Glu Val Tyr Gly Pro Glu Ser Ser Gly Lys Thr
                        70                        75                        80                        85

acc gtt gca ctg cac gca att gcg cag gca caa aag gcc ggc ggc atc 403
Thr Val Ala Leu His Ala Ile Ala Gln Ala Gln Lys Ala Gly Gly Ile
                        90                        95                        100

gct gca ttc att gac gcc gag cac gcg ttg gat cca gat tat gct cgc 451
Ala Ala Phe Ile Asp Ala Glu His Ala Leu Asp Pro Asp Tyr Ala Arg
                        105                        110                        115

aag ctt ggt gta gat act gat gcg ctt ctg gtt tcg cag cca gac act 499
Lys Leu Gly Val Asp Thr Asp Ala Leu Leu Val Ser Gln Pro Asp Thr
                        120                        125                        130

ggt gag caa gca cta gaa atc gcc gac atg ctg gtt cgt tcc ggc gca 547
Gly Glu Gln Ala Leu Glu Ile Ala Asp Met Leu Val Arg Ser Gly Ala
                        135                        140                        145

atc gac atc atc gtg att gac tcg gtg gct gcg ctg aca cca aag gct 595
Ile Asp Ile Ile Val Ile Asp Ser Val Ala Ala Leu Thr Pro Lys Ala
                        150                        155                        160                        165

gaa att gaa ggc gaa atg ggc gat agc cac gtt ggt ctt cag gcc cgc 643
Glu Ile Glu Gly Glu Met Gly Asp Ser His Val Gly Leu Gln Ala Arg
                        170                        175                        180

ctc atg agc cag gcg ctt cgt aag atg aca ggt gcg ctg tac aac tcg 691
Leu Met Ser Gln Ala Leu Arg Lys Met Thr Gly Ala Leu Tyr Asn Ser
                        185                        190                        195

ggt acc acc gcg atc ttc att aac cag ctg cgt gaa aag atc ggt gtg 739
Gly Thr Thr Ala Ile Phe Ile Asn Gln Leu Arg Glu Lys Ile Gly Val
                        200                        205                        210

atg ttc ggt tcc cca gaa acc acc acc ggt ggt aag gcc ctg aag ttc 787

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Met	Phe	Gly	Ser	Pro	Glu	Thr	Thr	Thr	Gly	Gly	Lys	Ala	Leu	Lys	Phe		
	215					220					225						
tac	gca	tct	gtt	cgt	tgt	gac	att	cga	cga	atc	cag	act	ctg	aag	gac	835	
Tyr	Ala	Ser	Val	Arg	Cys	Asp	Ile	Arg	Arg	Ile	Gln	Thr	Leu	Lys	Asp		
230					235					240					245		
gga	cag	gat	gcc	att	ggg	aac	cgc	acc	cgc	ttg	aag	gtc	gtt	aag	aac	883	
Gly	Gln	Asp	Ala	Ile	Gly	Asn	Arg	Thr	Arg	Leu	Lys	Val	Val	Lys	Asn		
				250					255					260			
aag	gtc	tcc	cca	ccg	ttc	aag	atc	gct	gaa	ttc	gac	atc	atg	tac	ggc	931	
Lys	Val	Ser	Pro	Pro	Phe	Lys	Ile	Ala	Glu	Phe	Asp	Ile	Met	Tyr	Gly		
			265					270					275				
gaa	ggc	atc	tcc	cgt	gaa	tcc	tcc	gtc	att	gac	ttg	gca	gtg	gac	aac	979	
Glu	Gly	Ile	Ser	Arg	Glu	Ser	Ser	Val	Ile	Asp	Leu	Ala	Val	Asp	Asn		
			280				285					290					
ggc	att	gtg	aag	aag	tca	ggg	tcc	tgg	ttc	acc	tac	gag	ggc	gaa	cag	1027	
Gly	Ile	Val	Lys	Lys	Ser	Gly	Ser	Trp	Phe	Thr	Tyr	Glu	Gly	Glu	Gln		
	295					300					305						
ctt	ggg	caa	ggg	aag	gaa	aag	gtg	cgt	ctt	tcc	ctc	aag	gag	aac	cct	1075	
Leu	Gly	Gln	Gly	Lys	Glu	Lys	Val	Arg	Leu	Ser	Leu	Lys	Glu	Asn	Pro		
310					315					320					325		
gaa	ctc	acc	gat	gag	ctg	gaa	gat	aag	atc	ttc	aag	aag	ctg	gga	gta	1123	
Glu	Leu	Thr	Asp	Glu	Leu	Glu	Asp	Lys	Ile	Phe	Lys	Lys	Leu	Gly	Val		
				330					335					340			
ggc	aag	tac	gct	gca	gcc	tca	gat	gaa	ctc	acc	gac	gat	cca	gta	gag	1171	
Gly	Lys	Tyr	Ala	Ala	Ala	Ser	Asp	Glu	Leu	Thr	Asp	Asp	Pro	Val	Glu		
			345					350					355				
ctc	gtg	cct	aac	gtt	gac	ttc	gat	gat	gaa	gcc	gac	acc	gaa	gcc	gac	1219	
Leu	Val	Pro	Asn	Val	Asp	Phe	Asp	Asp	Glu	Ala	Asp	Thr	Glu	Ala	Asp		
		360					365					370					
acc	gaa	gca	gac	gct	gaa	gac	taagcaccag ttttaacaaa gca									1263	
Thr	Glu	Ala	Asp	Ala	Glu	Asp											
	375				380												

&lt;210&gt; 138

&lt;211&gt; 380

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 138

Met	Ala	Pro	Lys	Lys	Thr	Ala	Thr	Lys	Ala	Thr	Ala	Ala	Lys	Gly	Asn		
1				5					10					15			
Asp	Arg	Gln	Lys	Ala	Leu	Asp	Ala	Ala	Leu	Ala	Leu	Ile	Glu	Lys	Asp		
			20					25					30				
Phe	Gly	Lys	Gly	Ala	Val	Met	Arg	Leu	Gly	Asp	Glu	Asn	Arg	Pro	Pro		
		35					40					45					
Ile	Gln	Thr	Ile	Ser	Ser	Gly	Asn	Thr	Ala	Ile	Asp	Ile	Ala	Leu	Gly		
	50					55					60						

Ile	Gly	Gly	Phe	Pro	Arg	Gly	Arg	Ile	Val	Glu	Val	Tyr	Gly	Pro	Glu	65	70	75	80
Ser	Ser	Gly	Lys	Thr	Thr	Val	Ala	Leu	His	Ala	Ile	Ala	Gln	Ala	Gln	85	90	95	
Lys	Ala	Gly	Gly	Ile	Ala	Ala	Phe	Ile	Asp	Ala	Glu	His	Ala	Leu	Asp	100	105	110	
Pro	Asp	Tyr	Ala	Arg	Lys	Leu	Gly	Val	Asp	Thr	Asp	Ala	Leu	Leu	Val	115	120	125	
Ser	Gln	Pro	Asp	Thr	Gly	Glu	Gln	Ala	Leu	Glu	Ile	Ala	Asp	Met	Leu	130	135	140	
Val	Arg	Ser	Gly	Ala	Ile	Asp	Ile	Ile	Val	Ile	Asp	Ser	Val	Ala	Ala	145	150	155	160
Leu	Thr	Pro	Lys	Ala	Glu	Ile	Glu	Gly	Glu	Met	Gly	Asp	Ser	His	Val	165	170	175	
Gly	Leu	Gln	Ala	Arg	Leu	Met	Ser	Gln	Ala	Leu	Arg	Lys	Met	Thr	Gly	180	185	190	
Ala	Leu	Tyr	Asn	Ser	Gly	Thr	Thr	Ala	Ile	Phe	Ile	Asn	Gln	Leu	Arg	195	200	205	
Glu	Lys	Ile	Gly	Val	Met	Phe	Gly	Ser	Pro	Glu	Thr	Thr	Thr	Gly	Gly	210	215	220	
Lys	Ala	Leu	Lys	Phe	Tyr	Ala	Ser	Val	Arg	Cys	Asp	Ile	Arg	Arg	Ile	225	230	235	240
Gln	Thr	Leu	Lys	Asp	Gly	Gln	Asp	Ala	Ile	Gly	Asn	Arg	Thr	Arg	Leu	245	250	255	
Lys	Val	Val	Lys	Asn	Lys	Val	Ser	Pro	Pro	Phe	Lys	Ile	Ala	Glu	Phe	260	265	270	
Asp	Ile	Met	Tyr	Gly	Glu	Gly	Ile	Ser	Arg	Glu	Ser	Ser	Val	Ile	Asp	275	280	285	
Leu	Ala	Val	Asp	Asn	Gly	Ile	Val	Lys	Lys	Ser	Gly	Ser	Trp	Phe	Thr	290	295	300	
Tyr	Glu	Gly	Glu	Gln	Leu	Gly	Gln	Gly	Lys	Glu	Lys	Val	Arg	Leu	Ser	305	310	315	320
Leu	Lys	Glu	Asn	Pro	Glu	Leu	Thr	Asp	Glu	Leu	Glu	Asp	Lys	Ile	Phe	325	330	335	
Lys	Lys	Leu	Gly	Val	Gly	Lys	Tyr	Ala	Ala	Ala	Ser	Asp	Glu	Leu	Thr	340	345	350	
Asp	Asp	Pro	Val	Glu	Leu	Val	Pro	Asn	Val	Asp	Phe	Asp	Asp	Glu	Ala	355	360	365	
Asp	Thr	Glu	Ala	Asp	Thr	Glu	Ala	Asp	Ala	Glu	Asp					370	375	380	

<400> 139																
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Met Ser Thr Arg Thr 1 5																
acg cca caa gac cgt tat acc gac gaa tac ggc atc gaa cgc gtc aac 163																
Thr Pro Gln Asp Arg Tyr Thr Asp Glu Tyr Gly Ile Glu Arg Val Asn 10 15 20																
aag gat gaa ccc ggc ctg gtg gac aaa ctc cgg gac aag cac gac tgg 211																
Lys Asp Glu Pro Gly Leu Val Asp Lys Leu Arg Asp Lys His Asp Trp 25 30 35																
ttt gat cat ctc atg cgc atg aat gaa cgt ttc ggc gca aaa ggt ggc 259																
Phe Asp His Leu Met Arg Met Asn Glu Arg Phe Gly Ala Lys Gly Gly 40 45 50																
aac caa ttg tcg gcg ggt att acg tat ttc tcc gtg ctg tcg atc ttc 307																
Asn Gln Leu Ser Ala Gly Ile Thr Tyr Phe Ser Val Leu Ser Ile Phe 55 60 65																
ccg att gcc atg ctt gtc ttc ggt att gca ggt gtc atc ctt gcc gga 355																
Pro Ile Ala Met Leu Val Phe Gly Ile Ala Gly Val Ile Leu Ala Gly 70 75 80 85																
aac cct gaa gtt ctc aca gat att caa aat cga atc aac gat gct tta 403																
Asn Pro Glu Val Leu Thr Asp Ile Gln Asn Arg Ile Asn Asp Ala Leu 90 95 100																
gaa ggc gag atc ggt aac acc gtc aac ggc atc att gat tcc gcg att 451																
Glu Gly Glu Ile Gly Asn Thr Val Asn Gly Ile Ile Asp Ser Ala Ile 105 110 115																
gcg cag cgt ggt gct gtg ttg ggc att ggt ggt gta act gcc ctg tgg 499																
Ala Gln Arg Gly Ala Val Leu Gly Ile Gly Gly Val Thr Ala Leu Trp 120 125 130																
tct gga ctg ggg tgg atg gcg aac ctg cgc ttt gga gtt tcc cgc atg 547																
Ser Gly Leu Gly Trp Met Ala Asn Leu Arg Phe Gly Val Ser Arg Met 135 140 145																
tgg gcc att gac cca act gaa ggc aac ttc att caa aag aag ctc acc 595																
Trp Ala Ile Asp Pro Thr Glu Gly Asn Phe Ile Gln Lys Lys Leu Thr 150 155 160 165																
gac ttg gtc gcg ctg atc gtc ttg ctg ctg gcc atg ggc gta gcc ttc 643																
Asp Leu Val Ala Leu Ile Val Leu Leu Ala Met Gly Val Ala Phe 170 175 180																

ggt atc acg gcg ctc ggt gct tcc gga cta acc aaa aac ctg ctg gac 691  
 Gly Ile Thr Ala Leu Gly Ala Ser Gly Leu Thr Lys Asn Leu Leu Asp  
 185 190 195

ttt gtg ggc ctg ggg gag att ccg ggc att agc tac atc acc tgg gtg 739  
 Phe Val Gly Leu Gly Glu Ile Pro Gly Ile Ser Tyr Ile Thr Trp Val  
 200 205 210

gtc gca gca ctt gtt ggt gtc ttg gct aac ttc ctg gtg ttc atg tgg 787  
 Val Ala Ala Leu Val Gly Val Leu Ala Asn Phe Leu Val Phe Met Trp  
 215 220 225

ctg att ttc tcc ctg cca cgt acc aaa gtt ccc atg aaa ccg ggt ctt 835  
 Leu Ile Phe Ser Leu Pro Arg Thr Lys Val Pro Met Lys Pro Gly Leu  
 230 235 240 245

cag gca gca ctg ctt ggc gca atc ggt ttt gag gtg gtc aag cag gtt 883  
 Gln Ala Ala Leu Leu Gly Ala Ile Gly Phe Glu Val Val Lys Gln Val  
 250 255 260

gga tcg ctg ttg gct tca aat gca ttg agt aac ccc gcg ggt gca gca 931  
 Gly Ser Leu Leu Ala Ser Asn Ala Leu Ser Asn Pro Ala Gly Ala Ala  
 265 270 275

ttc ggt ccg atc atc ggc atc atg gtt gtg ctg tat ttg atc tgg cgc 979  
 Phe Gly Pro Ile Ile Gly Ile Met Val Val Leu Tyr Leu Ile Trp Arg  
 280 285 290

atc ctc atg tat tgc tct gcg tgg gct gcc acc agt gaa gaa gcg ttg 1027  
 Ile Leu Met Tyr Cys Ser Ala Trp Ala Ala Thr Ser Glu Glu Ala Leu  
 295 300 305

cgt ctt gcg act gtt cca gca cca gag cct gcg atc att cgg gtt cgc 1075  
 Arg Leu Ala Thr Val Pro Ala Pro Glu Pro Ala Ile Ile Arg Val Arg  
 310 315 320 325

cat gaa att gat cca ggt gaa gaa gtc tcc caa tct gct cga aaa gtg 1123  
 His Glu Ile Asp Pro Gly Glu Glu Val Ser Gln Ser Ala Arg Lys Val  
 330 335 340

ggc att gga gtg gcc gtg ggt gcc gcg act gcg ggt gct ttt gcg ctg 1171  
 Gly Ile Gly Val Ala Val Gly Ala Ala Thr Ala Gly Ala Phe Ala Leu  
 345 350 355

ttg cgt aaa aaa tagtttttat taagggcatt ccc 1206  
 Leu Arg Lys Lys  
 360

&lt;210&gt; 140

&lt;211&gt; 361

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 140

Met Ser Thr Arg Thr Thr Pro Gln Asp Arg Tyr Thr Asp Glu Tyr Gly  
 1 5 10 15

Ile Glu Arg Val Asn Lys Asp Glu Pro Gly Leu Val Asp Lys Leu Arg  
 20 25 30

Asp	Lys	His 35	Asp	Trp	Phe	Asp	His 40	Leu	Met	Arg	Met	Asn 45	Glu	Arg	Phe
Gly	Ala 50	Lys	Gly	Gly	Asn	Gln 55	Leu	Ser	Ala	Gly	Ile 60	Thr	Tyr	Phe	Ser
Val 65	Leu	Ser	Ile	Phe	Pro 70	Ile	Ala	Met	Leu	Val 75	Phe	Gly	Ile	Ala	Gly 80
Val	Ile	Leu	Ala	Gly 85	Asn	Pro	Glu	Val	Leu 90	Thr	Asp	Ile	Gln	Asn 95	Arg
Ile	Asn	Asp	Ala 100	Leu	Glu	Gly	Glu 105	Ile	Gly	Asn	Thr	Val	Asn 110	Gly	Ile
Ile	Asp	Ser 115	Ala	Ile	Ala	Gln	Arg 120	Gly	Ala	Val	Leu	Gly 125	Ile	Gly	Gly
Val	Thr 130	Ala	Leu	Trp	Ser	Gly 135	Leu	Gly	Trp	Met	Ala 140	Asn	Leu	Arg	Phe
Gly 145	Val	Ser	Arg	Met	Trp 150	Ala	Ile	Asp	Pro	Thr 155	Glu	Gly	Asn	Phe	Ile 160
Gln	Lys	Lys	Leu	Thr 165	Asp	Leu	Val	Ala	Leu 170	Ile	Val	Leu	Leu	Leu 175	Ala
Met	Gly	Val	Ala 180	Phe	Gly	Ile	Thr	Ala 185	Leu	Gly	Ala	Ser	Gly 190	Leu	Thr
Lys	Asn 195	Leu	Leu	Asp	Phe	Val	Gly 200	Leu	Gly	Glu	Ile	Pro 205	Gly	Ile	Ser
Tyr 210	Ile	Thr	Trp	Val	Val	Ala 215	Ala	Leu	Val	Gly	Val 220	Leu	Ala	Asn	Phe
Leu 225	Val	Phe	Met	Trp	Leu 230	Ile	Phe	Ser	Leu	Pro 235	Arg	Thr	Lys	Val	Pro 240
Met	Lys	Pro	Gly	Leu 245	Gln	Ala	Ala	Leu	Leu 250	Gly	Ala	Ile	Gly	Phe 255	Glu
Val	Val	Lys	Gln 260	Val	Gly	Ser	Leu 265	Leu	Ala	Ser	Asn	Ala	Leu 270	Ser	Asn
Pro	Ala 275	Gly	Ala	Ala	Phe	Gly	Pro 280	Ile	Ile	Gly	Ile	Met 285	Val	Val	Leu
Tyr 290	Leu	Ile	Trp	Arg	Ile	Leu 295	Met	Tyr	Cys	Ser	Ala 300	Trp	Ala	Ala	Thr
Ser 305	Glu	Glu	Ala	Leu	Arg 310	Leu	Ala	Thr	Val	Pro 315	Ala	Pro	Glu	Pro	Ala 320
Ile	Ile	Arg	Val	Arg 325	His	Glu	Ile	Asp	Pro 330	Gly	Glu	Glu	Val	Ser 335	Gln
Ser	Ala	Arg	Lys 340	Val	Gly	Ile	Gly 345	Val	Ala	Val	Gly	Ala	Ala 350	Thr	Ala

Gly Ala Phe Ala Leu Leu Arg Lys Lys  
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 Ser Lys Leu Ala Ser Met Gly Val Glu Thr Ile Gly Asp Leu Ala Ala  
 20 25 30  
 cta acc caa aaa gaa gta gaa atc agc ctc ggt gca acc atc gga ata 144  
 Leu Thr Gln Lys Glu Val Glu Ile Ser Leu Gly Ala Thr Ile Gly Ile  
 35 40 45  
 tca ctg tgg aac ctt gcc cga gga atc gac gac cgc cct gtg gaa ccc 192  
 Ser Leu Trp Asn Leu Ala Arg Gly Ile Asp Asp Arg Pro Val Glu Pro  
 50 55 60  
 cgc gcc gaa gca aaa cag atc tcc caa gag cac acc tat gaa aaa gac 240  
 Arg Ala Glu Ala Lys Gln Ile Ser Gln Glu His Thr Tyr Glu Lys Asp  
 65 70 75 80  
 ctc ctc acc agg caa caa gta gat gct gcc atc att cga tca gcc gaa 288  
 Leu Leu Thr Arg Gln Gln Val Asp Ala Ala Ile Ile Arg Ser Ala Glu  
 85 90 95  
 ggc gca cac cga cgg ctc ctc aaa gac gga cgc ggt gcc aga act gtc 336  
 Gly Ala His Arg Arg Leu Leu Lys Asp Gly Arg Gly Ala Arg Thr Val  
 100 105 110  
 agc gtg aaa ctg cgg atg gcc gac ttt cgt att gag tct cgt tcc tac 384  
 Ser Val Lys Leu Arg Met Ala Asp Phe Arg Ile Glu Ser Arg Ser Tyr  
 115 120 125  
 acc ttg tcc tat gcc acc gat gat tac gca act ctt gag gca aca gca 432  
 Thr Leu Ser Tyr Ala Thr Asp Asp Tyr Ala Thr Leu Glu Ala Thr Ala  
 130 135 140  
 ttc cga ctt gcc cgc tac ccc gga gaa gta ggc ccc atc cgc ctt gtc 480  
 Phe Arg Leu Ala Arg Tyr Pro Gly Glu Val Gly Pro Ile Arg Leu Val  
 145 150 155 160  
 gga gta agt ttt tct ggt ttg gaa gaa tcc cgc caa gac atc ctc ttc 528  
 Gly Val Ser Phe Ser Gly Leu Glu Glu Ser Arg Gln Asp Ile Leu Phe  
 165 170 175  
 ccg gaa ctt gac caa caa atc atc gta cca cca gca ccc gac acc gat 576  
 Pro Glu Leu Asp Gln Gln Ile Ile Val Pro Pro Ala Pro Asp Thr Asp

180	185	190	
tat gag gta ggc gtg caa tcc tct tct agt tcc gaa agt act caa gtt			624
Tyr Glu Val Gly Val Gln Ser Ser Ser Ser Ser Glu Ser Thr Gln Val			
195	200	205	
gaa gcg ccg caa gat gtc gcg ttg agt atg tgg tgc gca acg caa gat			672
Glu Ala Pro Gln Asp Val Ala Leu Ser Met Trp Cys Ala Thr Gln Asp			
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gtc tac cac cca gaa tat ggc cac ggt tgg gta caa ggt gcc ggt cac			720
Val Tyr His Pro Glu Tyr Gly His Gly Trp Val Gln Gly Ala Gly His			
225	230	235	240
ggg gtt gta tca gta cgt ttt gaa acc cgc agc acc aca aaa ggg cga			768
Gly Val Val Ser Val Arg Phe Glu Thr Arg Ser Thr Thr Lys Gly Arg			
245	250	255	
act aaa agt ttt tcc atg gat gac ccg gac ctc acc ccg gca gac cct			816
Thr Lys Ser Phe Ser Met Asp Asp Pro Asp Leu Thr Pro Ala Asp Pro			
260	265	270	
cta gat agt ttg gat tgg gct gac tgg ttt gct gaa aat ggt gaa acg			864
Leu Asp Ser Leu Asp Trp Ala Asp Trp Phe Ala Glu Asn Gly Glu Thr			
275	280	285	
ggg gat gac gaa taggggtttca tcggggtttcg ggg			899
Gly Asp Asp Glu			
290			

&lt;210&gt; 142

&lt;211&gt; 292

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 142

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Ser Lys Leu Ala Ser Met Gly Val Glu Thr Ile Gly Asp Leu Ala Ala			
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Leu Thr Gln Lys Glu Val Glu Ile Ser Leu Gly Ala Thr Ile Gly Ile			
35	40	45	
Ser Leu Trp Asn Leu Ala Arg Gly Ile Asp Asp Arg Pro Val Glu Pro			
50	55	60	
Arg Ala Glu Ala Lys Gln Ile Ser Gln Glu His Thr Tyr Glu Lys Asp			
65	70	75	80
Leu Leu Thr Arg Gln Gln Val Asp Ala Ala Ile Ile Arg Ser Ala Glu			
85	90	95	
Gly Ala His Arg Arg Leu Leu Lys Asp Gly Arg Gly Ala Arg Thr Val			
100	105	110	
Ser Val Lys Leu Arg Met Ala Asp Phe Arg Ile Glu Ser Arg Ser Tyr			
115	120	125	

Thr Leu Ser Tyr Ala Thr Asp Asp Tyr Ala Thr Leu Glu Ala Thr Ala  
 130 135 140  
 Phe Arg Leu Ala Arg Tyr Pro Gly Glu Val Gly Pro Ile Arg Leu Val  
 145 150 155 160  
 Gly Val Ser Phe Ser Gly Leu Glu Glu Ser Arg Gln Asp Ile Leu Phe  
 165 170 175  
 Pro Glu Leu Asp Gln Gln Ile Ile Val Pro Pro Ala Pro Asp Thr Asp  
 180 185 190  
 Tyr Glu Val Gly Val Gln Ser Ser Ser Ser Glu Ser Thr Gln Val  
 195 200 205  
 Glu Ala Pro Gln Asp Val Ala Leu Ser Met Trp Cys Ala Thr Gln Asp  
 210 215 220  
 Val Tyr His Pro Glu Tyr Gly His Gly Trp Val Gln Gly Ala Gly His  
 225 230 235 240  
 Gly Val Val Ser Val Arg Phe Glu Thr Arg Ser Thr Thr Lys Gly Arg  
 245 250 255  
 Thr Lys Ser Phe Ser Met Asp Asp Pro Asp Leu Thr Pro Ala Asp Pro  
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 Gly Asp Asp Glu  
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 Met Arg Leu Glu Ser  
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tat gcc atg gct aag aaa gta gac acc tcg aac gct acc ccc gct cta 163  
 Tyr Ala Met Ala Lys Lys Val Asp Thr Ser Asn Ala Thr Pro Ala Leu  
 10 15 20

gcc ctt ctt acg gag agg cag att cct ttt gag ctg gat gtt cat gat 211  
 Ala Leu Leu Thr Glu Arg Gln Ile Pro Phe Glu Leu Asp Val His Asp  
 25 30 35

gta gat cca aaa tca tca aag ggc ttt gca ttg gat gcc tct gaa gta 259  
 Val Asp Pro Lys Ser Ser Lys Gly Phe Ala Leu Asp Ala Ser Glu Val

40                                      45                                      50  
 atg ggt gtg gag ccg gaa gtg gtg ttt aaa acg ctc atg gca gat att 307  
 Met Gly Val Glu Pro Glu Val Val Phe Lys Thr Leu Met Ala Asp Ile  
     55                                      60                                      65  
 gat ggt gaa cac gtg gtc gcg att gtt cca gcc agc aga acg ttg aat 355  
 Asp Gly Glu His Val Val Ala Ile Val Pro Ala Ser Arg Thr Leu Asn  
     70                                      75                                      80                                      85  
 ctc aag cag ttg gct aag gct gga aaa ggt aag cat gca aac atg atg 403  
 Leu Lys Gln Leu Ala Lys Ala Gly Lys Gly Lys His Ala Asn Met Met  
                                     90                                      95                                      100  
 gat cgc agc cgt gca cag gta gtt acg ggg taagtcctg gtggaatctc acc 456  
 Asp Arg Ser Arg Ala Gln Val Val Thr Gly  
                                     105                                      110

&lt;210&gt; 144

&lt;211&gt; 111

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 144

Met Arg Leu Glu Ser Tyr Ala Met Ala Lys Lys Val Asp Thr Ser Asn  
     1                                      5                                      10                                      15  
 Ala Thr Pro Ala Leu Ala Leu Leu Thr Glu Arg Gln Ile Pro Phe Glu  
                                     20                                      25                                      30  
 Leu Asp Val His Asp Val Asp Pro Lys Ser Ser Lys Gly Phe Ala Leu  
                                     35                                      40                                      45  
 Asp Ala Ser Glu Val Met Gly Val Glu Pro Glu Val Val Phe Lys Thr  
                                     50                                      55                                      60  
 Leu Met Ala Asp Ile Asp Gly Glu His Val Val Ala Ile Val Pro Ala  
                                     65                                      70                                      75                                      80  
 Ser Arg Thr Leu Asn Leu Lys Gln Leu Ala Lys Ala Gly Lys Gly Lys  
                                     85                                      90                                      95  
 His Ala Asn Met Met Asp Arg Ser Arg Ala Gln Val Val Thr Gly  
                                     100                                      105                                      110

&lt;210&gt; 145

&lt;211&gt; 261

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(238)

&lt;223&gt; RXN02986

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Val Phe Leu Asp Glu  
1 5

tct gca att ctc cag gag cga atc tac gtc agc gca ggg cga cgc ggg 163  
Ser Ala Ile Leu Gln Glu Arg Ile Tyr Val Ser Ala Gly Arg Arg Gly  
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tgg tcc ctg att atc gcc ccg gat gat gtt ctt ctg gct acc gat ggt 211  
Trp Ser Leu Ile Ile Ala Pro Asp Asp Val Leu Leu Ala Thr Asp Gly  
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Val Thr Glu Lys Thr  
1 5

gac cag acc tta atg ctt atc gac ggc cac tcg atg gct ttc cgc gca 163  
Asp Gln Thr Leu Met Leu Ile Asp Gly His Ser Met Ala Phe Arg Ala  
10 15 20

ttc ttt gct ttg ccg gct gag aat ttc tcc acg tcg ggc ggg cag gcc 211  
Phe Phe Ala Leu Pro Ala Glu Asn Phe Ser Thr Ser Gly Gly Gln Ala  
25 30 35

acc aat gct gtc tat ggc ttt ctc tcg atg ctg tcc acg ttg ttg aag 259  
Thr Asn Ala Val Tyr Gly Phe Leu Ser Met Leu Ser Thr Leu Leu Lys  
40 45 50

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Asp	Glu	Gln	Pro	Thr	His	Val	Ala	Val	Ala	Phe	Asp	Val	Gly	Arg	Lys	
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Thr	Phe	Arg	Thr	Asp	Met	Phe	Pro	Ala	Tyr	Lys	Ala	Gln	Arg	Glu	Ala	
	70				75					80					85	
acg	cca	cct	gag	ttt	aag	ggc	cag	gtg	gaa	atc	ctc	aag	gag	gtg	ttg	403
Thr	Pro	Pro	Glu	Phe	Lys	Gly	Gln	Val	Glu	Ile	Leu	Lys	Glu	Val	Leu	
				90					95					100		
tcc	act	ttg	gga	att	acg	act	att	gag	aaa	atc	gat	ttt	gag	gct	gat	451
Ser	Thr	Leu	Gly	Ile	Thr	Thr	Ile	Glu	Lys	Ile	Asp	Phe	Glu	Ala	Asp	
			105					110					115			
gat	gtg	atc	gcc	acg	ttg	tct	gtg	gcg	gcg	aaa	cct	tta	ggc	ttt	aag	499
Asp	Val	Ile	Ala	Thr	Leu	Ser	Val	Ala	Ala	Lys	Pro	Leu	Gly	Phe	Lys	
		120					125					130				
acg	ctg	att	gtt	acg	ggc	gac	cgt	gat	tcc	ttc	cag	ttg	gtc	aat	gac	547
Thr	Leu	Ile	Val	Thr	Gly	Asp	Arg	Asp	Ser	Phe	Gln	Leu	Val	Asn	Asp	
	135					140					145					
acc	acc	acg	gtg	ttg	tat	ccg	atg	aag	ggc	gtg	tct	gtg	ctg	cac	cgt	595
Thr	Thr	Thr	Val	Leu	Tyr	Pro	Met	Lys	Gly	Val	Ser	Val	Leu	His	Arg	
	150				155					160					165	
ttc	acg	ccg	gaa	gca	gtg	gag	gag	aag	tat	gga	ctg	aca	ccg	agg	cag	643
Phe	Thr	Pro	Glu	Ala	Val	Glu	Glu	Lys	Tyr	Gly	Leu	Thr	Pro	Arg	Gln	
			170						175					180		
tat	ccg	gag	ttt	gca	gcg	ctg	cgt	ggc	gat	cct	tcc	gat	aac	ttg	cct	691
Tyr	Pro	Glu	Phe	Ala	Ala	Leu	Arg	Gly	Asp	Pro	Ser	Asp	Asn	Leu	Pro	
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Asn	Ile	Pro	Gly	Val	Gly	Glu	Lys	Thr	Ala	Thr	Lys	Trp	Ile	Ala	Gln	
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Tyr	Glu	Thr	Leu	Asp	Asn	Leu	Leu	Asp	His	Ala	Asp	Glu	Ile	Lys	Gly	
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Lys	Val	Gly	Ala	Ser	Leu	Arg	Glu	Arg	Ile	Glu	Gln	Val	Arg	Met	Asn	
	230				235					240					245	
cgc	aag	ctc	acg	gag	atg	gtg	aag	gat	ctg	gag	ctg	ccg	ctt	ggc	ccg	883
Arg	Lys	Leu	Thr	Glu	Met	Val	Lys	Asp	Leu	Glu	Leu	Pro	Leu	Gly	Pro	
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gac	gat	ttt	gag	atg	aag	cct	gtg	cag	gtt	gcg	gag	gtt	gcg	gcg	aag	931
Asp	Asp	Phe	Glu	Met	Lys	Pro	Val	Gln	Val	Ala	Glu	Val	Ala	Ala	Lys	
			265					270					275			
ttt	gac	gat	ctg	gag	ttt	ggc	acc	aat	ttg	cgt	gag	cgg	gtg	ctg	gcg	979
Phe	Asp	Asp	Leu	Glu	Phe	Gly	Thr	Asn	Leu	Arg	Glu	Arg	Val	Leu	Ala	
		280					285					290				
gtg	gtg	aag	gcc	gag	ggc	tcc	gct	gcc	ccc	gtg	gag	gaa	gtg	gaa	gcg	1027

Val	Val	Lys	Ala	Glu	Gly	Ser	Ala	Ala	Pro	Val	Glu	Glu	Val	Glu	Ala	
	295					300					305					
gaa	cag	gtt	gtc	gtc	gat	acg	caa	tct	ttg	gcg	caa	tggt	ctg	cct	gct	1075
Glu	Gln	Val	Val	Val	Asp	Thr	Gln	Ser	Leu	Ala	Gln	Trp	Leu	Pro	Ala	
310					315					320					325	
agg	gct	ggc	cag	gcg	ctt	gct	tta	gcg	ctg	gct	gga	gtg	gct	aaa	cct	1123
Arg	Ala	Gly	Gln	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Gly	Val	Ala	Lys	Pro	
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gct	gct	ggc	gac	acg	tat	gcg	cta	gcg	att	gcg	gat	acc	aag	cg	cat	1171
Ala	Ala	Gly	Asp	Thr	Tyr	Ala	Leu	Ala	Ile	Ala	Asp	Thr	Lys	Arg	His	
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gcg	gtg	ttg	gtt	gat	gtg	gct	gat	att	tca	gcg	gag	gat	gaa	aag	gcg	1219
Ala	Val	Leu	Val	Asp	Val	Ala	Asp	Ile	Ser	Ala	Glu	Asp	Glu	Lys	Ala	
		360					365						370			
ctg	gcc	acg	tggt	ttg	gcg	tcg	gaa	gat	cca	aag	atg	ctg	cac	ggc	gct	1267
Leu	Ala	Thr	Trp	Leu	Ala	Ser	Glu	Asp	Pro	Lys	Met	Leu	His	Gly	Ala	
		375				380					385					
aag	gcc	gcc	tat	cat	atg	ctc	gct	ggg	cg	ggt	ttt	gag	ctg	cac	ggc	1315
Lys	Ala	Ala	Tyr	His	Met	Leu	Ala	Gly	Arg	Gly	Phe	Glu	Leu	His	Gly	
390					395					400					405	
gtg	gtg	cat	gac	acg	gcg	atc	gcg	gca	tac	ttg	ctg	cgt	ccg	ggc	caa	1363
Val	Val	His	Asp	Thr	Ala	Ile	Ala	Ala	Tyr	Leu	Leu	Arg	Pro	Gly	Gln	
				410					415					420		
cg	acc	tat	gag	ctt	gcc	gac	gtc	tac	cag	cg	cat	ctt	caa	cga	cag	1411
Arg	Thr	Tyr	Glu	Leu	Ala	Asp	Val	Tyr	Gln	Arg	His	Leu	Gln	Arg	Gln	
			425					430					435			
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Leu	Ser	Thr	Asn	Asp	Asn	Gly	Gly	Gln	Leu	Thr	Leu	Leu	Asp	Ala	Ala	
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Asp	Asp	Gln	Ser	Leu	Val	Asp	Asp	Val	Ile	Ala	Ile	Leu	Glu	Leu	Ser	
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gaa	gaa	ttg	acc	aaa	cag	ctt	cag	gag	att	caa	gct	ttt	gag	ctt	tac	1555
Glu	Glu	Leu	Thr	Lys	Gln	Leu	Gln	Glu	Ile	Gln	Ala	Phe	Glu	Leu	Tyr	
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His	Asp	Leu	Glu	Ile	Pro	Leu	Ser	Gly	Ile	Leu	Ala	Arg	Met	Glu	Ala	
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Ile	Gly	Ile	Ala	Val	Asp	Val	Ala	Thr	Leu	Glu	Glu	Gln	Leu	Lys	Thr	
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Phe	Ile	Gly	Gln	Val	Ala	Gln	Glu	Glu	Glu	Ala	Ala	Arg	Glu	Leu	Ala	
		520					525					530				
gag	gat	cca	acc	ctg	aat	ctc	tcg	agc	ccg	aag	cag	ctg	caa	gtg	gtg	1747
Glu	Asp	Pro	Thr	Leu	Asn	Leu	Ser	Ser	Pro	Lys	Gln	Leu	Gln	Val	Val	

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cac cca ttc cta gat cac ctg ttg gca cac cgt cag tac caa aag atg His Pro Phe Leu Asp His Leu Leu Ala His Arg Gln Tyr Gln Lys Met 585 590 595			1891
aag acc act ctg gaa ggt ctc atc cgt gag gtg gct cct gat ggc cgt Lys Thr Thr Leu Glu Gly Leu Ile Arg Glu Val Ala Pro Asp Gly Arg 600 605 610			1939
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tcc act gat ccc aac ctg caa aac att cct gtg cgc act gag gct ggc Ser Thr Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Glu Ala Gly 630 635 640 645			2035
cga aag att cgt tcg gga ttc gtc gta ggc gag ggg tat gaa acc ttg Arg Lys Ile Arg Ser Gly Phe Val Val Gly Glu Gly Tyr Glu Thr Leu 650 655 660			2083
ctg act gcc gac tat tcg cag att gaa atg cgc gtg atg gct cac ctt Leu Thr Ala Asp Tyr Ser Gln Ile Glu Met Arg Val Met Ala His Leu 665 670 675			2131
tcc cag gac cca ggc ttg att gag gcg tac cgc gaa ggc gaa gac ctg Ser Gln Asp Pro Gly Leu Ile Glu Ala Tyr Arg Glu Gly Glu Asp Leu 680 685 690			2179
cac aat tac gtg ggt tcc aag gtg ttt aat gtg ccc atc gat ggc gtg His Asn Tyr Val Gly Ser Lys Val Phe Asn Val Pro Ile Asp Gly Val 695 700 705			2227
acc cct gag ctg cgt cgc cag gtc aag gcc atg tct tac ggt ctg gtg Thr Pro Glu Leu Arg Arg Gln Val Lys Ala Met Ser Tyr Gly Leu Val 710 715 720 725			2275
tac ggc ttg tcc gcg ttt ggt ttg tct cag cag ctg agc att cct gct Tyr Gly Leu Ser Ala Phe Gly Leu Ser Gln Gln Leu Ser Ile Pro Ala 730 735 740			2323
ggc gaa gcg aag cag atc atg gag tcc tac ttc gag cgc ttc ggc gga Gly Glu Ala Lys Gln Ile Met Glu Ser Tyr Phe Glu Arg Phe Gly Gly 745 750 755			2371
gta cag cgc tac ctc cgg gag atc gtg gag gag gct cga aaa gct ggc Val Gln Arg Tyr Leu Arg Glu Ile Val Glu Glu Ala Arg Lys Ala Gly 760 765 770			2419
tac acg gaa acg ctc ttt ggg cgt cgt cgc tac ctg ccg gaa ctg acc Tyr Thr Glu Thr Leu Phe Gly Arg Arg Arg Tyr Leu Pro Glu Leu Thr 775 780 785			2467

tcg gat aac cgt gtc gct cgt gaa aac gct gaa cgt gcc gca ctg aac 2515  
 Ser Asp Asn Arg Val Ala Arg Glu Asn Ala Glu Arg Ala Ala Leu Asn  
 790 795 800 805  
  
 gcc ccg att cag gga act gcc gca gac atc atc aag gtg gcc atg atc 2563  
 Ala Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Val Ala Met Ile  
 810 815 820  
  
 cgg gtg gac cgt tca ctc aag gaa gct gcc gtg aaa tct cgc gtg ctg 2611  
 Arg Val Asp Arg Ser Leu Lys Glu Ala Ala Val Lys Ser Arg Val Leu  
 825 830 835  
  
 ctt cag gtg cat gat gaa ttg gtc gtg gaa gta gcg gcc ggt gag ttg 2659  
 Leu Gln Val His Asp Glu Leu Val Val Glu Val Ala Ala Gly Glu Leu  
 840 845 850  
  
 gaa caa gtc cgt gag att ctg gaa cgc gaa atg gat aac gcc atc aag 2707  
 Glu Gln Val Arg Glu Ile Leu Glu Arg Glu Met Asp Asn Ala Ile Lys  
 855 860 865  
  
 ctg tcc gtt cct ttg gaa gtt tca gct ggt gat ggc gtt aac tgg gat 2755  
 Leu Ser Val Pro Leu Glu Val Ser Ala Gly Asp Gly Val Asn Trp Asp  
 870 875 880 885  
  
 gct gca gcg cac taagaggtaa ctgccttttc gtc 2790  
 Ala Ala Ala His

&lt;210&gt; 148

&lt;211&gt; 889

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 148

Val Thr Glu Lys Thr Asp Gln Thr Leu Met Leu Ile Asp Gly His Ser  
 1 5 10 15

Met Ala Phe Arg Ala Phe Phe Ala Leu Pro Ala Glu Asn Phe Ser Thr  
 20 25 30

Ser Gly Gly Gln Ala Thr Asn Ala Val Tyr Gly Phe Leu Ser Met Leu  
 35 40 45

Ser Thr Leu Leu Lys Asp Glu Gln Pro Thr His Val Ala Val Ala Phe  
 50 55 60

Asp Val Gly Arg Lys Thr Phe Arg Thr Asp Met Phe Pro Ala Tyr Lys  
 65 70 75 80

Ala Gln Arg Glu Ala Thr Pro Pro Glu Phe Lys Gly Gln Val Glu Ile  
 85 90 95

Leu Lys Glu Val Leu Ser Thr Leu Gly Ile Thr Thr Ile Glu Lys Ile  
 100 105 110

Asp Phe Glu Ala Asp Asp Val Ile Ala Thr Leu Ser Val Ala Ala Lys  
 115 120 125

Pro Leu Gly Phe Lys Thr Leu Ile Val Thr Gly Asp Arg Asp Ser Phe

130	135	140
Gln Leu Val Asn Asp Thr Thr Thr Val Leu Tyr Pro Met Lys Gly Val 145 150 155 160		
Ser Val Leu His Arg Phe Thr Pro Glu Ala Val Glu Glu Lys Tyr Gly 165 170 175		
Leu Thr Pro Arg Gln Tyr Pro Glu Phe Ala Ala Leu Arg Gly Asp Pro 180 185 190		
Ser Asp Asn Leu Pro Asn Ile Pro Gly Val Gly Glu Lys Thr Ala Thr 195 200 205		
Lys Trp Ile Ala Gln Tyr Glu Thr Leu Asp Asn Leu Leu Asp His Ala 210 215 220		
Asp Glu Ile Lys Gly Lys Val Gly Ala Ser Leu Arg Glu Arg Ile Glu 225 230 235 240		
Gln Val Arg Met Asn Arg Lys Leu Thr Glu Met Val Lys Asp Leu Glu 245 250 255		
Leu Pro Leu Gly Pro Asp Asp Phe Glu Met Lys Pro Val Gln Val Ala 260 265 270		
Glu Val Ala Ala Lys Phe Asp Asp Leu Glu Phe Gly Thr Asn Leu Arg 275 280 285		
Glu Arg Val Leu Ala Val Val Lys Ala Glu Gly Ser Ala Ala Pro Val 290 295 300		
Glu Glu Val Glu Ala Glu Gln Val Val Val Asp Thr Gln Ser Leu Ala 305 310 315 320		
Gln Trp Leu Pro Ala Arg Ala Gly Gln Ala Leu Ala Leu Ala Leu Ala 325 330 335		
Gly Val Ala Lys Pro Ala Ala Gly Asp Thr Tyr Ala Leu Ala Ile Ala 340 345 350		
Asp Thr Lys Arg His Ala Val Leu Val Asp Val Ala Asp Ile Ser Ala 355 360 365		
Glu Asp Glu Lys Ala Leu Ala Thr Trp Leu Ala Ser Glu Asp Pro Lys 370 375 380		
Met Leu His Gly Ala Lys Ala Ala Tyr His Met Leu Ala Gly Arg Gly 385 390 395 400		
Phe Glu Leu His Gly Val Val His Asp Thr Ala Ile Ala Ala Tyr Leu 405 410 415		
Leu Arg Pro Gly Gln Arg Thr Tyr Glu Leu Ala Asp Val Tyr Gln Arg 420 425 430		
His Leu Gln Arg Gln Leu Ser Thr Asn Asp Asn Gly Gly Gln Leu Thr 435 440 445		
Leu Leu Asp Ala Ala Asp Asp Gln Ser Leu Val Asp Asp Val Ile Ala 450 455 460		

Ile	Leu	Glu	Leu	Ser	Glu	Glu	Leu	Thr	Lys	Gln	Leu	Gln	Glu	Ile	Gln	465	470	475	480
Ala	Phe	Glu	Leu	Tyr	His	Asp	Leu	Glu	Ile	Pro	Leu	Ser	Gly	Ile	Leu	485	490	495	
Ala	Arg	Met	Glu	Ala	Ile	Gly	Ile	Ala	Val	Asp	Val	Ala	Thr	Leu	Glu	500	505	510	
Glu	Gln	Leu	Lys	Thr	Phe	Ile	Gly	Gln	Val	Ala	Gln	Glu	Glu	Glu	Ala	515	520	525	
Ala	Arg	Glu	Leu	Ala	Glu	Asp	Pro	Thr	Leu	Asn	Leu	Ser	Ser	Pro	Lys	530	535	540	
Gln	Leu	Gln	Val	Val	Leu	Phe	Glu	Thr	Phe	Gly	Met	Pro	Lys	Thr	Lys	545	550	555	560
Lys	Thr	Lys	Thr	Gly	Tyr	Ser	Thr	Ala	Ala	Ala	Glu	Ile	Glu	Ala	Leu	565	570	575	
Ala	Ile	Lys	Asn	Pro	His	Pro	Phe	Leu	Asp	His	Leu	Leu	Ala	His	Arg	580	585	590	
Gln	Tyr	Gln	Lys	Met	Lys	Thr	Thr	Leu	Glu	Gly	Leu	Ile	Arg	Glu	Val	595	600	605	
Ala	Pro	Asp	Gly	Arg	Ile	His	Thr	Thr	Phe	Asn	Gln	Thr	Val	Ala	Ser	610	615	620	
Thr	Gly	Arg	Leu	Ser	Ser	Thr	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	625	630	635	640
Arg	Thr	Glu	Ala	Gly	Arg	Lys	Ile	Arg	Ser	Gly	Phe	Val	Val	Gly	Glu	645	650	655	
Gly	Tyr	Glu	Thr	Leu	Leu	Thr	Ala	Asp	Tyr	Ser	Gln	Ile	Glu	Met	Arg	660	665	670	
Val	Met	Ala	His	Leu	Ser	Gln	Asp	Pro	Gly	Leu	Ile	Glu	Ala	Tyr	Arg	675	680	685	
Glu	Gly	Glu	Asp	Leu	His	Asn	Tyr	Val	Gly	Ser	Lys	Val	Phe	Asn	Val	690	695	700	
Pro	Ile	Asp	Gly	Val	Thr	Pro	Glu	Leu	Arg	Arg	Gln	Val	Lys	Ala	Met	705	710	715	720
Ser	Tyr	Gly	Leu	Val	Tyr	Gly	Leu	Ser	Ala	Phe	Gly	Leu	Ser	Gln	Gln	725	730	735	
Leu	Ser	Ile	Pro	Ala	Gly	Glu	Ala	Lys	Gln	Ile	Met	Glu	Ser	Tyr	Phe	740	745	750	
Glu	Arg	Phe	Gly	Gly	Val	Gln	Arg	Tyr	Leu	Arg	Glu	Ile	Val	Glu	Glu	755	760	765	
Ala	Arg	Lys	Ala	Gly	Tyr	Thr	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	770	775	780	

Leu Pro Glu Leu Thr Ser Asp Asn Arg Val Ala Arg Glu Asn Ala Glu  
 785 790 795 800  
 Arg Ala Ala Leu Asn Ala Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile  
 805 810 815  
 Lys Val Ala Met Ile Arg Val Asp Arg Ser Leu Lys Glu Ala Ala Val  
 820 825 830  
 Lys Ser Arg Val Leu Leu Gln Val His Asp Glu Leu Val Val Glu Val  
 835 840 845  
 Ala Ala Gly Glu Leu Glu Gln Val Arg Glu Ile Leu Glu Arg Glu Met  
 850 855 860  
 Asp Asn Ala Ile Lys Leu Ser Val Pro Leu Glu Val Ser Ala Gly Asp  
 865 870 875 880  
 Gly Val Asn Trp Asp Ala Ala Ala His  
 885

<210> 149

<211> 1683

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1660)

<223> RXS00212

<400> 149

ttagagcgtg ccgctactcg tggatgatggt cgcgtgggcg aggacatcac ggccaatgct 60  
 cgcgtgatcg aagatatccc gcaccagctt cagggcactg atg aat atc ctg tgc 115  
 Met Asn Ile Leu Cys  
 1 5  
 ctg ctg tgc tgg aaa ttc gcg gtg agg tgt tca tca ctg tgg agg att 163  
 Leu Leu Cys Trp Lys Phe Ala Val Arg Cys Ser Ser Leu Trp Arg Ile  
 10 15 20  
 tcc cag gag gtc aac gcg cag cgc att gct gat ggt ggc aag ccg ttt 211  
 Ser Gln Glu Val Asn Ala Gln Arg Ile Ala Asp Gly Gly Lys Pro Phe  
 25 30 35  
 gcc aac ccg cgt aat gct gcg gct ggt tct ctg cgt cag aaa aat att 259  
 Ala Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu Arg Gln Lys Asn Ile  
 40 45 50  
 gag gac gtg aag aag cgc cgc ctg cgg atg atc agc cat ggc atc ggt 307  
 Glu Asp Val Lys Lys Arg Arg Leu Arg Met Ile Ser His Gly Ile Gly  
 55 60 65  
 ttc act gaa ggc ttt agc cct gcg tct cag cat gat gcg tat ctg gca 355  
 Phe Thr Glu Gly Phe Ser Pro Ala Ser Gln His Asp Ala Tyr Leu Ala  
 70 75 80 85  
 ttg gct gcc tgg ggt ttg ccc acc tcg ccg tac aca gag gct gtg act 403  
 Leu Ala Ala Trp Gly Leu Pro Thr Ser Pro Tyr Thr Glu Ala Val Thr

90										95					100					
gat	cca	gaa	gat	gtg	gtg	aaa	aag	gtc	agc	tac	tgg	gct	gat	cac	cgc	451				
Asp	Pro	Glu	Asp	Val	Val	Lys	Lys	Val	Ser	Tyr	Trp	Ala	Asp	His	Arg					
			105					110					115							
cac	gac	gca	ctc	cat	gag	atg	gat	ggc	ctg	gtg	att	aag	gtc	gat	gac	499				
His	Asp	Ala	Leu	His	Glu	Met	Asp	Gly	Leu	Val	Ile	Lys	Val	Asp	Asp					
		120					125					130								
atc	gca	tct	cag	cgt	gct	ttg	ggc	tcc	acc	agc	cgc	gcg	cct	cgc	tgg	547				
Ile	Ala	Ser	Gln	Arg	Ala	Leu	Gly	Ser	Thr	Ser	Arg	Ala	Pro	Arg	Trp					
	135					140					145									
gcc	att	gcg	tac	aag	tac	cct	ccg	gag	gag	gtc	acc	acc	aag	ctg	ctt	595				
Ala	Ile	Ala	Tyr	Lys	Tyr	Pro	Pro	Glu	Glu	Val	Thr	Thr	Lys	Leu	Leu					
150					155					160					165					
gat	att	cag	gtt	ggc	gtt	ggc	cgc	acc	ggc	cgt	gtc	acc	cca	ttc	gcg	643				
Asp	Ile	Gln	Val	Gly	Val	Gly	Arg	Thr	Gly	Arg	Val	Thr	Pro	Phe	Ala					
				170					175					180						
gtc	atg	gag	ccg	gtt	ctt	gtt	gca	gga	tca	acg	gtg	tct	atg	gcg	acg	691				
Val	Met	Glu	Pro	Val	Leu	Val	Ala	Gly	Ser	Thr	Val	Ser	Met	Ala	Thr					
			185					190					195							
ctg	cat	aac	cag	agc	gaa	gtc	aag	cgt	aaa	ggc	gtg	ctc	atc	ggc	gac	739				
Leu	His	Asn	Gln	Ser	Glu	Val	Lys	Arg	Lys	Gly	Val	Leu	Ile	Gly	Asp					
		200					205					210								
acc	gtg	gtt	atc	cgc	aag	gcg	ggc	gag	gtt	atc	cca	gag	gtg	ctt	ggc	787				
Thr	Val	Val	Ile	Arg	Lys	Ala	Gly	Glu	Val	Ile	Pro	Glu	Val	Leu	Gly					
	215					220				225										
cct	gtc	gta	gag	ctt	cgt	gac	ggc	aca	gag	cgc	gag	tac	atc	ttc	cca	835				
Pro	Val	Val	Glu	Leu	Arg	Asp	Gly	Thr	Glu	Arg	Glu	Tyr	Ile	Phe	Pro					
230					235					240					245					
acg	ctg	tgc	cct	gaa	tgc	ggc	acc	cgt	ctg	gcg	ccc	gcg	aag	gcc	gat	883				
Thr	Leu	Cys	Pro	Glu	Cys	Gly	Thr	Arg	Leu	Ala	Pro	Ala	Lys	Ala	Asp					
				250				255						260						
gac	gtg	gat	tgg	cgt	tgc	ccc	aac	atg	caa	agc	tgt	cca	ggc	cag	ctg	931				
Asp	Val	Asp	Trp	Arg	Cys	Pro	Asn	Met	Gln	Ser	Cys	Pro	Gly	Gln	Leu					
			265					270					275							
tcc	acg	cgt	ttg	acc	tac	ctt	gct	ggc	cgt	ggc	gct	ttt	gat	att	gaa	979				
Ser	Thr	Arg	Leu	Thr	Tyr	Leu	Ala	Gly	Arg	Gly	Ala	Phe	Asp	Ile	Glu					
		280					285					290								
gca	ttg	ggc	gaa	aag	ggc	gct	gaa	gac	ctc	att	cgc	acc	ggc	att	ttg	1027				
Ala	Leu	Gly	Glu	Lys	Gly	Ala	Glu	Asp	Leu	Ile	Arg	Thr	Gly	Ile	Leu					
	295					300					305									
ctt	gac	gag	tct	ggc	ctg	ttc	gac	ctc	aca	gag	gac	gat	ctg	ctg	agc	1075				
Leu	Asp	Glu	Ser	Gly	Leu	Phe	Asp	Leu	Thr	Glu	Asp	Asp	Leu	Leu	Ser					
310					315					320					325					
tcc	aat	gtc	tac	acc	acc	aac	gcc	ggc	aaa	gta	aat	gcc	agc	ggc	aag	1123				
Ser	Asn	Val	Tyr	Thr	Thr	Asn	Ala	Gly	Lys	Val	Asn	Ala	Ser	Gly	Lys					
				330					335					340						

aaa ctg ctg gac aac ctg caa aaa tcc aag cag acc gac ctc tgg cga 1171  
 Lys Leu Leu Asp Asn Leu Gln Lys Ser Lys Gln Thr Asp Leu Trp Arg  
 345 350 355  
  
 gtc ctc gtg gca tta tct atc agg cac gta ggc ccc acc gca gcg cgc 1219  
 Val Leu Val Ala Leu Ser Ile Arg His Val Gly Pro Thr Ala Ala Arg  
 360 365 370  
  
 gcc ctt gca ggt cgc tac cac tcc atc cag gcg ctt atc gac gcc ccc 1267  
 Ala Leu Ala Gly Arg Tyr His Ser Ile Gln Ala Leu Ile Asp Ala Pro  
 375 380 385  
  
 ctc gag gaa ctc tcc gaa acc gat gga gta ggt acc atc att gcc caa 1315  
 Leu Glu Glu Leu Ser Glu Thr Asp Gly Val Gly Thr Ile Ile Ala Gln  
 390 395 400 405  
  
 tcc ttc aag gac tgg ttc gag gtt gat tgg cac aag gcc atc gtg gac 1363  
 Ser Phe Lys Asp Trp Phe Glu Val Asp Trp His Lys Ala Ile Val Asp  
 410 415 420  
  
 aag tgg gca gcc gct ggt gtg act atg gag gaa gaa gta ggg gag gtc 1411  
 Lys Trp Ala Ala Ala Gly Val Thr Met Glu Glu Glu Val Gly Glu Val  
 425 430 435  
  
 gct gaa caa acc ctt gaa ggc cta acc atc gtg gtc acc gga ggg ttg 1459  
 Ala Glu Gln Thr Leu Glu Gly Leu Thr Ile Val Val Thr Gly Gly Leu  
 440 445 450  
  
 gaa ggc ttc acc aga gat tcg gtg aag gaa gcc atc atc tcc cgt ggc 1507  
 Glu Gly Phe Thr Arg Asp Ser Val Lys Glu Ala Ile Ile Ser Arg Gly  
 455 460 465  
  
 gga aaa gcc tct gga tct gtc tcg aag aaa act gac tac gtg gtg att 1555  
 Gly Lys Ala Ser Gly Ser Val Ser Lys Lys Thr Asp Tyr Val Val Ile  
 470 475 480 485  
  
 ggt gaa aac gca ggt tcc aag gcc acc aag gca gaa gaa cta ggg ctg 1603  
 Gly Glu Asn Ala Gly Ser Lys Ala Thr Lys Ala Glu Glu Leu Gly Leu  
 490 495 500  
  
 cgc att ctg gat gag gca gga ttc gtc cgt ttg ctc aat acc ggc tca 1651  
 Arg Ile Leu Asp Glu Ala Gly Phe Val Arg Leu Leu Asn Thr Gly Ser  
 505 510 515  
  
 gct gac gaa tagtcgcaca tgaaaatgcc cca 1683  
 Ala Asp Glu  
 520

&lt;210&gt; 150

&lt;211&gt; 520

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 150

Met Asn Ile Leu Cys Leu Leu Cys Trp Lys Phe Ala Val Arg Cys Ser  
 1 5 10 15

Ser Leu Trp Arg Ile Ser Gln Glu Val Asn Ala Gln Arg Ile Ala Asp  
 20 25 30

Gly Gly Lys Pro Phe Ala Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu  
 35 40 45  
 Arg Gln Lys Asn Ile Glu Asp Val Lys Lys Arg Arg Leu Arg Met Ile  
 50 55 60  
 Ser His Gly Ile Gly Phe Thr Glu Gly Phe Ser Pro Ala Ser Gln His  
 65 70 75 80  
 Asp Ala Tyr Leu Ala Leu Ala Ala Trp Gly Leu Pro Thr Ser Pro Tyr  
 85 90 95  
 Thr Glu Ala Val Thr Asp Pro Glu Asp Val Val Lys Lys Val Ser Tyr  
 100 105 110  
 Trp Ala Asp His Arg His Asp Ala Leu His Glu Met Asp Gly Leu Val  
 115 120 125  
 Ile Lys Val Asp Asp Ile Ala Ser Gln Arg Ala Leu Gly Ser Thr Ser  
 130 135 140  
 Arg Ala Pro Arg Trp Ala Ile Ala Tyr Lys Tyr Pro Pro Glu Glu Val  
 145 150 155 160  
 Thr Thr Lys Leu Leu Asp Ile Gln Val Gly Val Gly Arg Thr Gly Arg  
 165 170 175  
 Val Thr Pro Phe Ala Val Met Glu Pro Val Leu Val Ala Gly Ser Thr  
 180 185 190  
 Val Ser Met Ala Thr Leu His Asn Gln Ser Glu Val Lys Arg Lys Gly  
 195 200 205  
 Val Leu Ile Gly Asp Thr Val Val Ile Arg Lys Ala Gly Glu Val Ile  
 210 215 220  
 Pro Glu Val Leu Gly Pro Val Val Glu Leu Arg Asp Gly Thr Glu Arg  
 225 230 235 240  
 Glu Tyr Ile Phe Pro Thr Leu Cys Pro Glu Cys Gly Thr Arg Leu Ala  
 245 250 255  
 Pro Ala Lys Ala Asp Asp Val Asp Trp Arg Cys Pro Asn Met Gln Ser  
 260 265 270  
 Cys Pro Gly Gln Leu Ser Thr Arg Leu Thr Tyr Leu Ala Gly Arg Gly  
 275 280 285  
 Ala Phe Asp Ile Glu Ala Leu Gly Glu Lys Gly Ala Glu Asp Leu Ile  
 290 295 300  
 Arg Thr Gly Ile Leu Leu Asp Glu Ser Gly Leu Phe Asp Leu Thr Glu  
 305 310 315 320  
 Asp Asp Leu Leu Ser Ser Asn Val Tyr Thr Thr Asn Ala Gly Lys Val  
 325 330 335  
 Asn Ala Ser Gly Lys Lys Leu Leu Asp Asn Leu Gln Lys Ser Lys Gln  
 340 345 350

Thr Asp Leu Trp Arg Val Leu Val Ala Leu Ser Ile Arg His Val Gly  
 355 360 365  
 Pro Thr Ala Ala Arg Ala Leu Ala Gly Arg Tyr His Ser Ile Gln Ala  
 370 375 380  
 Leu Ile Asp Ala Pro Leu Glu Glu Leu Ser Glu Thr Asp Gly Val Gly  
 385 390 395 400  
 Thr Ile Ile Ala Gln Ser Phe Lys Asp Trp Phe Glu Val Asp Trp His  
 405 410 415  
 Lys Ala Ile Val Asp Lys Trp Ala Ala Ala Gly Val Thr Met Glu Glu  
 420 425 430  
 Glu Val Gly Glu Val Ala Glu Gln Thr Leu Glu Gly Leu Thr Ile Val  
 435 440 445  
 Val Thr Gly Gly Leu Glu Gly Phe Thr Arg Asp Ser Val Lys Glu Ala  
 450 455 460  
 Ile Ile Ser Arg Gly Gly Lys Ala Ser Gly Ser Val Ser Lys Lys Thr  
 465 470 475 480  
 Asp Tyr Val Val Ile Gly Glu Asn Ala Gly Ser Lys Ala Thr Lys Ala  
 485 490 495  
 Glu Glu Leu Gly Leu Arg Ile Leu Asp Glu Ala Gly Phe Val Arg Leu  
 500 505 510  
 Leu Asn Thr Gly Ser Ala Asp Glu  
 515 520

<210> 151  
 <211> 696  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(673)  
 <223> RXS00213

<400> 151  
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cgaatggccg tgtccaccct tagggttaga atcgggaacc gtg act gaa gat aat 115  
 Val Thr Glu Asp Asn  
 1 5

gct caa ctg cgt aga acg tgg aac gac tta gcc gag aag gtt cgt tat 163  
 Ala Gln Leu Arg Arg Thr Trp Asn Asp Leu Ala Glu Lys Val Arg Tyr  
 10 15 20

cac cga gat cgt tat tac aac gaa cag cca gag atc cct gat gct gat 211  
 His Arg Asp Arg Tyr Tyr Asn Glu Gln Pro Glu Ile Pro Asp Ala Asp  
 25 30 35

ttt gat gcg ctt ttt aag cag ctt cag cag ttg gaa gaa gac cac ccg 259  
 Phe Asp Ala Leu Phe Lys Gln Leu Gln Gln Leu Glu Glu Asp His Pro

40					45					50						
gag	ctc	gcc	gtc	cct	gat	agc	ccc	acc	atg	gtt	gtg	ggc	gct	ccg	gtg	307
Glu	Leu	Ala	Val	Pro	Asp	Ser	Pro	Thr	Met	Val	Val	Gly	Ala	Pro	Val	
	55						60				65					
gca	gag	caa	tca	agc	ttt	gac	aat	gtt	gag	cac	ttg	gag	cga	atg	ctc	355
Ala	Glu	Gln	Ser	Ser	Phe	Asp	Asn	Val	Glu	His	Leu	Glu	Arg	Met	Leu	
	70				75				80						85	
agc	ttg	gac	aat	gtt	ttt	gat	gag	cag	gag	ttg	cgt	gat	tgg	ttg	ggc	403
Ser	Leu	Asp	Asn	Val	Phe	Asp	Glu	Gln	Glu	Leu	Arg	Asp	Trp	Leu	Gly	
				90					95					100		
agg	acg	cca	gcc	aag	cag	tat	ttg	acg	gag	ttg	aaa	att	gat	ggc	ttg	451
Arg	Thr	Pro	Ala	Lys	Gln	Tyr	Leu	Thr	Glu	Leu	Lys	Ile	Asp	Gly	Leu	
			105					110					115			
tcc	atc	gac	ttg	gtg	tat	cgc	aat	ggc	cag	tta	gag	cgt	gcc	gct	act	499
Ser	Ile	Asp	Leu	Val	Tyr	Arg	Asn	Gly	Gln	Leu	Glu	Arg	Ala	Ala	Thr	
		120					125					130				
cgt	ggt	gat	ggt	cgc	gtg	ggc	gag	gac	atc	acg	gcc	aat	gct	cgc	gtg	547
Arg	Gly	Asp	Gly	Arg	Val	Gly	Glu	Asp	Ile	Thr	Ala	Asn	Ala	Arg	Val	
	135					140					145					
atc	gaa	gat	atc	ccg	cac	cag	ctt	cag	ggc	act	gat	gaa	tat	cct	gtg	595
Ile	Glu	Asp	Ile	Pro	His	Gln	Leu	Gln	Gly	Thr	Asp	Glu	Tyr	Pro	Val	
	150				155				160						165	
cct	gct	gtg	ctg	gaa	att	cgc	ggt	gag	gtg	ttc	atc	act	gtg	gag	gat	643
Pro	Ala	Val	Leu	Glu	Ile	Arg	Gly	Glu	Val	Phe	Ile	Thr	Val	Glu	Asp	
			170					175						180		
ttc	cca	gga	ggt	caa	cgc	gca	gcg	cat	tgc	tgatggtggc	aagccgtttg	cca				696
Phe	Pro	Gly	Gly	Gln	Arg	Ala	Ala	His	Cys							
		185						190								

&lt;210&gt; 152

&lt;211&gt; 191

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 152

Val	Thr	Glu	Asp	Asn	Ala	Gln	Leu	Arg	Arg	Thr	Trp	Asn	Asp	Leu	Ala
1				5					10					15	

Glu	Lys	Val	Arg	Tyr	His	Arg	Asp	Arg	Tyr	Tyr	Asn	Glu	Gln	Pro	Glu
		20					25						30		

Ile	Pro	Asp	Ala	Asp	Phe	Asp	Ala	Leu	Phe	Lys	Gln	Leu	Gln	Gln	Leu
		35					40					45			

Glu	Glu	Asp	His	Pro	Glu	Leu	Ala	Val	Pro	Asp	Ser	Pro	Thr	Met	Val
	50					55					60				

Val	Gly	Ala	Pro	Val	Ala	Glu	Gln	Ser	Ser	Phe	Asp	Asn	Val	Glu	His
	65				70					75				80	

Leu	Glu	Arg	Met	Leu	Ser	Leu	Asp	Asn	Val	Phe	Asp	Glu	Gln	Glu	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85					90					95					
Arg	Asp	Trp	Leu	Gly	Arg	Thr	Pro	Ala	Lys	Gln	Tyr	Leu	Thr	Glu	Leu
			100					105					110		
Lys	Ile	Asp	Gly	Leu	Ser	Ile	Asp	Leu	Val	Tyr	Arg	Asn	Gly	Gln	Leu
		115					120					125			
Glu	Arg	Ala	Ala	Thr	Arg	Gly	Asp	Gly	Arg	Val	Gly	Glu	Asp	Ile	Thr
	130					135					140				
Ala	Asn	Ala	Arg	Val	Ile	Glu	Asp	Ile	Pro	His	Gln	Leu	Gln	Gly	Thr
145						150					155				160
Asp	Glu	Tyr	Pro	Val	Pro	Ala	Val	Leu	Glu	Ile	Arg	Gly	Glu	Val	Phe
				165					170					175	
Ile	Thr	Val	Glu	Asp	Phe	Pro	Gly	Gly	Gln	Arg	Ala	Ala	His	Cys	
			180					185					190		

&lt;210&gt; 153

&lt;211&gt; 2100

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2077)

&lt;223&gt; RXS00724

&lt;400&gt; 153

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tccgccacca	tgtgcgcaaa	tactccacca	cggtcttggc	gtg	gga	att	ggt	gat	115
				Val	Gly	Ile	Gly	Asp	
				1				5	

gcc	act	gag	ggc	gat	ctt	gtt	acc	atc	gtg	ggt	cag	gtc	gcc	ttt	gcc	163
Ala	Thr	Glu	Gly	Asp	Leu	Val	Thr	Ile	Val	Gly	Gln	Val	Ala	Phe	Ala	
				10					15					20		

aag	cag	tcc	tat	acc	cag	tcc	ggc	aag	atg	ctg	tac	aag	gtt	aca	gtc	211
Lys	Gln	Ser	Tyr	Thr	Gln	Ser	Gly	Lys	Met	Leu	Tyr	Lys	Val	Thr	Val	
			25					30					35			

ttg	act	gag	acg	gaa	cgc	atc	ggc	att	tcc	ttc	ttc	gga	gcc	aag	cac	259
Leu	Thr	Glu	Thr	Glu	Arg	Ile	Gly	Ile	Ser	Phe	Phe	Gly	Ala	Lys	His	
		40					45					50				

att	ccg	cgt	ctt	ctc	cca	gaa	ggc	act	cgt	gcg	ctt	ttt	acc	ggc	aag	307
Ile	Pro	Arg	Leu	Leu	Pro	Glu	Gly	Thr	Arg	Ala	Leu	Phe	Thr	Gly	Lys	
		55				60					65					

gtg	aag	ttt	ttt	cgc	aac	gaa	cct	cag	cta	tct	cat	cca	gag	ttc	att	355
Val	Lys	Phe	Phe	Arg	Asn	Glu	Pro	Gln	Leu	Ser	His	Pro	Glu	Phe	Ile	
	70				75				80						85	

gtg	atc	cca	gat	cct	gga	tca	ggc	cgc	cga	ctc	acc	gcc	act	ggc	ggt	403
Val	Ile	Pro	Asp	Pro	Gly	Ser	Gly	Arg	Arg	Leu	Thr	Ala	Thr	Gly	Gly	
				90					95						100	

atg aaa tct ctg gct gcc tac ggc gat gtg gaa gaa gtg gca ctt cgt	451
Met Lys Ser Leu Ala Ala Tyr Gly Asp Val Glu Glu Val Ala Leu Arg	
105 110 115	
ttg gtg gat cgc gaa tac atc ccg atc tat gcc ggc acc gcc acc atg	499
Leu Val Asp Arg Glu Tyr Ile Pro Ile Tyr Ala Gly Thr Ala Thr Met	
120 125 130	
act acc tgg cgg atc atg gct gca gtg caa cgg gta ctg gaa acc atg	547
Thr Thr Trp Arg Ile Met Ala Ala Val Gln Arg Val Leu Glu Thr Met	
135 140 145	
ccg gtg atc aaa gaa cca ctg agc gtg gtg ccc gaa ggc atg ccc agt	595
Pro Val Ile Lys Glu Pro Leu Ser Val Val Pro Glu Gly Met Pro Ser	
150 155 160 165	
ttc gac gag gcc atc cgc ggc att cac gat cca ggc cat gaa tct ccc	643
Phe Asp Glu Ala Ile Arg Gly Ile His Asp Pro Gly His Glu Ser Pro	
170 175 180	
agc acg ttt atc aac cgt ctg aaa tac aac gaa gca cta tcg ctg gcc	691
Ser Thr Phe Ile Asn Arg Leu Lys Tyr Asn Glu Ala Leu Ser Leu Ala	
185 190 195	
acg gtg atg gcg atc cgg cgt gcc gat acc aag aac cgc aaa gca cca	739
Thr Val Met Ala Ile Arg Arg Ala Asp Thr Lys Asn Arg Lys Ala Pro	
200 205 210	
ccc atg ccg cgc gca ctc aaa ggg cat cag cac atg ctc atc gat gca	787
Pro Met Pro Arg Ala Leu Lys Gly His Gln His Met Leu Ile Asp Ala	
215 220 225	
ctc aac ttt cag ctc aca gtg gga cag aag caa gtg atc cgt gag atc	835
Leu Asn Phe Gln Leu Thr Val Gly Gln Lys Gln Val Ile Arg Glu Ile	
230 235 240 245	
agc gcg gac att gaa caa cgc gtt ccc atg tct cgt ctg ctc caa ggt	883
Ser Ala Asp Ile Glu Gln Arg Val Pro Met Ser Arg Leu Leu Gln Gly	
250 255 260	
gag gtt ggt tcg ggt aaa acc atc gtg tcg ttg atc gcg atg ctg cag	931
Glu Val Gly Ser Gly Lys Thr Ile Val Ser Leu Ile Ala Met Leu Gln	
265 270 275	
gca att gat tcc ggt agg cag tgc gcc atg ctc gcc ccg acg gaa gtg	979
Ala Ile Asp Ser Gly Arg Gln Cys Ala Met Leu Ala Pro Thr Glu Val	
280 285 290	
ttg gcc acc cag cat gcc cgc agc ctg agc aaa act ctc gac gac gca	1027
Leu Ala Thr Gln His Ala Arg Ser Leu Ser Lys Thr Leu Asp Asp Ala	
295 300 305	
ggc ctt gat atc aat gtt gtg ctc ttg act ggc tcg atg ccc acg gga	1075
Gly Leu Asp Ile Asn Val Val Leu Leu Thr Gly Ser Met Pro Thr Gly	
310 315 320 325	
gcc aag aag gag gct ctg ctg gaa atc atc tcc ggt gac gca gac att	1123
Ala Lys Lys Glu Ala Leu Leu Glu Ile Ile Ser Gly Asp Ala Asp Ile	
330 335 340	

gtg gtc ggc acg cat gcg ctg atc cag gac acc gtg gag ttc ttc gac	1171
Val Val Gly Thr His Ala Leu Ile Gln Asp Thr Val Glu Phe Phe Asp	
345 350 355	
ctt ggc ctc gtg gtg gtg gat gag cag cac cgt ttc ggc gtg gag caa	1219
Leu Gly Leu Val Val Val Asp Glu Gln His Arg Phe Gly Val Glu Gln	
360 365 370	
cgc gat caa ctg cgg acc aag ggc agg gaa ggc ctg acc ccg cac cta	1267
Arg Asp Gln Leu Arg Thr Lys Gly Arg Glu Gly Leu Thr Pro His Leu	
375 380 385	
ttg gtt atg act gcg acc cca att ccg cgc acc atc gcc atg acg gtg	1315
Leu Val Met Thr Ala Thr Pro Ile Pro Arg Thr Ile Ala Met Thr Val	
390 395 400 405	
ttc ggc gac ttg gcg gtg tcc acg ttg cgt gaa ctt cca ggc ggg cgc	1363
Phe Gly Asp Leu Ala Val Ser Thr Leu Arg Glu Leu Pro Gly Gly Arg	
410 415 420	
cgg ccg att caa acc tcg gtg ata ccc gat cac aaa cct ggc tgg gtt	1411
Arg Pro Ile Gln Thr Ser Val Ile Pro Asp His Lys Pro Gly Trp Val	
425 430 435	
aaa cgc ggt tgg gaa cgc atc ggt gag gaa gtc ctc gcc gga cgc caa	1459
Lys Arg Gly Trp Glu Arg Ile Gly Glu Glu Val Leu Ala Gly Arg Gln	
440 445 450	
gcc tat gtg gtg tgt ccg cgc att gaa ggc gaa ggc gcc gtg ctg gaa	1507
Ala Tyr Val Val Cys Pro Arg Ile Glu Gly Glu Gly Gly Val Leu Glu	
455 460 465	
atc cac gcc tat ctt tcc gaa cag gta tat cca gga ttg aat gtt gga	1555
Ile His Ala Tyr Leu Ser Glu Gln Val Tyr Pro Gly Leu Asn Val Gly	
470 475 480 485	
atg ctg cac ggt cgc atg gac acg gat ctc aaa gat tcg gtc atg cag	1603
Met Leu His Gly Arg Met Asp Thr Asp Leu Lys Asp Ser Val Met Gln	
490 495 500	
gaa ttc gcc caa ggt gag atc gat att ttg gtc gcc acc acg gtc att	1651
Glu Phe Ala Gln Gly Glu Ile Asp Ile Leu Val Ala Thr Thr Val Ile	
505 510 515	
gag gtc ggt att gac gtt gcc aac gcc acc gtc atg ctc atc cgc gag	1699
Glu Val Gly Ile Asp Val Ala Asn Ala Thr Val Met Leu Ile Arg Glu	
520 525 530	
gcg gaa cgc ttc ggc gtt tcc cag atc cac cag ctg cgc ggc cgt gtt	1747
Ala Glu Arg Phe Gly Val Ser Gln Ile His Gln Leu Arg Gly Arg Val	
535 540 545	
ggc cgt ggg cag cac gat tcc ctc tgc ctg ctg cac acc acc ttc gac	1795
Gly Arg Gly Gln His Asp Ser Leu Cys Leu Leu His Thr Thr Phe Asp	
550 555 560 565	
gag gac tcc cca caa ggc caa cgc ctc gcc gca att tcc acc aca acc	1843
Glu Asp Ser Pro Gln Gly Gln Arg Leu Ala Ala Ile Ser Thr Thr Thr	
570 575 580	
gac ggt ttt caa ctc tct gaa ctt gat ttg cag gta cgc caa gaa ggc	1891

Asp Gly Phe Gln Leu Ser Glu Leu Asp Leu Gln Val Arg Gln Glu Gly  
 585 590 595  
 gac gtg ttg ggc acc cgc cag tcc ggc agc gac acc aaa ctc cgt cac 1939  
 Asp Val Leu Gly Thr Arg Gln Ser Gly Ser Asp Thr Lys Leu Arg His  
 600 605 610  
 ctc tcg ttt atc agc gac caa aaa atc atc gag cgt gcg ctt atc gac 1987  
 Leu Ser Phe Ile Ser Asp Gln Lys Ile Ile Glu Arg Ala Leu Ile Asp  
 615 620 625  
 gcc acc gag ctg gtt gcc gcc agc cgt tcc agg gcg ctt gag ctg gtc 2035  
 Ala Thr Glu Leu Val Ala Ala Ser Arg Ser Arg Ala Leu Glu Leu Val  
 630 635 640 645  
 agc gac atc gca atg atc aac cag gaa tac ctg gaa aag agc 2077  
 Ser Asp Ile Ala Met Ile Asn Gln Glu Tyr Leu Glu Lys Ser  
 650 655  
 tgatattgat agggtttaag tca 2100

<210> 154  
 <211> 659  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 154

Val Gly Ile Gly Asp Ala Thr Glu Gly Asp Leu Val Thr Ile Val Gly  
 1 5 10 15  
 Gln Val Ala Phe Ala Lys Gln Ser Tyr Thr Gln Ser Gly Lys Met Leu  
 20 25 30  
 Tyr Lys Val Thr Val Leu Thr Glu Thr Glu Arg Ile Gly Ile Ser Phe  
 35 40 45  
 Phe Gly Ala Lys His Ile Pro Arg Leu Leu Pro Glu Gly Thr Arg Ala  
 50 55 60  
 Leu Phe Thr Gly Lys Val Lys Phe Phe Arg Asn Glu Pro Gln Leu Ser  
 65 70 75 80  
 His Pro Glu Phe Ile Val Ile Pro Asp Pro Gly Ser Gly Arg Arg Leu  
 85 90 95  
 Thr Ala Thr Gly Gly Met Lys Ser Leu Ala Ala Tyr Gly Asp Val Glu  
 100 105 110  
 Glu Val Ala Leu Arg Leu Val Asp Arg Glu Tyr Ile Pro Ile Tyr Ala  
 115 120 125  
 Gly Thr Ala Thr Met Thr Thr Trp Arg Ile Met Ala Ala Val Gln Arg  
 130 135 140  
 Val Leu Glu Thr Met Pro Val Ile Lys Glu Pro Leu Ser Val Val Pro  
 145 150 155 160  
 Glu Gly Met Pro Ser Phe Asp Glu Ala Ile Arg Gly Ile His Asp Pro  
 165 170 175

Gly	His	Glu	Ser	Pro	Ser	Thr	Phe	Ile	Asn	Arg	Leu	Lys	Tyr	Asn	Glu		
			180					185					190				
Ala	Leu	Ser	Leu	Ala	Thr	Val	Met	Ala	Ile	Arg	Arg	Ala	Asp	Thr	Lys		
		195					200					205					
Asn	Arg	Lys	Ala	Pro	Pro	Met	Pro	Arg	Ala	Leu	Lys	Gly	His	Gln	His		
	210					215					220						
Met	Leu	Ile	Asp	Ala	Leu	Asn	Phe	Gln	Leu	Thr	Val	Gly	Gln	Lys	Gln		
225					230					235					240		
Val	Ile	Arg	Glu	Ile	Ser	Ala	Asp	Ile	Glu	Gln	Arg	Val	Pro	Met	Ser		
				245					250					255			
Arg	Leu	Leu	Gln	Gly	Glu	Val	Gly	Ser	Gly	Lys	Thr	Ile	Val	Ser	Leu		
			260					265					270				
Ile	Ala	Met	Leu	Gln	Ala	Ile	Asp	Ser	Gly	Arg	Gln	Cys	Ala	Met	Leu		
		275					280					285					
Ala	Pro	Thr	Glu	Val	Leu	Ala	Thr	Gln	His	Ala	Arg	Ser	Leu	Ser	Lys		
	290					295					300						
Thr	Leu	Asp	Asp	Ala	Gly	Leu	Asp	Ile	Asn	Val	Val	Leu	Leu	Thr	Gly		
305					310					315					320		
Ser	Met	Pro	Thr	Gly	Ala	Lys	Lys	Glu	Ala	Leu	Leu	Glu	Ile	Ile	Ser		
				325					330					335			
Gly	Asp	Ala	Asp	Ile	Val	Val	Gly	Thr	His	Ala	Leu	Ile	Gln	Asp	Thr		
			340					345					350				
Val	Glu	Phe	Phe	Asp	Leu	Gly	Leu	Val	Val	Val	Asp	Glu	Gln	His	Arg		
		355					360					365					
Phe	Gly	Val	Glu	Gln	Arg	Asp	Gln	Leu	Arg	Thr	Lys	Gly	Arg	Glu	Gly		
	370					375					380						
Leu	Thr	Pro	His	Leu	Leu	Val	Met	Thr	Ala	Thr	Pro	Ile	Pro	Arg	Thr		
385					390					395					400		
Ile	Ala	Met	Thr	Val	Phe	Gly	Asp	Leu	Ala	Val	Ser	Thr	Leu	Arg	Glu		
				405					410					415			
Leu	Pro	Gly	Gly	Arg	Arg	Pro	Ile	Gln	Thr	Ser	Val	Ile	Pro	Asp	His		
			420					425					430				
Lys	Pro	Gly	Trp	Val	Lys	Arg	Gly	Trp	Glu	Arg	Ile	Gly	Glu	Glu	Val		
		435					440					445					
Leu	Ala	Gly	Arg	Gln	Ala	Tyr	Val	Val	Cys	Pro	Arg	Ile	Glu	Gly	Glu		
	450					455					460						
Gly	Gly	Val	Leu	Glu	Ile	His	Ala	Tyr	Leu	Ser	Glu	Gln	Val	Tyr	Pro		
465					470					475					480		
Gly	Leu	Asn	Val	Gly	Met	Leu	His	Gly	Arg	Met	Asp	Thr	Asp	Leu	Lys		
				485					490					495			
Asp	Ser	Val	Met	Gln	Glu	Phe	Ala	Gln	Gly	Glu	Ile	Asp	Ile	Leu	Val		

500					505					510					
Ala	Thr	Thr	Val	Ile	Glu	Val	Gly	Ile	Asp	Val	Ala	Asn	Ala	Thr	Val
		515					520					525			
Met	Leu	Ile	Arg	Glu	Ala	Glu	Arg	Phe	Gly	Val	Ser	Gln	Ile	His	Gln
	530					535					540				
Leu	Arg	Gly	Arg	Val	Gly	Arg	Gly	Gln	His	Asp	Ser	Leu	Cys	Leu	Leu
545					550					555					560
His	Thr	Thr	Phe	Asp	Glu	Asp	Ser	Pro	Gln	Gly	Gln	Arg	Leu	Ala	Ala
			565						570					575	
Ile	Ser	Thr	Thr	Thr	Asp	Gly	Phe	Gln	Leu	Ser	Glu	Leu	Asp	Leu	Gln
			580					585					590		
Val	Arg	Gln	Glu	Gly	Asp	Val	Leu	Gly	Thr	Arg	Gln	Ser	Gly	Ser	Asp
		595					600					605			
Thr	Lys	Leu	Arg	His	Leu	Ser	Phe	Ile	Ser	Asp	Gln	Lys	Ile	Ile	Glu
	610					615					620				
Arg	Ala	Leu	Ile	Asp	Ala	Thr	Glu	Leu	Val	Ala	Ala	Ser	Arg	Ser	Arg
625					630					635					640
Ala	Leu	Glu	Leu	Val	Ser	Asp	Ile	Ala	Met	Ile	Asn	Gln	Glu	Tyr	Leu
				645					650					655	
Glu Lys Ser															

&lt;210&gt; 155

&lt;211&gt; 903

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(880)

&lt;223&gt; RXS00823

&lt;400&gt; 155

caaatgcaaa aagcatcagc aagagcggga tgatcaccac aagcaaacct gtcattgggag 60

tcattcta	at	gatgaat	caa	atccgcg	cta	acttaagg	gt	atg	ggt	tcc	att	act			115
								Met	Gly	Ser	Ile	Thr			5
								1							

ccg	cag	aag	cgg	cct	cgc	gtg	ggg	tct	cac	atc	gcg	aac	aag	ggt	caa	163
Pro	Gln	Lys	Arg	Pro	Arg	Val	Gly	Ser	His	Ile	Ala	Asn	Lys	Gly	Gln	
				10					15					20		

gag	act	gat	atc	ggg	cga	aaa	cgc	cga	gct	cga	cgc	atc	aat	cgc	aca	211
Glu	Thr	Asp	Ile	Gly	Arg	Lys	Arg	Arg	Ala	Arg	Arg	Ile	Asn	Arg	Thr	
			25					30					35			

ctc	acc	gtg	gca	tat	ccg	gat	gcg	cac	tgc	gaa	tta	gat	ttc	acc	aat	259
Leu	Thr	Val	Ala	Tyr	Pro	Asp	Ala	His	Cys	Glu	Leu	Asp	Phe	Thr	Asn	
		40					45					50				

ccg cta gaa ctc acg gtc gcc acc att ttg tcc gcc cag tgc acg gac 307  
 Pro Leu Glu Leu Thr Val Ala Thr Ile Leu Ser Ala Gln Cys Thr Asp  
 55 60 65

gtt cgc gtg aac cag gtg acg ccc gcg ttg ttc aag cgc tat ccg acg 355  
 Val Arg Val Asn Gln Val Thr Pro Ala Leu Phe Lys Arg Tyr Pro Thr  
 70 75 80 85

gcc aca gat tac gcc aac gcc gat cgc acg gaa ttg gag gag ttc atc 403  
 Ala Thr Asp Tyr Ala Asn Ala Asp Arg Thr Glu Leu Glu Glu Phe Ile  
 90 95 100

cgt ccg aca ggc ttt tac cgc aac aag gcc act tct tta atc ggc ctg 451  
 Arg Pro Thr Gly Phe Tyr Arg Asn Lys Ala Thr Ser Leu Ile Gly Leu  
 105 110 115

ggt gag gca cta att tcg ctt cac gac ggc cag gtc ccc ggt acc ctt 499  
 Gly Glu Ala Leu Ile Ser Leu His Asp Gly Gln Val Pro Gly Thr Leu  
 120 125 130

gag cag cta gtt gag ctg ccg ggg gtc ggg cgg aaa acc gcc aac gtg 547  
 Glu Gln Leu Val Glu Leu Pro Gly Val Gly Arg Lys Thr Ala Asn Val  
 135 140 145

gtg ctg gga aat gct ttc ggt gtt ccg gga atc acg gtg gat aca cac 595  
 Val Leu Gly Asn Ala Phe Gly Val Pro Gly Ile Thr Val Asp Thr His  
 150 155 160 165

ttt ggc agg ttg gtg cgt cgc ctg aag ctc act gat gaa gaa gat ccc 643  
 Phe Gly Arg Leu Val Arg Arg Leu Lys Leu Thr Asp Glu Glu Asp Pro  
 170 175 180

gtc aag gtg gaa aaa gtg atg aac gaa ctc atc gaa aag cct gag tgg 691  
 Val Lys Val Glu Lys Val Met Asn Glu Leu Ile Glu Lys Pro Glu Trp  
 185 190 195

acc atg ttt tca cat agg ctg atc ttc cac gga cgt agg ata tgt cat 739  
 Thr Met Phe Ser His Arg Leu Ile Phe His Gly Arg Arg Ile Cys His  
 200 205 210

agt cga cgc gcc gcc tgt gga gcc tgc atg ctg gca gct gat tgc cca 787  
 Ser Arg Arg Ala Ala Cys Gly Ala Cys Met Leu Ala Ala Asp Cys Pro  
 215 220 225

tcc ttt ggt ttg gag ggg ccg tca gat cca ttt gag gcg caa aaa ctc 835  
 Ser Phe Gly Leu Glu Gly Pro Ser Asp Pro Phe Glu Ala Gln Lys Leu  
 230 235 240 245

att aaa agt gat gat agg gag cac ctg ctg aaa atg gca gga atg 880  
 Ile Lys Ser Asp Arg Glu His Leu Leu Lys Met Ala Gly Met  
 250 255 260

tagaaaacaa atgacaagca gtg 903

&lt;210&gt; 156

&lt;211&gt; 260

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 156

Met Gly Ser Ile Thr Pro Gln Lys Arg Pro Arg Val Gly Ser His Ile  
 1 5 10 15  
 Ala Asn Lys Gly Gln Glu Thr Asp Ile Gly Arg Lys Arg Arg Ala Arg  
 20 25 30  
 Arg Ile Asn Arg Thr Leu Thr Val Ala Tyr Pro Asp Ala His Cys Glu  
 35 40 45  
 Leu Asp Phe Thr Asn Pro Leu Glu Leu Thr Val Ala Thr Ile Leu Ser  
 50 55 60  
 Ala Gln Cys Thr Asp Val Arg Val Asn Gln Val Thr Pro Ala Leu Phe  
 65 70 75 80  
 Lys Arg Tyr Pro Thr Ala Thr Asp Tyr Ala Asn Ala Asp Arg Thr Glu  
 85 90 95  
 Leu Glu Glu Phe Ile Arg Pro Thr Gly Phe Tyr Arg Asn Lys Ala Thr  
 100 105 110  
 Ser Leu Ile Gly Leu Gly Glu Ala Leu Ile Ser Leu His Asp Gly Gln  
 115 120 125  
 Val Pro Gly Thr Leu Glu Gln Leu Val Glu Leu Pro Gly Val Gly Arg  
 130 135 140  
 Lys Thr Ala Asn Val Val Leu Gly Asn Ala Phe Gly Val Pro Gly Ile  
 145 150 155 160  
 Thr Val Asp Thr His Phe Gly Arg Leu Val Arg Arg Leu Lys Leu Thr  
 165 170 175  
 Asp Glu Glu Asp Pro Val Lys Val Glu Lys Val Met Asn Glu Leu Ile  
 180 185 190  
 Glu Lys Pro Glu Trp Thr Met Phe Ser His Arg Leu Ile Phe His Gly  
 195 200 205  
 Arg Arg Ile Cys His Ser Arg Arg Ala Ala Cys Gly Ala Cys Met Leu  
 210 215 220  
 Ala Ala Asp Cys Pro Ser Phe Gly Leu Glu Gly Pro Ser Asp Pro Phe  
 225 230 235 240  
 Glu Ala Gln Lys Leu Ile Lys Ser Asp Asp Arg Glu His Leu Leu Lys  
 245 250 255  
 Met Ala Gly Met  
 260

&lt;210&gt; 157

&lt;211&gt; 912

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(889)

<400> 157

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aac	gga	aatt	ctaaa	aat	cca	aaac	agct	ag	ggt	tata	aat	atg	cgc	atc	ggt	aat	115	
												Met	Arg	Ile	Val	Asn	5	
1																		
tgg	aac	gtc	aac	tct	gct	cgc	act	cgt	gtg	gac	cgg	atg	gtc	gat	ttt		163	
Trp	Asn	Val	Asn	Ser	Ala	Arg	Thr	Arg	Val	Asp	Arg	Met	Val	Asp	Phe			
				10					15					20				
ttg	ctt	cgc	cat	gat	gtt	gat	gta	tta	gcg	gtg	cag	gaa	acc	aag	tgt		211	
Leu	Leu	Arg	His	Asp	Val	Asp	Val	Leu	Ala	Val	Gln	Glu	Thr	Lys	Cys			
			25					30					35					
aaa	gat	gag	caa	ttt	ccc	acc	gag	cgt	ttc	acc	gaa	atc	ggc	tat	gag		259	
Lys	Asp	Glu	Gln	Phe	Pro	Thr	Glu	Arg	Phe	Thr	Glu	Ile	Gly	Tyr	Glu			
		40					45					50						
gta	gcc	cat	ttc	ggc	ctt	aac	cag	tgg	aat	ggg	gtc	gcc	att	att	tcc		307	
Val	Ala	His	Phe	Gly	Leu	Asn	Gln	Trp	Asn	Gly	Val	Ala	Ile	Ile	Ser			
	55					60					65							
cgc	gtt	ggc	att	gaa	aat	gtg	gaa	acc	cac	ttc	cct	gcc	caa	ccg	gga		355	
Arg	Val	Gly	Ile	Glu	Asn	Val	Glu	Thr	His	Phe	Pro	Ala	Gln	Pro	Gly			
	70				75					80					85			
ttc	aac	aaa	gac	atc	acc	aag	gaa	caa	tcc	atc	gaa	gcc	cgc	gcc	atc		403	
Phe	Asn	Lys	Asp	Ile	Thr	Lys	Glu	Gln	Ser	Ile	Glu	Ala	Arg	Ala	Ile			
				90					95					100				
ggc	gcc	cgc	tgc	ggg	ggg	gtc	cag	gtg	tgg	agc	ctc	tat	gtt	ccc	aac		451	
Gly	Ala	Arg	Cys	Gly	Gly	Val	Gln	Val	Trp	Ser	Leu	Tyr	Val	Pro	Asn			
			105					110					115					
ggc	cgc	gaa	atc	gca	gat	cct	cac	tac	gac	tac	aaa	ctg	cgc	tgg	cta		499	
Gly	Arg	Glu	Ile	Ala	Asp	Pro	His	Tyr	Asp	Tyr	Lys	Leu	Arg	Trp	Leu			
		120					125					130						
ttc	tcc	ctg	cgc	aac	tac	gtg	atc	gac	acc	ttg	gaa	tac	cgc	ccc	gag		547	
Phe	Ser	Leu	Arg	Asn	Tyr	Val	Ile	Asp	Thr	Leu	Glu	Tyr	Arg	Pro	Glu			
	135					140					145							
gaa	aaa	ctg	gtg	ttg	ctc	ggc	gac	ttc	aac	atc	gcg	ccc	aca	gac	atc		595	
Glu	Lys	Leu	Val	Leu	Leu	Gly	Asp	Phe	Asn	Ile	Ala	Pro	Thr	Asp	Ile			
	150				155					160					165			
gac	gtc	tgg	gac	atc	gca	gcc	ttc	gaa	gga	aaa	acc	cac	gtc	acc	gaa		643	
Asp	Val	Trp	Asp	Ile	Ala	Ala	Phe	Glu	Gly	Lys	Thr	His	Val	Thr	Glu			
				170					175					180				
cca	gaa</																	

cgc ttc ctc aaa ggc gaa ggc atg cgc atc gat ttc cag ctc gca tcc 787  
 Arg Phe Leu Lys Gly Glu Gly Met Arg Ile Asp Phe Gln Leu Ala Ser  
 215 220 225  
  
 ccg gcc ctt gct gca acc gcg ggt gaa acc ttt gtg gac gtt gaa gaa 835  
 Pro Ala Leu Ala Ala Thr Ala Gly Glu Thr Phe Val Asp Val Glu Glu  
 230 235 240 245  
  
 cgc agc gga acc ggc gcc tct gac cac gca cca gtc atc gtt gat tac 883  
 Arg Ser Gly Thr Gly Ala Ser Asp His Ala Pro Val Ile Val Asp Tyr  
 250 255 260  
  
 aag gtg taactgcgta tgatctttca gat 912  
 Lys Val

&lt;210&gt; 158

&lt;211&gt; 263

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 158

Met Arg Ile Val Asn Trp Asn Val Asn Ser Ala Arg Thr Arg Val Asp  
 1 5 10 15  
  
 Arg Met Val Asp Phe Leu Leu Arg His Asp Val Asp Val Leu Ala Val  
 20 25 30  
  
 Gln Glu Thr Lys Cys Lys Asp Glu Gln Phe Pro Thr Glu Arg Phe Thr  
 35 40 45  
  
 Glu Ile Gly Tyr Glu Val Ala His Phe Gly Leu Asn Gln Trp Asn Gly  
 50 55 60  
  
 Val Ala Ile Ile Ser Arg Val Gly Ile Glu Asn Val Glu Thr His Phe  
 65 70 75 80  
  
 Pro Ala Gln Pro Gly Phe Asn Lys Asp Ile Thr Lys Glu Gln Ser Ile  
 85 90 95  
  
 Glu Ala Arg Ala Ile Gly Ala Arg Cys Gly Gly Val Gln Val Trp Ser  
 100 105 110  
  
 Leu Tyr Val Pro Asn Gly Arg Glu Ile Ala Asp Pro His Tyr Asp Tyr  
 115 120 125  
  
 Lys Leu Arg Trp Leu Phe Ser Leu Arg Asn Tyr Val Ile Asp Thr Leu  
 130 135 140  
  
 Glu Tyr Arg Pro Glu Glu Lys Leu Val Leu Leu Gly Asp Phe Asn Ile  
 145 150 155 160  
  
 Ala Pro Thr Asp Ile Asp Val Trp Asp Ile Ala Ala Phe Glu Gly Lys  
 165 170 175  
  
 Thr His Val Thr Glu Pro Glu Arg Ala Ala Phe Asp Gly Leu Ile Glu  
 180 185 190  
  
 Ala Gly Leu Lys Glu Thr Thr Pro Gly Pro Gly Thr Tyr Thr Tyr Trp  
 195 200 205

Asp Tyr Lys Gly Ala Arg Phe Leu Lys Gly Glu Gly Met Arg Ile Asp  
 210 215 220  
 Phe Gln Leu Ala Ser Pro Ala Leu Ala Ala Thr Ala Gly Glu Thr Phe  
 225 230 235 240  
 Val Asp Val Glu Glu Arg Ser Gly Thr Gly Ala Ser Asp His Ala Pro  
 245 250 255  
 Val Ile Val Asp Tyr Lys Val  
 260

<210> 159  
 <211> 849  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(826)  
 <223> RXS01066

<400> 159  
 aaacgtattc cttgacctgc gcatcaaggt gctgaagaac tggcaatccg atccaaaggc 60  
 tttgaaccgc ctgggcttct agctttaagg ggggtgagttc atg cgt agg gac agt 115  
 Met Arg Arg Asp Ser  
 1 5  
 ttt cgg gac cgc gcg cta gta gtc aaa act tat gat ttt ggc gaa gcc 163  
 Phe Arg Asp Arg Ala Leu Val Val Lys Thr Tyr Asp Phe Gly Glu Ala  
 10 15 20  
 gac cgc att att gtg ctg ctc acc cga gac cac ggc atc gtg cgc gga 211  
 Asp Arg Ile Ile Val Leu Leu Thr Arg Asp His Gly Ile Val Arg Gly  
 25 30 35  
 gtt gcc aaa gga gta cgc cga tcc aaa tcc cgg ttt ggg tca agg ctg 259  
 Val Ala Lys Gly Val Arg Arg Ser Lys Ser Arg Phe Gly Ser Arg Leu  
 40 45 50  
 cag ctt ttt gtg gaa ctc gac gtg cag ctc tac cca ggt aga aaa ctg 307  
 Gln Leu Phe Val Glu Leu Asp Val Gln Leu Tyr Pro Gly Arg Lys Leu  
 55 60 65  
 tcc acc atc tct ggc gcg gac acc gtc ggc tac tac gca tca ggc atc 355  
 Ser Thr Ile Ser Gly Ala Asp Thr Val Gly Tyr Tyr Ala Ser Gly Ile  
 70 75 80 85  
 atc gag gac ttc act cgg tat tcc tgt gcg tcc gcc atc ctg gaa atc 403  
 Ile Glu Asp Phe Thr Arg Tyr Ser Cys Ala Ser Ala Ile Leu Glu Ile  
 90 95 100  
 gcc acc cac atc gca gga ctg gaa aac gat ccg cac ctg ttt gaa gaa 451  
 Ala Thr His Ile Ala Gly Leu Glu Asn Asp Pro His Leu Phe Glu Glu  
 105 110 115  
 acc acc cgg gcg ttg aaa aac att cag gac tcc cca gaa ccc atc ctc 499  
 Thr Thr Arg Ala Leu Lys Asn Ile Gln Asp Ser Pro Glu Pro Ile Leu

120	125	130	
aac cta gac gag ttc atg ctc cgc gcc atg aac cac gcc ggc tgg gca			547
Asn Leu Asp Glu Phe Met Leu Arg Ala Met Asn His Ala Gly Trp Ala			
135	140	145	
cca agc ctt ttc gac tgc gca gcc tgc ggc cga cca gga cct cac aac			595
Pro Ser Leu Phe Asp Cys Ala Ala Cys Gly Arg Pro Gly Pro His Asn			
150	155	160	165
gca ttc cac cca ggc gtc ggc ggg gca gtg tgc ctg tac tgc cga ccg			643
Ala Phe His Pro Gly Val Gly Gly Ala Val Cys Leu Tyr Cys Arg Pro			
	170	175	180
ccg gga agc gcc gaa gtc cca cca gaa gca cta cac atg atg tgg ttg			691
Pro Gly Ser Ala Glu Val Pro Pro Glu Ala Leu His Met Met Trp Leu			
	185	190	195
gtc gcc aac ggc caa gca gcc cgc att ccc cgg gaa cac cca gag cag			739
Val Ala Asn Gly Gln Ala Ala Arg Ile Pro Arg Glu His Pro Glu Gln			
	200	205	210
caa acc acc att cac caa ctg aca acc gcg cat ctg cag tgg cat att			787
Gln Thr Thr Ile His Gln Leu Thr Thr Ala His Leu Gln Trp His Ile			
	215	220	225
gaa aga aag ctg ccc acg ctg gcg gtg ctg gat cag gcc tagtgcttag			836
Glu Arg Lys Leu Pro Thr Leu Ala Val Leu Asp Gln Ala			
230	235	240	
gcttaggcgt ccg			849

&lt;210&gt; 160

&lt;211&gt; 242

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 160

Met Arg Arg Asp Ser Phe Arg Asp Arg Ala Leu Val Val Lys Thr Tyr
1 5 10 15

Asp Phe Gly Glu Ala Asp Arg Ile Ile Val Leu Leu Thr Arg Asp His
20 25 30

Gly Ile Val Arg Gly Val Ala Lys Gly Val Arg Arg Ser Lys Ser Arg
35 40 45

Phe Gly Ser Arg Leu Gln Leu Phe Val Glu Leu Asp Val Gln Leu Tyr
50 55 60

Pro Gly Arg Lys Leu Ser Thr Ile Ser Gly Ala Asp Thr Val Gly Tyr
65 70 75 80

Tyr Ala Ser Gly Ile Ile Glu Asp Phe Thr Arg Tyr Ser Cys Ala Ser
85 90 95

Ala Ile Leu Glu Ile Ala Thr His Ile Ala Gly Leu Glu Asn Asp Pro
100 105 110

His Leu Phe Glu Glu Thr Thr Arg Ala Leu Lys Asn Ile Gln Asp Ser
---

115	120	125
Pro Glu Pro Ile Leu Asn Leu Asp Glu Phe Met Leu Arg Ala Met Asn 130 135 140		
His Ala Gly Trp Ala Pro Ser Leu Phe Asp Cys Ala Ala Cys Gly Arg 145 150 155 160		
Pro Gly Pro His Asn Ala Phe His Pro Gly Val Gly Gly Ala Val Cys 165 170 175		
Leu Tyr Cys Arg Pro Pro Gly Ser Ala Glu Val Pro Pro Glu Ala Leu 180 185 190		
His Met Met Trp Leu Val Ala Asn Gly Gln Ala Ala Arg Ile Pro Arg 195 200 205		
Glu His Pro Glu Gln Gln Thr Thr Ile His Gln Leu Thr Thr Ala His 210 215 220		
Leu Gln Trp His Ile Glu Arg Lys Leu Pro Thr Leu Ala Val Leu Asp 225 230 235 240		
Gln Ala		

<210> 161  
 <211> 1740  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1717)  
 <223> RXS02145

<400> 161  
 cactgccaca gctgccaatt accgttgatg aagagggcta cctcatcgcc gctggtaact 60  
 tcattgagcc actcggccct gcattctggg agcgtaagtc atg agt cta gct acc 115  
 Met Ser Leu Ala Thr  
 1 5  
 gtg gga aac aat ctt gat tcc cgt tac acc atg gcg tcg ggt atc cgt 163  
 Val Gly Asn Asn Leu Asp Ser Arg Tyr Thr Met Ala Ser Gly Ile Arg  
 10 15 20  
 cgc cag atc aac aag gtc ttc cca act cac tgg tcc ttc atg ctc ggc 211  
 Arg Gln Ile Asn Lys Val Phe Pro Thr His Trp Ser Phe Met Leu Gly  
 25 30 35  
 gag att gcg ctt tac agc ttc atc gtc ttg ctg ctg act ggt gtc tac 259  
 Glu Ile Ala Leu Tyr Ser Phe Ile Val Leu Leu Leu Thr Gly Val Tyr  
 40 45 50  
 ctg acc ctg ttc ttc gac cca tca atc acc aag gtc att tat gac ggc 307  
 Leu Thr Leu Phe Phe Asp Pro Ser Ile Thr Lys Val Ile Tyr Asp Gly  
 55 60 65  
 ggc tac ctc cca ctg aac ggt gtg gag atg tcc cgt gca tac gca act 355

Gly 70	Tyr	Leu	Pro	Leu	Asn 75	Gly	Val	Glu	Met	Ser 80	Arg	Ala	Tyr	Ala	Thr 85	
gcg	ttg	gat	att	tcc	ttc	gag	gtt	cgc	ggt	ggt	ctg	ttc	atc	cgc	cag	403
Ala	Leu	Asp	Ile	Ser 90	Phe	Glu	Val	Arg	Gly 95	Gly	Leu	Phe	Ile	Arg	Gln 100	
atg	cac	cac	tgg	gca	gcc	ctg	ctg	ttc	gtt	gta	tcc	atg	ctg	gtt	cac	451
Met	His	His	Trp 105	Ala	Ala	Leu	Leu	Phe	Val 110	Val	Ser	Met	Leu	Val	His 115	
atg	ctc	cgt	att	ttc	ttc	acc	ggt	gcg	ttc	cgt	cgc	cca	cgt	gaa	gca	499
Met	Leu	Arg 120	Ile	Phe	Phe	Thr	Gly 125	Ala	Phe	Arg	Arg	Pro 130	Arg	Glu	Ala	
aac	tgg	atc	atc	ggt	gtt	gtt	ctg	atc	atc	ctg	ggt	atg	gct	gaa	ggc	547
Asn 135	Trp	Ile	Ile	Gly	Val	Val	Leu 140	Ile	Ile	Leu	Gly 145	Met	Ala	Glu	Gly	
ttc	atg	ggt	tac	tcc	ctg	cct	gat	gac	ctg	ctc	tct	ggt	gtt	ggt	ctt	595
Phe 150	Met	Gly	Tyr	Ser	Leu 155	Pro	Asp	Asp	Leu	Leu	Ser	Gly	Val	Gly	Leu 165	
cga	atc	atg	tcc	gcc	atc	atc	gtt	ggt	ctt	ccg	atc	ata	ggt	acc	tgg	643
Arg	Ile	Met	Ser 170	Ala	Ile	Ile	Val	Gly	Leu 175	Pro	Ile	Ile	Gly	Thr 180	Trp	
atg	cac	tgg	ctg	atc	ttc	ggt	gga	gac	ttc	cca	tcc	gat	ctg	atg	ctg	691
Met	His	Trp 185	Leu	Ile	Phe	Gly	Gly	Asp	Phe 190	Pro	Ser	Asp	Leu	Met	Leu 195	
gac	cgc	ttc	tac	atc	gca	cac	gtt	cta	atc	atc	cca	gct	atc	ctg	ctt	739
Asp	Arg	Phe 200	Tyr	Ile	Ala	His	Val 205	Leu	Ile	Ile	Pro	Ala	Ile	Leu	Leu 210	
ggc	ttg	atc	gca	gct	cac	ctg	gca	ctt	gtt	tgg	tac	cag	aag	cac	acc	787
Gly 215	Leu	Ile	Ala	Ala	His	Leu 220	Ala	Leu	Val	Trp	Tyr	Gln	Lys	His	Thr 225	
cag	ttc	cca	ggc	gct	ggc	cgc	act	gag	aac	aac	gtg	atc	ggt	atc	cga	835
Gln 230	Phe	Pro	Gly	Ala	Gly 235	Arg	Thr	Glu	Asn	Asn 240	Val	Ile	Gly	Ile	Arg 245	
atc	atg	cct	ctg	ttc	gca	gtt	aag	gct	gtt	gct	ttc	ggc	ctc	atc	gtc	883
Ile	Met	Pro	Leu	Phe 250	Ala	Val	Lys	Ala	Val 255	Ala	Phe	Gly	Leu	Ile	Val 260	
ttc	ggt	ttc	ctc	gca	ctg	ctt	gct	ggt	gtc	acc	acc	att	aac	gca	att	931
Phe	Gly	Phe	Leu 265	Ala	Leu	Leu	Ala	Gly 270	Val	Thr	Thr	Ile	Asn 275	Ala	Ile	
tgg	aat	ctt	gga	ccg	tac	aac	cct	tca	cag	gtg	tct	gct	ggt	tcc	cag	979
Trp	Asn 280	Leu	Gly	Pro	Tyr	Asn	Pro 285	Ser	Gln	Val	Ser	Ala	Gly	Ser	Gln 290	
cct	gac	gtt	tac	atg	ctg	tgg	aca	gat	ggt	gct	gct	cgt	gtc	atg	ccg	1027
Pro	Asp	Val	Tyr	Met	Leu	Trp 300	Thr	Asp	Gly	Ala	Ala	Arg	Val	Met	Pro 305	
gca	tgg	gag	ctc	tac	ctc	ggt	aac	tac	act	att	cca	gca	gtc	ttc	tgg	1075
Ala	Trp	Glu	Leu	Tyr	Leu	Gly	Asn	Tyr	Thr	Ile	Pro	Ala	Val	Phe	Trp	

310	315	320	325	
gtt gct gtg atg ctg ggt atc ctc gtg gtt ctg ctt gtg act tac cca				1123
Val Ala Val Met Leu Gly Ile Leu Val Val Leu Leu Val Thr Tyr Pro	330	335	340	
ttc att gag cgt aag ttc acc ggc gac gat gca cac cac aac ttg ctg				1171
Phe Ile Glu Arg Lys Phe Thr Gly Asp Asp Ala His His Asn Leu Leu	345	350	355	
cag cgt cct cgc gat gtt cca gtc cgc acc tca ctc ggt gtc atg gcg				1219
Gln Arg Pro Arg Asp Val Pro Val Arg Thr Ser Leu Gly Val Met Ala	360	365	370	
ctt gtc ttc tac atc ctg ctt acc gtt tct ggt ggt aac gat gtt tac				1267
Leu Val Phe Tyr Ile Leu Leu Thr Val Ser Gly Gly Asn Asp Val Tyr	375	380	385	
gca atg cag ttc cat gtt tca ctg aac gcg atg acc tgg atc ggt cgt				1315
Ala Met Gln Phe His Val Ser Leu Asn Ala Met Thr Trp Ile Gly Arg	390	395	400	405
atc ggc ctc atc gtt gga cca gct att gca tac ttc atc act tac cga				1363
Ile Gly Leu Ile Val Gly Pro Ala Ile Ala Tyr Phe Ile Thr Tyr Arg	410	415	420	
ctg tgc atc ggc ttg cag cgc tct gac cgc gag gtc ctg gag cac ggc				1411
Leu Cys Ile Gly Leu Gln Arg Ser Asp Arg Glu Val Leu Glu His Gly	425	430	435	
atc gag acc ggt atc atc aag cag atg cca aat ggt gcc ttc att gaa				1459
Ile Glu Thr Gly Ile Ile Lys Gln Met Pro Asn Gly Ala Phe Ile Glu	440	445	450	
gtt cac cag cca ctt ggc cca gtt gat gac cat ggt cac cca atc cca				1507
Val His Gln Pro Leu Gly Pro Val Asp Asp His Gly His Pro Ile Pro	455	460	465	
ctg cca tac gct ggc gct gcg gtt cca aag cag atg aac cag ctt ggt				1555
Leu Pro Tyr Ala Gly Ala Ala Val Pro Lys Gln Met Asn Gln Leu Gly	470	475	480	485
tac gct gag gtt gaa acc cgc ggt gga ttc ttc gga cct gat cca gaa				1603
Tyr Ala Glu Val Glu Thr Arg Gly Gly Phe Phe Gly Pro Asp Pro Glu	490	495	500	
gac atc cgt gcg aag gct aag gaa att gag cac gca aac cac att gag				1651
Asp Ile Arg Ala Lys Ala Lys Glu Ile Glu His Ala Asn His Ile Glu	505	510	515	
gaa gcg aac act ctt cgt gca ctc aac gag gca aac att gag cgt gac				1699
Glu Ala Asn Thr Leu Arg Ala Leu Asn Glu Ala Asn Ile Glu Arg Asp	520	525	530	
aag aat gag ggc aag aac tagtttctag gacttcatct ctg				1740
Lys Asn Glu Gly Lys Asn	535			

&lt;210&gt; 162

&lt;211&gt; 539

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 162

Met	Ser	Leu	Ala	Thr	Val	Gly	Asn	Asn	Leu	Asp	Ser	Arg	Tyr	Thr	Met
1				5					10					15	
Ala	Ser	Gly	Ile	Arg	Arg	Gln	Ile	Asn	Lys	Val	Phe	Pro	Thr	His	Trp
			20					25					30		
Ser	Phe	Met	Leu	Gly	Glu	Ile	Ala	Leu	Tyr	Ser	Phe	Ile	Val	Leu	Leu
		35					40					45			
Leu	Thr	Gly	Val	Tyr	Leu	Thr	Leu	Phe	Phe	Asp	Pro	Ser	Ile	Thr	Lys
	50					55					60				
Val	Ile	Tyr	Asp	Gly	Gly	Tyr	Leu	Pro	Leu	Asn	Gly	Val	Glu	Met	Ser
65					70					75					80
Arg	Ala	Tyr	Ala	Thr	Ala	Leu	Asp	Ile	Ser	Phe	Glu	Val	Arg	Gly	Gly
				85					90					95	
Leu	Phe	Ile	Arg	Gln	Met	His	His	Trp	Ala	Ala	Leu	Leu	Phe	Val	Val
			100					105					110		
Ser	Met	Leu	Val	His	Met	Leu	Arg	Ile	Phe	Phe	Thr	Gly	Ala	Phe	Arg
		115					120					125			
Arg	Pro	Arg	Glu	Ala	Asn	Trp	Ile	Ile	Gly	Val	Val	Leu	Ile	Ile	Leu
	130					135					140				
Gly	Met	Ala	Glu	Gly	Phe	Met	Gly	Tyr	Ser	Leu	Pro	Asp	Asp	Leu	Leu
145					150					155					160
Ser	Gly	Val	Gly	Leu	Arg	Ile	Met	Ser	Ala	Ile	Ile	Val	Gly	Leu	Pro
				165					170					175	
Ile	Ile	Gly	Thr	Trp	Met	His	Trp	Leu	Ile	Phe	Gly	Gly	Asp	Phe	Pro
			180					185					190		
Ser	Asp	Leu	Met	Leu	Asp	Arg	Phe	Tyr	Ile	Ala	His	Val	Leu	Ile	Ile
		195					200					205			
Pro	Ala	Ile	Leu	Leu	Gly	Leu	Ile	Ala	Ala	His	Leu	Ala	Leu	Val	Trp
	210					215					220				
Tyr	Gln	Lys	His	Thr	Gln	Phe	Pro	Gly	Ala	Gly	Arg	Thr	Glu	Asn	Asn
225					230					235					240
Val	Ile	Gly	Ile	Arg	Ile	Met	Pro	Leu	Phe	Ala	Val	Lys	Ala	Val	Ala
				245					250					255	
Phe	Gly	Leu	Ile	Val	Phe	Gly	Phe	Leu	Ala	Leu	Leu	Ala	Gly	Val	Thr
			260					265					270		
Thr	Ile	Asn	Ala	Ile	Trp	Asn	Leu	Gly	Pro	Tyr	Asn	Pro	Ser	Gln	Val
		275					280					285			
Ser	Ala	Gly	Ser	Gln	Pro	Asp	Val	Tyr	Met	Leu	Trp	Thr	Asp	Gly	Ala
	290					295					300				

Ala Arg Val Met Pro Ala Trp Glu Leu Tyr Leu Gly Asn Tyr Thr Ile  
 305 310 315 320  
 Pro Ala Val Phe Trp Val Ala Val Met Leu Gly Ile Leu Val Val Leu  
 325 330 335  
 Leu Val Thr Tyr Pro Phe Ile Glu Arg Lys Phe Thr Gly Asp Asp Ala  
 340 345 350  
 His His Asn Leu Leu Gln Arg Pro Arg Asp Val Pro Val Arg Thr Ser  
 355 360 365  
 Leu Gly Val Met Ala Leu Val Phe Tyr Ile Leu Leu Thr Val Ser Gly  
 370 375 380  
 Gly Asn Asp Val Tyr Ala Met Gln Phe His Val Ser Leu Asn Ala Met  
 385 390 395 400  
 Thr Trp Ile Gly Arg Ile Gly Leu Ile Val Gly Pro Ala Ile Ala Tyr  
 405 410 415  
 Phe Ile Thr Tyr Arg Leu Cys Ile Gly Leu Gln Arg Ser Asp Arg Glu  
 420 425 430  
 Val Leu Glu His Gly Ile Glu Thr Gly Ile Ile Lys Gln Met Pro Asn  
 435 440 445  
 Gly Ala Phe Ile Glu Val His Gln Pro Leu Gly Pro Val Asp Asp His  
 450 455 460  
 Gly His Pro Ile Pro Leu Pro Tyr Ala Gly Ala Ala Val Pro Lys Gln  
 465 470 475 480  
 Met Asn Gln Leu Gly Tyr Ala Glu Val Glu Thr Arg Gly Gly Phe Phe  
 485 490 495  
 Gly Pro Asp Pro Glu Asp Ile Arg Ala Lys Ala Lys Glu Ile Glu His  
 500 505 510  
 Ala Asn His Ile Glu Glu Ala Asn Thr Leu Arg Ala Leu Asn Glu Ala  
 515 520 525  
 Asn Ile Glu Arg Asp Lys Asn Glu Gly Lys Asn  
 530 535

&lt;210&gt; 163

&lt;211&gt; 1002

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(979)

&lt;223&gt; RXS02476

&lt;400&gt; 163

cgggcggagt tctatcaaca ttacgcaaag gcataagctt tattattcca ctcggtgtga 60

 catatgacct aaagtgcag tcagtacaat catttaggtc atg tca ttt aca gct 115  
 Met Ser Phe Thr Ala

															1	5	
ttt	caa	aca	gcc	ctg	ctc	gtg	tgg	ttt	aga	gca	aat	gcc	cgc	gat	ctt	163	
Phe	Gln	Thr	Ala	Leu	Leu	Val	Trp	Phe	Arg	Ala	Asn	Ala	Arg	Asp	Leu		
				10					15					20			
gcg	tgg	cgt	gat	ccc	aat	act	tca	gca	tgg	gga	att	ctc	ctt	tca	gag	211	
Ala	Trp	Arg	Asp	Pro	Asn	Thr	Ser	Ala	Trp	Gly	Ile	Leu	Leu	Ser	Glu		
				25					30					35			
gtg	atg	agc	caa	caa	act	ccc	gtc	gcg	cga	gtc	gag	ccg	att	tgg	cgt	259	
Val	Met	Ser	Gln	Gln	Thr	Pro	Val	Ala	Arg	Val	Glu	Pro	Ile	Trp	Arg		
				40					45					50			
gag	tgg	atg	gaa	aaa	tgg	ccc	act	ccg	gaa	gat	ttc	gcg	aat	gcg	agc	307	
Glu	Trp	Met	Glu	Lys	Trp	Pro	Thr	Pro	Glu	Asp	Phe	Ala	Asn	Ala	Ser		
				55					60					65			
acc	gat	gag	att	ttg	cgg	tcg	tgg	ggc	aag	ttg	ggc	tat	cca	cgt	agg	355	
Thr	Asp	Glu	Ile	Leu	Arg	Ser	Trp	Gly	Lys	Leu	Gly	Tyr	Pro	Arg	Arg		
				70					75					80	85		
gcg	ctg	agg	ttg	aag	gaa	tgt	gcg	gag	gtg	atc	gtc	gaa	aag	cat	gcc	403	
Ala	Leu	Arg	Leu	Lys	Glu	Cys	Ala	Glu	Val	Ile	Val	Glu	Lys	His	Ala		
				90					95					100			
ggc	gag	gtg	ccg	gat	acg	gtg	gag	gcg	ctg	ctc	gcg	ttg	ccg	ggg	atc	451	
Gly	Glu	Val	Pro	Asp	Thr	Val	Glu	Ala	Leu	Leu	Ala	Leu	Pro	Gly	Ile		
				105					110					115			
ggt	gat	tac	acg	gcg	cgc	gcg	gtc	gcg	gcg	ttt	cat	ttt	ggg	cag	cgc	499	
Gly	Asp	Tyr	Thr	Ala	Arg	Ala	Val	Ala	Ala	Phe	His	Phe	Gly	Gln	Arg		
				120					125					130			
gtg	ccg	gtg	gtc	gat	acg	aac	gtg	cgt	cgc	gtg	tac	cag	cgc	gcg	gta	547	
Val	Pro	Val	Val	Asp	Thr	Asn	Val	Arg	Arg	Val	Tyr	Gln	Arg	Ala	Val		
				135					140					145			
gcc	gga	cgt	tac	ctt	gcg	ggg	cct	gcg	aaa	aag	caa	gag	ctt	atc	gac	595	
Ala	Gly	Arg	Tyr	Leu	Ala	Gly	Pro	Ala	Lys	Lys	Gln	Glu	Leu	Ile	Asp		
				150					155					160	165		
gtc	tcc	ctt	ctc	ctt	ccc	aac	act	cac	gcc	cca	gaa	ttc	tct	gcc	gca	643	
Val	Ser	Leu	Leu	Leu	Pro	Asn	Thr	His	Ala	Pro	Glu	Phe	Ser	Ala	Ala		
				170					175					180			
ata	atg	gag	ttg	ggt	gct	ctt	atc	tgc	acg	gcc	act	tcc	cca	aag	tgt	691	
Ile	Met	Glu	Leu	Gly	Ala	Leu	Ile	Cys	Thr	Ala	Thr	Ser	Pro	Lys	Cys		
				185					190					195			
gac	acc	tgc	cca	ctg	ctt	gac	cag	tgt	caa	tgg	caa	aaa	ctt	ggc	tgt	739	
Asp	Thr	Cys	Pro	Leu	Leu	Asp	Gln	Cys	Gln	Trp	Gln	Lys	Leu	Gly	Cys		
				200					205					210			
ccc	tcc	ccg	agt	gaa	gag	gag	ctg	gct	tca	gcg	aaa	aag	cgt	gtg	cag	787	
Pro	Ser	Pro	Ser	Glu	Glu	Glu	Leu	Ala	Ser	Ala	Lys	Lys	Arg	Val	Gln		
				215					220					225			
aaa	ttt	gtg	gga	acc	gac	cga	caa	gtc	cgt	ggc	cta	atc	atg	gac	gta	835	
Lys	Phe	Val	Gly	Thr	Asp	Arg	Gln	Val	Arg	Gly	Leu	Ile	Met	Asp	Val		
				230					235					240	245		

ctg cgc aat gcc acc gca cct gtg cca cta tcc gcg att gat gtc gtg 883  
 Leu Arg Asn Ala Thr Ala Pro Val Pro Leu Ser Ala Ile Asp Val Val  
                   250                  255                  260

tgg cct gac gat gcc caa cgc tcc cgg gcg ctg ttt tcg ctc att gag 931  
 Trp Pro Asp Asp Ala Gln Arg Ser Arg Ala Leu Phe Ser Leu Ile Glu  
                   265                  270                  275

gac gga ctc gcg gaa caa aat gag gcg ggt tat ttc cac ctg cca cgg 979  
 Asp Gly Leu Ala Glu Gln Asn Glu Ala Gly Tyr Phe His Leu Pro Arg  
                   280                  285                  290

taaaccactg cgcgcctgca aaa 1002

<210> 164  
 <211> 293  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 164  
 Met Ser Phe Thr Ala Phe Gln Thr Ala Leu Leu Val Trp Phe Arg Ala  
   1                  5                  10                  15

Asn Ala Arg Asp Leu Ala Trp Arg Asp Pro Asn Thr Ser Ala Trp Gly  
                   20                  25                  30

Ile Leu Leu Ser Glu Val Met Ser Gln Gln Thr Pro Val Ala Arg Val  
                   35                  40                  45

Glu Pro Ile Trp Arg Glu Trp Met Glu Lys Trp Pro Thr Pro Glu Asp  
                   50                  55                  60

Phe Ala Asn Ala Ser Thr Asp Glu Ile Leu Arg Ser Trp Gly Lys Leu  
   65                  70                  75                  80

Gly Tyr Pro Arg Arg Ala Leu Arg Leu Lys Glu Cys Ala Glu Val Ile  
                   85                  90                  95

Val Glu Lys His Ala Gly Glu Val Pro Asp Thr Val Glu Ala Leu Leu  
                   100                  105                  110

Ala Leu Pro Gly Ile Gly Asp Tyr Thr Ala Arg Ala Val Ala Ala Phe  
                   115                  120                  125

His Phe Gly Gln Arg Val Pro Val Val Asp Thr Asn Val Arg Arg Val  
   130                  135                  140

Tyr Gln Arg Ala Val Ala Gly Arg Tyr Leu Ala Gly Pro Ala Lys Lys  
 145                  150                  155                  160

Gln Glu Leu Ile Asp Val Ser Leu Leu Leu Pro Asn Thr His Ala Pro  
                   165                  170                  175

Glu Phe Ser Ala Ala Ile Met Glu Leu Gly Ala Leu Ile Cys Thr Ala  
                   180                  185                  190

Thr Ser Pro Lys Cys Asp Thr Cys Pro Leu Leu Asp Gln Cys Gln Trp  
                   195                  200                  205

Gln Lys Leu Gly Cys Pro Ser Pro Ser Glu Glu Glu Leu Ala Ser Ala  
 210 215 220

Lys Lys Arg Val Gln Lys Phe Val Gly Thr Asp Arg Gln Val Arg Gly  
 225 230 235 240

Leu Ile Met Asp Val Leu Arg Asn Ala Thr Ala Pro Val Pro Leu Ser  
 245 250 255

Ala Ile Asp Val Val Trp Pro Asp Asp Ala Gln Arg Ser Arg Ala Leu  
 260 265 270

Phe Ser Leu Ile Glu Asp Gly Leu Ala Glu Gln Asn Glu Ala Gly Tyr  
 275 280 285

Phe His Leu Pro Arg  
 290

<210> 165  
 <211> 720  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(697)  
 <223> RXS02990

<400> 165  
 gaagactaag caccagtttt aacaaagcag ggacaatcca cacacttaaa ccatgatgtg 60

gcttgttcct gctttttcgt caacgaaggg caacaacgcg atg gat atc caa gcc 115  
 Met Asp Ile Gln Ala  
 1 5

gaa aag att gaa aag ctc aga aaa gca ctc gac aac ttt gaa cgc gct 163  
 Glu Lys Ile Glu Lys Leu Arg Lys Ala Leu Asp Asn Phe Glu Arg Ala  
 10 15 20

cat gcg cga ggc gaa tca gac ttc ttt gac cat gaa aaa gaa gaa aag 211  
 His Ala Arg Gly Glu Ser Asp Phe Phe Asp His Glu Lys Glu Glu Lys  
 25 30 35

aaa gcc aac gta cgc aga cgt gcc ctg ctg ctg ctt aac caa cgc gca 259  
 Lys Ala Asn Val Arg Arg Arg Ala Leu Leu Leu Leu Asn Gln Arg Ala  
 40 45 50

cga tca gtc aac gaa cta agc acc aga ctt aaa gca ctg gag ttt gag 307  
 Arg Ser Val Asn Glu Leu Ser Thr Arg Leu Lys Ala Leu Glu Phe Glu  
 55 60 65

gaa gac atc atc aat gag gtc att ggc gat ctc acc aga tcc aaa ctg 355  
 Glu Asp Ile Ile Asn Glu Val Ile Gly Asp Leu Thr Arg Ser Lys Leu  
 70 75 80 85

ctt gat gat gaa gtt ttt gcc act gag tgg gtt cgg caa cgt gct gcc 403  
 Leu Asp Asp Glu Val Phe Ala Thr Glu Trp Val Arg Gln Arg Ala Ala  
 90 95 100

agg cga gga aaa tct tcg cgt gcg ctg gac cgc gaa ctg cag gaa aaa 451

Arg Arg Gly Lys Ser Ser Arg Ala Leu Asp Arg Glu Leu Gln Glu Lys  
 105 110 115  
 ggc gtc gac aag caa acg cgt gct gcg gcg ctt gag caa atc gac cag 499  
 Gly Val Asp Lys Gln Thr Arg Ala Ala Leu Glu Gln Ile Asp Gln  
 120 125 130  
 gcc gat gag cgg gac acg gcg cgg gcg gtg gcc gtg aaa aag gcg cgc 547  
 Ala Asp Glu Arg Asp Thr Ala Arg Ala Val Ala Val Lys Lys Ala Arg  
 135 140 145  
 tca gag acc aag att ccg cag gac cgc gcc gac tac gac aaa gcg ctt 595  
 Ser Glu Thr Lys Ile Pro Gln Asp Arg Ala Asp Tyr Asp Lys Ala Leu  
 150 155 160 165  
 cgg cgc gtg gtt ggt gcg ctg gca cgg cgg gga ttt ccg gct gga atg 643  
 Arg Arg Val Val Gly Ala Leu Ala Arg Arg Gly Phe Pro Ala Gly Met  
 170 175 180  
 tcc atg gac ctt gcg cgg gaa gcg cta gac gcg cga atc gag gat ttg 691  
 Ser Met Asp Leu Ala Arg Glu Ala Leu Asp Ala Arg Ile Glu Asp Leu  
 185 190 195  
 aaa aac taaaccccg atgggaatca tcc 720  
 Lys Asn

&lt;210&gt; 166

&lt;211&gt; 199

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 166

Met Asp Ile Gln Ala Glu Lys Ile Glu Lys Leu Arg Lys Ala Leu Asp  
 1 5 10 15  
 Asn Phe Glu Arg Ala His Ala Arg Gly Glu Ser Asp Phe Phe Asp His  
 20 25 30  
 Glu Lys Glu Glu Lys Lys Ala Asn Val Arg Arg Arg Ala Leu Leu Leu  
 35 40 45  
 Leu Asn Gln Arg Ala Arg Ser Val Asn Glu Leu Ser Thr Arg Leu Lys  
 50 55 60  
 Ala Leu Glu Phe Glu Glu Asp Ile Ile Asn Glu Val Ile Gly Asp Leu  
 65 70 75 80  
 Thr Arg Ser Lys Leu Leu Asp Asp Glu Val Phe Ala Thr Glu Trp Val  
 85 90 95  
 Arg Gln Arg Ala Ala Arg Arg Gly Lys Ser Ser Arg Ala Leu Asp Arg  
 100 105 110  
 Glu Leu Gln Glu Lys Gly Val Asp Lys Gln Thr Arg Ala Ala Ala Leu  
 115 120 125  
 Glu Gln Ile Asp Gln Ala Asp Glu Arg Asp Thr Ala Arg Ala Val Ala  
 130 135 140

Val Lys Lys Ala Arg Ser Glu Thr Lys Ile Pro Gln Asp Arg Ala Asp  
 145 150 155 160

Tyr Asp Lys Ala Leu Arg Arg Val Val Gly Ala Leu Ala Arg Arg Gly  
 165 170 175

Phe Pro Ala Gly Met Ser Met Asp Leu Ala Arg Glu Ala Leu Asp Ala  
 180 185 190

Arg Ile Glu Asp Leu Lys Asn  
 195

<210> 167  
 <211> 747  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(724)  
 <223> RXS03098

<400> 167  
 gaccggttttg tcgatcgac cgctgctggc tcgcaccatc aacgagatct tcgaaaacgg 60

ttccgtcacc accctcttcg agggcgaggc ctaaaccacc atg ccc acc acg gac 115  
 Met Pro Thr Thr Asp  
 1 5

gtc ttc aac cgc gtc cgg ttg gca ttg gaa cct cta gct gat ccc gca 163  
 Val Phe Asn Arg Val Arg Leu Ala Leu Glu Pro Leu Ala Asp Pro Ala  
 10 15 20

cgt gcc acc gga atg gca agc tac atg cgg gat cag ttt tct ttt ctc 211  
 Arg Ala Thr Gly Met Ala Ser Tyr Met Arg Asp Gln Phe Ser Phe Leu  
 25 30 35

ggc atc cca tcc acc ccc aga aaa gaa gcc tgc aaa ccc gtg ctg tcc 259  
 Gly Ile Pro Ser Thr Pro Arg Lys Glu Ala Cys Lys Pro Val Leu Ser  
 40 45 50

gcg cta aaa gag ttg gac act gac ttt gtc tca gac tgc ttt ggc gca 307  
 Ala Leu Lys Glu Leu Asp Thr Asp Phe Val Ser Asp Cys Phe Gly Ala  
 55 60 65

gct gaa cgg gaa tac cag tat gtc gcc tgc gat cac atc aat cgc gtc 355  
 Ala Glu Arg Glu Tyr Gln Tyr Val Ala Cys Asp His Ile Asn Arg Val  
 70 75 80 85

ggc atc acc gat tta ggt ttt gcc aaa gca tta gtg cag acc aaa tcc 403  
 Gly Ile Thr Asp Leu Gly Phe Ala Lys Ala Leu Val Gln Thr Lys Ser  
 90 95 100

tgg tgg gac acc gtc gat tcc cta gca aaa ccg atc ggc gcc aaa cac 451  
 Trp Trp Asp Thr Val Asp Ser Leu Ala Lys Pro Ile Gly Ala Lys His  
 105 110 115

gat gat gat ctg atg aaa acg tgg gcg ctt gat gag gac ttc tgg gtg 499  
 Asp Asp Asp Leu Met Lys Thr Trp Ala Leu Asp Glu Asp Phe Trp Val  
 120 125 130

cgc cgc atc gcg atc atc cac caa ctg ggc cgc aag aaa aac acc gac 547  
 Arg Arg Ile Ala Ile Ile His Gln Leu Gly Arg Lys Lys Asn Thr Asp  
 135 140 145  
  
 gct gcc ctg ctg gcc tgg atc atc gag cag aac ctc ggc tcc agc gag 595  
 Ala Ala Leu Leu Ala Trp Ile Ile Glu Gln Asn Leu Gly Ser Ser Glu  
 150 155 160 165  
  
 ttc ttc atc aac aaa gcg atc ggc tgg gca ctg cgg gat ttc gcc cgc 643  
 Phe Phe Ile Asn Lys Ala Ile Gly Trp Ala Leu Arg Asp Phe Ala Arg  
 170 175 180  
  
 cac gac ccc agc tgg gtc cgg gct ttt gtc gac gcc acg gac ctt tcc 691  
 His Asp Pro Ser Trp Val Arg Ala Phe Val Asp Ala Thr Asp Leu Ser  
 185 190 195  
  
 cca ctg agc cgg cga gaa gcc ctg aag aat att tagccctcag gcatcatctg 744  
 Pro Leu Ser Arg Arg Glu Ala Leu Lys Asn Ile  
 200 205  
  
 agc 747

<210> 168  
 <211> 208  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 168  
 Met Pro Thr Thr Asp Val Phe Asn Arg Val Arg Leu Ala Leu Glu Pro  
 1 5 10 15  
  
 Leu Ala Asp Pro Ala Arg Ala Thr Gly Met Ala Ser Tyr Met Arg Asp  
 20 25 30  
  
 Gln Phe Ser Phe Leu Gly Ile Pro Ser Thr Pro Arg Lys Glu Ala Cys  
 35 40 45  
  
 Lys Pro Val Leu Ser Ala Leu Lys Glu Leu Asp Thr Asp Phe Val Ser  
 50 55 60  
  
 Asp Cys Phe Gly Ala Ala Glu Arg Glu Tyr Gln Tyr Val Ala Cys Asp  
 65 70 75 80  
  
 His Ile Asn Arg Val Gly Ile Thr Asp Leu Gly Phe Ala Lys Ala Leu  
 85 90 95  
  
 Val Gln Thr Lys Ser Trp Trp Asp Thr Val Asp Ser Leu Ala Lys Pro  
 100 105 110  
  
 Ile Gly Ala Lys His Asp Asp Asp Leu Met Lys Thr Trp Ala Leu Asp  
 115 120 125  
  
 Glu Asp Phe Trp Val Arg Arg Ile Ala Ile Ile His Gln Leu Gly Arg  
 130 135 140  
  
 Lys Lys Asn Thr Asp Ala Ala Leu Leu Ala Trp Ile Ile Glu Gln Asn  
 145 150 155 160  
  
 Leu Gly Ser Ser Glu Phe Phe Ile Asn Lys Ala Ile Gly Trp Ala Leu

			165						170						175
Arg	Asp	Phe	Ala	Arg	His	Asp	Pro	Ser	Trp	Val	Arg	Ala	Phe	Val	Asp
			180					185					190		
Ala	Thr	Asp	Leu	Ser	Pro	Leu	Ser	Arg	Arg	Glu	Ala	Leu	Lys	Asn	Ile
		195					200					205			

&lt;210&gt; 169

&lt;211&gt; 806

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(783)

&lt;223&gt; RXS03175

&lt;400&gt; 169

gtc	cgc	gca	agc	gaa	aaa	gac	acc	gcc	acc	gca	ctg	caa	ccc	gcc	tta	48
Val	Arg	Ala	Ser	Glu	Lys	Asp	Thr	Ala	Thr	Ala	Leu	Gln	Pro	Ala	Leu	
1				5				10						15		
gat	aac	gga	tgg	cac	tac	att	ggt	gcc	cca	gca	gct	gcc	aag	gga	cgt	96
Asp	Asn	Gly	Trp	His	Tyr	Ile	Gly	Ala	Pro	Ala	Ala	Ala	Lys	Gly	Arg	
			20					25					30			
gcc	ggt	gtc	ggc	att	ttg	tct	agg	cat	gaa	ctt	gaa	gat	gtg	aac	atc	144
Ala	Gly	Val	Gly	Ile	Leu	Ser	Arg	His	Glu	Leu	Glu	Asp	Val	Asn	Ile	
		35					40					45				
ggt	ttt	gga	tct	ttc	ctt	gac	tcc	ggc	cgc	tac	att	gaa	gca	acc	atc	192
Gly	Phe	Gly	Ser	Phe	Leu	Asp	Ser	Gly	Arg	Tyr	Ile	Glu	Ala	Thr	Ile	
	50					55					60					
aaa	gac	acc	acc	ctg	gat	gtg	cca	gta	acc	gtg	gca	tct	ctt	tac	ctc	240
Lys	Asp	Thr	Thr	Leu	Asp	Val	Pro	Val	Thr	Val	Ala	Ser	Leu	Tyr	Leu	
	65				70				75						80	
ccc	tca	ggt	tca	gcg	ggc	acc	gac	aag	cag	gat	gaa	aag	tac	cgc	ttc	288
Pro	Ser	Gly	Ser	Ala	Gly	Thr	Asp	Lys	Gln	Asp	Glu	Lys	Tyr	Arg	Phe	
			85					90						95		
ctc	gat	gaa	ttc	gaa	ggg	ttc	ctg	gac	cag	cgc	gct	aaa	gaa	cgc	tcc	336
Leu	Asp	Glu	Phe	Glu	Gly	Phe	Leu	Asp	Gln	Arg	Ala	Lys	Glu	Arg	Ser	
		100					105						110			
cac	atg	gtc	atc	ggt	ggc	gac	tgg	aac	atc	tgc	cac	cgc	cgc	gaa	gac	384
His	Met	Val	Ile	Gly	Gly	Asp	Trp	Asn	Ile	Cys	His	Arg	Arg	Glu	Asp	
		115					120					125				
ctg	aaa	aac	tgg	aaa	acc	aac	caa	aag	aaa	tcc	ggt	ttc	ctt	ccc	gac	432
Leu	Lys	Asn	Trp	Lys	Thr	Asn	Gln	Lys	Lys	Ser	Gly	Phe	Leu	Pro	Asp	
	130					135					140					
gaa	cgc	gca	ttc	atg	gat	tca	gtc	ttt	ggc	acc	ttc	cca	gat	gag	gca	480
Glu	Arg	Ala	Phe	Met	Asp	Ser	Val	Phe	Gly	Thr	Phe	Pro	Asp	Glu	Ala	
	145				150				155					160		
acc	cag	gtt	gca	ggg	gcc	ggc	gac	ttc	ttc	ggt	gcc	gtg	gac	tat	gaa	528

Thr Gln Val Ala Gly Ala Gly Asp Phe Phe Gly Ala Val Asp Tyr Glu  
 165 170 175  
 gga acg agg cgt cga gaa gca act acg gac cct gcg tgg ttc gac gtt 576  
 Gly Thr Arg Arg Arg Glu Ala Thr Thr Asp Pro Ala Trp Phe Asp Val  
 180 185 190  
 gca cgt cgc ctg caa cct gaa ggc gac ggc ccc tac act tgg tgg acc 624  
 Ala Arg Arg Leu Gln Pro Glu Gly Asp Gly Pro Tyr Thr Trp Trp Thr  
 195 200 205  
 tac cgc gga aaa gcc ttc gac acc ggc gcc gga tgg cgc atc gac tac 672  
 Tyr Arg Gly Lys Ala Phe Asp Thr Gly Ala Gly Trp Arg Ile Asp Tyr  
 210 215 220  
 caa gca gca acc gca gcg atg ctc gaa cgc gca gaa cgc tcc tgg gta 720  
 Gln Ala Ala Thr Ala Ala Met Leu Glu Arg Ala Glu Arg Ser Trp Val  
 225 230 235 240  
 gac aaa gcc gct gca tac gat ttg cgc tgg tca gat cac tca cca ctg 768  
 Asp Lys Ala Ala Ala Tyr Asp Leu Arg Trp Ser Asp His Ser Pro Leu  
 245 250 255  
 aac gtg atc tac tcc taaaatgctg ctgacaattc tat 806  
 Asn Val Ile Tyr Ser  
 260

&lt;210&gt; 170

&lt;211&gt; 261

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 170

Val Arg Ala Ser Glu Lys Asp Thr Ala Thr Ala Leu Gln Pro Ala Leu  
 1 5 10 15  
 Asp Asn Gly Trp His Tyr Ile Gly Ala Pro Ala Ala Ala Lys Gly Arg  
 20 25 30  
 Ala Gly Val Gly Ile Leu Ser Arg His Glu Leu Glu Asp Val Asn Ile  
 35 40 45  
 Gly Phe Gly Ser Phe Leu Asp Ser Gly Arg Tyr Ile Glu Ala Thr Ile  
 50 55 60  
 Lys Asp Thr Thr Leu Asp Val Pro Val Thr Val Ala Ser Leu Tyr Leu  
 65 70 75 80  
 Pro Ser Gly Ser Ala Gly Thr Asp Lys Gln Asp Glu Lys Tyr Arg Phe  
 85 90 95  
 Leu Asp Glu Phe Glu Gly Phe Leu Asp Gln Arg Ala Lys Glu Arg Ser  
 100 105 110  
 His Met Val Ile Gly Gly Asp Trp Asn Ile Cys His Arg Arg Glu Asp  
 115 120 125  
 Leu Lys Asn Trp Lys Thr Asn Gln Lys Lys Ser Gly Phe Leu Pro Asp  
 130 135 140

Glu Arg Ala Phe Met Asp Ser Val Phe Gly Thr Phe Pro Asp Glu Ala  
 145 150 155 160  
 Thr Gln Val Ala Gly Ala Gly Asp Phe Phe Gly Ala Val Asp Tyr Glu  
 165 170 175  
 Gly Thr Arg Arg Arg Glu Ala Thr Thr Asp Pro Ala Trp Phe Asp Val  
 180 185 190  
 Ala Arg Arg Leu Gln Pro Glu Gly Asp Gly Pro Tyr Thr Trp Trp Thr  
 195 200 205  
 Tyr Arg Gly Lys Ala Phe Asp Thr Gly Ala Gly Trp Arg Ile Asp Tyr  
 210 215 220  
 Gln Ala Ala Thr Ala Ala Met Leu Glu Arg Ala Glu Arg Ser Trp Val  
 225 230 235 240  
 Asp Lys Ala Ala Ala Tyr Asp Leu Arg Trp Ser Asp His Ser Pro Leu  
 245 250 255  
 Asn Val Ile Tyr Ser  
 260

<210> 171  
 <211> 1206  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1183)  
 <223> RXN03069

<400> 171  
 actatgcgga aaagtggaag aggggtttgtg atatatgtca cgatcgagga attggggaga 60  
 gatcgagaag ttgcgctcgg ggaggtacag ggcacgcttc atg cac gag ggt agg 115  
 Met His Glu Gly Arg  
 1 5  
 cga tac tct gcc ccg tat acc ttc ggt acc aag ggt gag gcg cag gag 163  
 Arg Tyr Ser Ala Pro Tyr Thr Phe Gly Thr Lys Gly Glu Ala Gln Glu  
 10 15 20  
 ttc ttg gcc tct gaa cgc acg gcc atc atc aat ggc aca tgg atg gat 211  
 Phe Leu Ala Ser Glu Arg Thr Ala Ile Ile Asn Gly Thr Trp Met Asp  
 25 30 35  
 ttt gag atg cgg gag agg ttc gag cag gca cag cgc gaa gcc gaa gaa 259  
 Phe Glu Met Arg Glu Arg Phe Glu Gln Ala Gln Arg Glu Ala Glu Glu  
 40 45 50  
 cgc atg atg gag acc ttc ttc agt tat gca tcg agg tgg ata gaa acc 307  
 Arg Met Met Glu Thr Phe Phe Ser Tyr Ala Ser Arg Trp Ile Glu Thr  
 55 60 65  
 cgg aca aat gcc caa gga aag aaa ctc agc caa ggg gtg aaa gat gat 355  
 Arg Thr Asn Ala Gln Gly Lys Lys Leu Ser Gln Gly Val Lys Asp Asp  
 70 75 80 85

tac ttt cgt tat ata aaa tca gat cga cta agt tat tgg gct gat tat	403
Tyr Phe Arg Tyr Ile Lys Ser Asp Arg Leu Ser Tyr Trp Ala Asp Tyr	
90 95 100	
gcg ctc tgt gaa atc act gtc gct gat gtc cgt gag tgg tat agc gat	451
Ala Leu Cys Glu Ile Thr Val Ala Asp Val Arg Glu Trp Tyr Ser Asp	
105 110 115	
act att cag gac ggt aaa ttg acc tca atg gcg cgg agt tac agc atg	499
Thr Ile Gln Asp Gly Lys Leu Thr Ser Met Ala Arg Ser Tyr Ser Met	
120 125 130	
atg aag tct gtc atg gag act gca gtg gag gat ggc att atc ccg atg	547
Met Lys Ser Val Met Glu Thr Ala Val Glu Asp Gly Ile Ile Pro Met	
135 140 145	
aat ccg tgc aaa gtc cgt ggc ggg ggt aat acg aaa aca ggc aaa aag	595
Asn Pro Cys Lys Val Arg Gly Gly Gly Asn Thr Lys Thr Gly Lys Lys	
150 155 160 165	
gtt gat gtc cca acc gat gcc gag ctt gag gcg atc att ggt gca ctg	643
Val Asp Val Pro Thr Asp Ala Glu Leu Glu Ala Ile Ile Gly Ala Leu	
170 175 180	
ccg agt aag tac ttt tgt ttg gct att gtt gct gcc gct ggt gca ctt	691
Pro Ser Lys Tyr Phe Cys Leu Ala Ile Val Ala Ala Ala Gly Ala Leu	
185 190 195	
cga ttc ggt gaa atc gtt gcg ctg cgt acc act gat gtg gat gtt tat	739
Arg Phe Gly Glu Ile Val Ala Leu Arg Thr Thr Asp Val Asp Val Tyr	
200 205 210	
ttt gat cgc agc gga ttt gta gat tgt gtt cga ata agg att tct cgg	787
Phe Asp Arg Ser Gly Phe Val Asp Cys Val Arg Ile Arg Ile Ser Arg	
215 220 225	
agc att agg cac acg aga tac cat ggc cga gtt gaa ggt ccg cct aaa	835
Ser Ile Arg His Thr Arg Tyr His Gly Arg Val Glu Gly Pro Pro Lys	
230 235 240 245	
act gaa gct ggt gtt cgt agc ctc tat atc tat ggc aaa gat gca gca	883
Thr Glu Ala Gly Val Arg Ser Leu Tyr Ile Tyr Gly Lys Asp Ala Ala	
250 255 260	
gaa att gcc aag cat gtg gac acg att gat gtg ggt ttg cga cta tgg	931
Glu Ile Ala Lys His Val Asp Thr Ile Asp Val Gly Leu Arg Leu Trp	
265 270 275	
agc tcg atg aga gat cct gat gaa ccc atg ccg tat cac acc ttt aag	979
Ser Ser Met Arg Asp Pro Asp Glu Pro Met Pro Tyr His Thr Phe Lys	
280 285 290	
cac aac tgg gat agg gcg cgg gaa agt gtc cac agt aaa gcg acc gtt	1027
His Asn Trp Asp Arg Ala Arg Glu Ser Val His Ser Lys Ala Thr Val	
295 300 305	
cac tcg atg agg cat tat tcg ggt acg aag tat gca cag gtt ggg gcg	1075
His Ser Met Arg His Tyr Ser Gly Thr Lys Tyr Ala Gln Val Gly Ala	
310 315 320 325	

aca ctc aag gag gtg atg gcg cgg ctg ggg cac tca aca cct agt gca 1123  
 Thr Leu Lys Glu Val Met Ala Arg Leu Gly His Ser Thr Pro Ser Ala  
                   330                                  335                                  340

gca ctg cgt tat cag cac tca ggc gag cgt gat gaa gag cta gca aag 1171  
 Ala Leu Arg Tyr Gln His Ser Gly Glu Arg Asp Glu Glu Leu Ala Lys  
                   345                                  350                                  355

cgc atg gcg cgc taaacactcg gcagtgagtt tca 1206  
 Arg Met Ala Arg  
                   360

<210> 172

<211> 361

<212> PRT

<213> Corynebacterium glutamicum

<400> 172

Met His Glu Gly Arg Arg Tyr Ser Ala Pro Tyr Thr Phe Gly Thr Lys  
   1                                  5                                  10                                  15

Gly Glu Ala Gln Glu Phe Leu Ala Ser Glu Arg Thr Ala Ile Ile Asn  
                   20                                  25                                  30

Gly Thr Trp Met Asp Phe Glu Met Arg Glu Arg Phe Glu Gln Ala Gln  
                   35                                  40                                  45

Arg Glu Ala Glu Glu Arg Met Met Glu Thr Phe Phe Ser Tyr Ala Ser  
   50                                  55                                  60

Arg Trp Ile Glu Thr Arg Thr Asn Ala Gln Gly Lys Lys Leu Ser Gln  
   65                                  70                                  75                                  80

Gly Val Lys Asp Asp Tyr Phe Arg Tyr Ile Lys Ser Asp Arg Leu Ser  
                   85                                  90                                  95

Tyr Trp Ala Asp Tyr Ala Leu Cys Glu Ile Thr Val Ala Asp Val Arg  
                   100                                  105                                  110

Glu Trp Tyr Ser Asp Thr Ile Gln Asp Gly Lys Leu Thr Ser Met Ala  
                   115                                  120                                  125

Arg Ser Tyr Ser Met Met Lys Ser Val Met Glu Thr Ala Val Glu Asp  
   130                                  135                                  140

Gly Ile Ile Pro Met Asn Pro Cys Lys Val Arg Gly Gly Gly Asn Thr  
   145                                  150                                  155                                  160

Lys Thr Gly Lys Lys Val Asp Val Pro Thr Asp Ala Glu Leu Glu Ala  
                   165                                  170                                  175

Ile Ile Gly Ala Leu Pro Ser Lys Tyr Phe Cys Leu Ala Ile Val Ala  
                   180                                  185                                  190

Ala Ala Gly Ala Leu Arg Phe Gly Glu Ile Val Ala Leu Arg Thr Thr  
                   195                                  200                                  205

Asp Val Asp Val Tyr Phe Asp Arg Ser Gly Phe Val Asp Cys Val Arg  
   210                                  215                                  220

Ile Arg Ile Ser Arg Ser Ile Arg His Thr Arg Tyr His Gly Arg Val  
 225 230 235 240  
 Glu Gly Pro Pro Lys Thr Glu Ala Gly Val Arg Ser Leu Tyr Ile Tyr  
 245 250 255  
 Gly Lys Asp Ala Ala Glu Ile Ala Lys His Val Asp Thr Ile Asp Val  
 260 265 270  
 Gly Leu Arg Leu Trp Ser Ser Met Arg Asp Pro Asp Glu Pro Met Pro  
 275 280 285  
 Tyr His Thr Phe Lys His Asn Trp Asp Arg Ala Arg Glu Ser Val His  
 290 295 300  
 Ser Lys Ala Thr Val His Ser Met Arg His Tyr Ser Gly Thr Lys Tyr  
 305 310 315 320  
 Ala Gln Val Gly Ala Thr Leu Lys Glu Val Met Ala Arg Leu Gly His  
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 Glu Glu Leu Ala Lys Arg Met Ala Arg  
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 Met His Glu Gly Arg  
 1 5  
 cga tac tct gcc ccg cat acc ttc ggt acc aag ggt gag gcg cag gag 163  
 Arg Tyr Ser Ala Pro His Thr Phe Gly Thr Lys Gly Glu Ala Gln Glu  
 10 15 20  
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 Phe Leu Ala Ser Glu Arg Thr Ala Ile Ile Asn Gly Thr Trp Met Asp  
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 Phe Glu Met Arg Glu Arg Phe Glu Gln Ala Gln Arg Glu Ala Glu Glu  
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 Arg Met Met Glu Thr Phe Phe Ser Tyr Ala Ser Arg Trp Ile Glu Thr  
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Arg Thr Asn Ala Gln Gly Lys Lys Leu Ser Gln Gly Val Lys Asp Asp	
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Tyr Phe Arg Tyr Ile Lys Ser Asp Arg Leu Ser Tyr Trp Ala Asp Tyr	
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Ala Leu Cys Glu Ile Thr Val Ala Asp Val Arg Glu Trp Tyr Ser Asp	
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Thr Ile Gln Asp Gly Lys Leu Thr Ser Met Ala Arg Ser Tyr Ser Met	
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Met Lys Ser Val Met Glu Thr Ala Val Glu Asp Gly Ile Ile Pro Met	
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Asn Pro Cys Lys Val Arg Gly Gly Gly Asn Thr Lys Thr Gly Lys Lys	
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Val Asp Val Pro Thr Asp Ala Glu Leu Glu Ala Ile Ile Gly Ala Leu	
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Pro Ser Lys Tyr Phe Cys Leu Ala Ile Val Ala Ala Ala Gly Ala Leu	
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Arg Phe Gly Glu Ile Val Ala Leu Arg Thr Thr Asp Val Asp Val Tyr	
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Phe Asp Arg Ser Gly Phe Val Asp Cys Val Arg Ile Arg Ile Ser Arg	
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Ser Ile Arg His Thr Arg Tyr His Gly Arg Val Glu Gly Pro Pro Lys	
230 235 240 245	
act gaa gct ggt gtt cgt agc ctc tat atc tat ggc aaa gat gca gca	883
Thr Glu Ala Gly Val Arg Ser Leu Tyr Ile Tyr Gly Lys Asp Ala Ala	
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Glu Ile Ala Lys His Val Asp Thr Ile Asp Val Gly Leu Arg Leu Trp	
265 270 275	
agc tcg atg aga gat cct gat gaa ccc atg ccg tat cac acc ttt aag	979
Ser Ser Met Arg Asp Pro Asp Glu Pro Met Pro Tyr His Thr Phe Lys	
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His Asn Trp Asp Arg Ala Arg Glu Ser Val His Ser Lys Ala Thr Val	
295 300 305	
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His Ser Met Arg His Tyr Ser Gly Thr Lys Tyr Ala Gln Val Gly Ala  
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 Thr Leu Lys Glu Val Met Ala Arg Leu Gly His Ser Thr Pro Ser Ala  
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 gca ctg cgt tat cag cac tca ggc gag cgt gat gaa gag cta gca aag 1171  
 Ala Leu Arg Tyr Gln His Ser Gly Glu Arg Asp Glu Glu Leu Ala Lys  
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 <212> PRT  
 <213> Corynebacterium glutamicum

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 Arg Glu Ala Glu Glu Arg Met Met Glu Thr Phe Phe Ser Tyr Ala Ser  
 50 55 60  
 Arg Trp Ile Glu Thr Arg Thr Asn Ala Gln Gly Lys Lys Leu Ser Gln  
 65 70 75 80  
 Gly Val Lys Asp Asp Tyr Phe Arg Tyr Ile Lys Ser Asp Arg Leu Ser  
 85 90 95  
 Tyr Trp Ala Asp Tyr Ala Leu Cys Glu Ile Thr Val Ala Asp Val Arg  
 100 105 110  
 Glu Trp Tyr Ser Asp Thr Ile Gln Asp Gly Lys Leu Thr Ser Met Ala  
 115 120 125  
 Arg Ser Tyr Ser Met Met Lys Ser Val Met Glu Thr Ala Val Glu Asp  
 130 135 140  
 Gly Ile Ile Pro Met Asn Pro Cys Lys Val Arg Gly Gly Gly Asn Thr  
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 Lys Thr Gly Lys Lys Val Asp Val Pro Thr Asp Ala Glu Leu Glu Ala  
 165 170 175  
 Ile Ile Gly Ala Leu Pro Ser Lys Tyr Phe Cys Leu Ala Ile Val Ala  
 180 185 190  
 Ala Ala Gly Ala Leu Arg Phe Gly Glu Ile Val Ala Leu Arg Thr Thr  
 195 200 205

Asp Val Asp Val Tyr Phe Asp Arg Ser Gly Phe Val Asp Cys Val Arg  
 210 215 220  
 Ile Arg Ile Ser Arg Ser Ile Arg His Thr Arg Tyr His Gly Arg Val  
 225 230 235 240  
 Glu Gly Pro Pro Lys Thr Glu Ala Gly Val Arg Ser Leu Tyr Ile Tyr  
 245 250 255  
 Gly Lys Asp Ala Ala Glu Ile Ala Lys His Val Asp Thr Ile Asp Val  
 260 265 270  
 Gly Leu Arg Leu Trp Ser Ser Met Arg Asp Pro Asp Glu Pro Met Pro  
 275 280 285  
 Tyr His Thr Phe Lys His Asn Trp Asp Arg Ala Arg Glu Ser Val His  
 290 295 300  
 Ser Lys Ala Thr Val His Ser Met Arg His Tyr Ser Gly Thr Lys Tyr  
 305 310 315 320  
 Ala Gln Val Gly Ala Thr Leu Lys Glu Val Met Ala Arg Leu Gly His  
 325 330 335  
 Ser Thr Pro Ser Ala Ala Leu Arg Tyr Gln His Ser Gly Glu Arg Asp  
 340 345 350  
 Glu Glu Leu Ala Lys Arg Met Ala Arg  
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&lt;210&gt; 175

&lt;211&gt; 1035

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1012)

&lt;223&gt; RXA01601

&lt;400&gt; 175

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 Met Lys Ala Arg Val  
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 Leu Ala Lys Thr Trp Leu Thr His Leu Ala Val Glu Arg Gly Leu Ser  
 10 15 20

gca aat acg ctg agt aat tat cgg cgc gat gtg gaa cgc tat tgc gac 211  
 Ala Asn Thr Leu Ser Asn Tyr Arg Arg Asp Val Glu Arg Tyr Cys Asp  
 25 30 35

tgg ctc gag gca gct ggg ctg gat gat att cgt gat atc acc acc gcg 259  
 Trp Leu Glu Ala Ala Gly Leu Asp Asp Ile Arg Asp Ile Thr Thr Ala  
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cat gtg gaa agt tat gtc aaa gac ctg cgc cgc ggg att gat gga caa 307

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Gln	Ala	Leu	Ser	Ala	Ser	Ser	Ala	Gly	Arg	Ala	Leu	Ile	Val	Ala	Arg	85	
70					75				80								
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Gly	Leu	His	Lys	Phe	Ala	Leu	Met	Glu	Gly	Glu	Val	Ala	Ala	Asp	Val		
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Ala	Ala	Asp	Val	Ser	Pro	Pro	Ala	Met	Gly	Arg	His	Leu	Pro	Asp	Thr		
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ctc	agc	atc	aac	gag	gta	gcc	ctg	ctt	atc	gac	gcg	atc	cca	cat	tca	499	
Leu	Ser	Ile	Asn	Glu	Val	Ala	Leu	Leu	Ile	Asp	Ala	Ile	Pro	His	Ser		
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gat	atc	gcc	act	ccc	gtt	gat	ctc	cgt	gac	cga	gcg	ctg	gtg	gaa	tta	547	
Asp	Ile	Ala	Thr	Pro	Val	Asp	Leu	Arg	Asp	Arg	Ala	Leu	Val	Glu	Leu		
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ctt	tat	gga	act	ggc	gcg	cgt	atc	tct	gag	gcg	att	ggg	ctg	gca	gtt	595	
Leu	Tyr	Gly	Thr	Gly	Ala	Arg	Ile	Ser	Glu	Ala	Ile	Gly	Leu	Ala	Val		
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Asp	Asp	Val	Ser	Glu	Met	Pro	Glu	Val	Leu	Arg	Ile	Thr	Gly	Lys	Gly		
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Ser	Lys	Gln	Arg	Ile	Val	Pro	Phe	Gly	Ser	Met	Ala	Gln	Gln	Ala	Val		
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Arg	Glu	Tyr	Leu	Val	Arg	Ala	Arg	Pro	Ala	Leu	Ser	Lys	Gly	Lys	Ser		
		200					205					210					
cat	gcg	ctt	ttt	ctc	aac	caa	cgc	ggc	ggt	cgg	cta	tct	cgg	caa	tct	787	
His	Ala	Leu	Phe	Leu	Asn	Gln	Arg	Gly	Gly	Pro	Leu	Ser	Arg	Gln	Ser		
	215					220					225						
gcg	tgg	gca	gtg	ctg	aag	aaa	acg	gtt	gag	cgc	gca	ggt	tta	gat	aaa	835	
Ala	Trp	Ala	Val	Leu	Lys	Lys	Thr	Val	Glu	Arg	Ala	Gly	Leu	Asp	Lys		
230					235					240					245		
gat	att	tct	ccc	cac	acc	ctg	cgg	cac	agc	ttt	gcc	acc	cat	ctc	ctc	883	
Asp	Ile	Ser	Pro	His	Thr	Leu	Arg	His	Ser	Phe	Ala	Thr	His	Leu	Leu		
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gaa	ggt	ggc	gcc	gat	gtc	cgt	gtg	gtg	cag	gaa	ctc	ctg	ggt	cat	tct	931	
Glu	Gly	Gly	Ala	Asp	Val	Arg	Val	Val	Gln	Glu	Leu	Leu	Gly	His	Ser		
			265				270						275				
tct	gtg	acg	acc	act	cag	att	tac	acg	cac	atc	aca	gcc	gat	agc	ttg	979	
Ser	Val	Thr	Thr	Thr	Gln	Ile	Tyr	Thr	His	Ile	Thr	Ala	Asp	Ser	Leu		
		280				285						290					
cgg	gaa	gtg	tgg	cgc	ggg	gct	cat	cct	cgt	gcg	tgaaagccct	tgcaattct	1032				
Arg	Glu	Val	Trp	Arg	Gly	Ala	His	Pro	Arg	Ala							

295

300

taa

1035

&lt;210&gt; 176

&lt;211&gt; 304

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 176

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Glu Arg Gly Leu Ser Ala Asn Thr Leu Ser Asn Tyr Arg Arg Asp Val  
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Glu Arg Tyr Cys Asp Trp Leu Glu Ala Ala Gly Leu Asp Asp Ile Arg  
 35 40 45

Asp Ile Thr Thr Ala His Val Glu Ser Tyr Val Lys Asp Leu Arg Arg  
 50 55 60

Gly Ile Asp Gly Gln Gln Ala Leu Ser Ala Ser Ser Ala Gly Arg Ala  
 65 70 75 80

Leu Ile Val Ala Arg Gly Leu His Lys Phe Ala Leu Met Glu Gly Glu  
 85 90 95

Val Ala Ala Asp Val Ala Ala Asp Val Ser Pro Pro Ala Met Gly Arg  
 100 105 110

His Leu Pro Asp Thr Leu Ser Ile Asn Glu Val Ala Leu Leu Ile Asp  
 115 120 125

Ala Ile Pro His Ser Asp Ile Ala Thr Pro Val Asp Leu Arg Asp Arg  
 130 135 140

Ala Leu Val Glu Leu Leu Tyr Gly Thr Gly Ala Arg Ile Ser Glu Ala  
 145 150 155 160

Ile Gly Leu Ala Val Asp Asp Val Ser Glu Met Pro Glu Val Leu Arg  
 165 170 175

Ile Thr Gly Lys Gly Ser Lys Gln Arg Ile Val Pro Phe Gly Ser Met  
 180 185 190

Ala Gln Gln Ala Val Arg Glu Tyr Leu Val Arg Ala Arg Pro Ala Leu  
 195 200 205

Ser Lys Gly Lys Ser His Ala Leu Phe Leu Asn Gln Arg Gly Gly Pro  
 210 215 220

Leu Ser Arg Gln Ser Ala Trp Ala Val Leu Lys Lys Thr Val Glu Arg  
 225 230 235 240

Ala Gly Leu Asp Lys Asp Ile Ser Pro His Thr Leu Arg His Ser Phe  
 245 250 255

Ala Thr His Leu Leu Glu Gly Gly Ala Asp Val Arg Val Val Gln Glu  
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Val His Phe Ile Lys  
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Glu Asn Leu Ile Phe Ser Ala Glu Ser Asn Ala Leu Arg Ala Gln Leu  
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Met Leu Ser Ile Leu Gly Ser Phe Ala Glu Phe Glu Arg Ser Ile Ile  
25 30 35  
  
cgg gag cgc caa gcc gag ggg atc gcc tgg cga aaa agg ccg gca agt 259  
Arg Glu Arg Gln Ala Glu Gly Ile Ala Trp Arg Lys Arg Pro Ala Ser  
40 45 50  
  
aca agg gcc gca aac gcg ccc tca ccc cgg acg acg tcg aga aag ccc 307  
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<213> Corynebacterium glutamicum

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Met Lys Ser Thr Gly 5															
aac atc atc gct gac acc atc tgc cgc act gcg gaa cta gga ctc acc 163															
Asn Ile Ile Ala Asp Thr Ile Cys Arg Thr Ala Glu Leu Gly Leu Thr 20															
atc acc ggc gct tcc gat gca ggt gat tac acc ctg atc gaa gca gac 211															
Ile Thr Gly Ala Ser Asp Ala Gly Asp Tyr Thr Leu Ile Glu Ala Asp 35															
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Ala Leu Asp Tyr Thr Ser Thr Cys Pro Glu Cys Ser Gln Pro Gly Val 50															
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Phe Arg His His Thr His Arg Met Leu Ile Asp Leu Pro Ile Val Gly 65															
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Phe Pro Thr Lys Leu Phe Ile Arg Leu Pro Arg Tyr Arg Cys Thr Asn 85															
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Pro Thr Cys Lys Gln Lys Tyr Phe Gln Ala Glu Leu Ser Cys Ala Asp 100															
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His Gly Lys Lys Val Thr His Arg Val Thr Arg Trp Ile Leu Gln Arg 115															
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Leu Ala Ile Asp Arg Met Ser Val His Ala Thr Ala Lys Ala Leu Gly 130															
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Leu Gly Trp Asp Leu Thr Cys Gln Leu Ala Leu Asp Met Cys Arg Glu 145															
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Cys	Pro	Ala 200	Arg	Leu	Leu	Asp	Val 205	Val	Pro	Gly	Arg	Ser 210	Ala	Asp	Ala	
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Arg	Ile	Val	Ser	Met	Asp 235	Gly	Phe	Gln	Gly	Tyr 240	Ala	Thr	Ala	Ser	Lys 245	
gaa	ctc	att	cct	tct	gct	cgt	cgc	gtg	atg	gat	cca	ttc	cat	gtt	gtg	883
Glu	Leu	Ile	Pro	Ser 250	Ala	Arg	Arg	Val 255	Met	Asp	Pro	Phe	His	Val 260	Val	
cgg	ctt	gct	ggt	gac	aag	ctc	acc	gcc	tgc	cgg	caa	cgc	ctc	cag	cgg	931
Arg	Leu	Ala	Gly	Asp 265	Lys	Leu	Thr	Ala 270	Cys	Arg	Gln	Arg	Leu	Gln 275	Arg	
gag	aaa	tac	cag	cgt	cgt	ggt	tta	agc	cag	gat	ccg	ttg	tat	aaa	aac	979
Glu	Lys	Tyr 280	Gln	Arg	Arg	Gly	Leu 285	Ser	Gln	Asp	Pro	Leu	Tyr	Lys	Asn 290	
cgg	aag	acc	ttg	ttg	acc	acg	cac	aag	tgg	ttg	agt	cct	cgt	cag	caa	1027
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gaa	agc	ttg	gag	cag	ttg	tgg	gcg	tat	gac	aaa	gac	tac	ggg	gcg	tta	1075
Glu	Ser	Leu	Glu	Gln	Leu 315	Trp	Ala	Tyr	Asp	Lys 320	Asp	Tyr	Gly	Ala	Leu 325	
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Lys	Leu	Ala	Trp	Leu 330	Ala	Tyr	Gln	Ala	Ile 335	Ile	Asp	Cys	Tyr	Gln 340	Met	
ggt	aat	aag	cgt	gaa	gcg	aag	aag	aaa	atg	cgg	acc	att	att	gat	cag	1171
Gly	Asn	Lys	Arg 345	Glu	Ala	Lys	Lys	Lys 350	Met	Arg	Thr	Ile 355	Ile	Asp	Gln	
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Ser	Leu	Phe 375	Lys	Arg	Leu	Gly 380	Asp	Val	Leu	Ala	Tyr 385	Phe	Asp	Val	Gly	
gtc	tcc	aac	ggt	ccg	gtc	gaa	gcg	atc	aac	gga	cgg	ttg	gag	cat	ttg	1315
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Arg Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn His Tyr Ile Leu Arg				
	410	415	420	
tgc ctt atc cat tca ggg cag ttg gtc cat aag atc aat gca ctc				1408
Cys Leu Ile His Ser Gly Gln Leu Val His Lys Ile Asn Ala Leu				
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taaaacagga agagcccgta aac				1431

&lt;210&gt; 180

&lt;211&gt; 436

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 180

Met Lys Ser Thr Gly Asn Ile Ile Ala Asp Thr Ile Cys Arg Thr Ala
1 5 10 15

Glu Leu Gly Leu Thr Ile Thr Gly Ala Ser Asp Ala Gly Asp Tyr Thr
20 25 30

Leu Ile Glu Ala Asp Ala Leu Asp Tyr Thr Ser Thr Cys Pro Glu Cys
35 40 45

Ser Gln Pro Gly Val Phe Arg His His Thr His Arg Met Leu Ile Asp
50 55 60

Leu Pro Ile Val Gly Phe Pro Thr Lys Leu Phe Ile Arg Leu Pro Arg
65 70 75 80

Tyr Arg Cys Thr Asn Pro Thr Cys Lys Gln Lys Tyr Phe Gln Ala Glu
85 90 95

Leu Ser Cys Ala Asp His Gly Lys Lys Val Thr His Arg Val Thr Arg
100 105 110

Trp Ile Leu Gln Arg Leu Ala Ile Asp Arg Met Ser Val His Ala Thr
115 120 125

Ala Lys Ala Leu Gly Leu Gly Trp Asp Leu Thr Cys Gln Leu Ala Leu
130 135 140

Asp Met Cys Arg Glu Leu Val Tyr Asn Asp Pro His His Leu Asp Gly
145 150 155 160

Val Tyr Val Ile Gly Val Asp Glu His Lys Trp Ser His Asn Arg Ala
165 170 175

Lys His Gly Asp Gly Phe Val Thr Val Ile Val Asp Met Thr Gly His
180 185 190

Arg Tyr Asp Ser Arg Cys Pro Ala Arg Leu Leu Asp Val Val Pro Gly
195 200 205

Arg Ser Ala Asp Ala Leu Arg Ser Trp Leu Gly Ser Arg Gly Glu Gln
210 215 220

Phe Arg Asn Gln Ile Arg Ile Val Ser Met Asp Gly Phe Gln Gly Tyr  
 225 230 235 240  
 Ala Thr Ala Ser Lys Glu Leu Ile Pro Ser Ala Arg Arg Val Met Asp  
 245 250 255  
 Pro Phe His Val Val Arg Leu Ala Gly Asp Lys Leu Thr Ala Cys Arg  
 260 265 270  
 Gln Arg Leu Gln Arg Glu Lys Tyr Gln Arg Arg Gly Leu Ser Gln Asp  
 275 280 285  
 Pro Leu Tyr Lys Asn Arg Lys Thr Leu Leu Thr Thr His Lys Trp Leu  
 290 295 300  
 Ser Pro Arg Gln Gln Glu Ser Leu Glu Gln Leu Trp Ala Tyr Asp Lys  
 305 310 315 320  
 Asp Tyr Gly Ala Leu Lys Leu Ala Trp Leu Ala Tyr Gln Ala Ile Ile  
 325 330 335  
 Asp Cys Tyr Gln Met Gly Asn Lys Arg Glu Ala Lys Lys Lys Met Arg  
 340 345 350  
 Thr Ile Ile Asp Gln Leu Arg Val Leu Lys Gly Pro Asn Lys Glu Leu  
 355 360 365  
 Ala Gln Leu Gly Arg Ser Leu Phe Lys Arg Leu Gly Asp Val Leu Ala  
 370 375 380  
 Tyr Phe Asp Val Gly Val Ser Asn Gly Pro Val Glu Ala Ile Asn Gly  
 385 390 395 400  
 Arg Leu Glu His Leu Arg Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn  
 405 410 415  
 His Tyr Ile Leu Arg Cys Leu Ile His Ser Gly Gln Leu Val His Lys  
 420 425 430  
 Ile Asn Ala Leu  
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 <223> RXN01969

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 gaagtgggtt agtcctcgtc agcaagaaag cttggagcag ttg tgg gcg tat gac 115  
 Leu Trp Ala Tyr Asp  
 1 5  
 aaa gcc tac ggg gcg tta aag ctt gcg tgg ctt gcg tat cag gcg att 163

Lys Ala Tyr Gly Ala Leu Lys Leu Ala Trp Leu Ala Tyr Gln Ala Ile  
                     10                    15                    20  
 att gat tgt tat cag atg ggt aat aag cgt gaa gcg aag aag aaa atg 211  
 Ile Asp Cys Tyr Gln Met Gly Asn Lys Arg Glu Ala Lys Lys Lys Met  
                     25                    30                    35  
 cgg acc att att gat cag ctt cgg gtg ttg aag ggg ccg aat aag gaa 259  
 Arg Thr Ile Ile Asp Gln Leu Arg Val Leu Lys Gly Pro Asn Lys Glu  
                     40                    45                    50  
 ctc gcg cag ttg ggt cgt agt ttg ttt aaa cga ctt ggt gat gtg ttg 307  
 Leu Ala Gln Leu Gly Arg Ser Leu Phe Lys Arg Leu Gly Asp Val Leu  
                     55                    60                    65  
 gcg tat ttc gat gtt ggt gtc tcc aac ggt ccg gtc gaa gcg atc aac 355  
 Ala Tyr Phe Asp Val Gly Val Ser Asn Gly Pro Val Glu Ala Ile Asn  
                     70                    75                    80                    85  
 gga cgg ttg gag cat ttg cgt ggg att gct cta ggt ttc cgt aat ttg 403  
 Gly Arg Leu Glu His Leu Arg Gly Ile Ala Leu Gly Phe Arg Asn Leu  
                     90                    95                    100  
 aac cac tac att ctg cgg tgc ctt atc cat tca ggg cag ttg gtc cat 451  
 Asn His Tyr Ile Leu Arg Cys Leu Ile His Ser Gly Gln Leu Val His  
                     105                    110                    115  
 aag atc aat gca ctc taaaacagga agagccactt aag 489  
 Lys Ile Asn Ala Leu  
                     120

&lt;210&gt; 182

&lt;211&gt; 122

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 182

Leu Trp Ala Tyr Asp Lys Ala Tyr Gly Ala Leu Lys Leu Ala Trp Leu  
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 Ala Tyr Gln Ala Ile Ile Asp Cys Tyr Gln Met Gly Asn Lys Arg Glu  
                     20                    25                    30  
 Ala Lys Lys Lys Met Arg Thr Ile Ile Asp Gln Leu Arg Val Leu Lys  
                     35                    40                    45  
 Gly Pro Asn Lys Glu Leu Ala Gln Leu Gly Arg Ser Leu Phe Lys Arg  
                     50                    55                    60  
 Leu Gly Asp Val Leu Ala Tyr Phe Asp Val Gly Val Ser Asn Gly Pro  
   65                    70                    75                    80  
 Val Glu Ala Ile Asn Gly Arg Leu Glu His Leu Arg Gly Ile Ala Leu  
                     85                    90                    95  
 Gly Phe Arg Asn Leu Asn His Tyr Ile Leu Arg Cys Leu Ile His Ser  
                     100                    105                    110  
 Gly Gln Leu Val His Lys Ile Asn Ala Leu  
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<222> (101)..(1408)
<223> FRXA00263
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Met Lys Ser Thr Gly																5
1																
aac atc atc gct gac acc atc tgc cgc act gcg gaa cta gga ctc acc	163															
Asn Ile Ile Ala Asp Thr Ile Cys Arg Thr Ala Glu Leu Gly Leu Thr																
10 15 20																
atc acc ggc gct tcc gat gca ggt gat tac acc ctg atc gaa gca gac	211															
Ile Thr Gly Ala Ser Asp Ala Gly Asp Tyr Thr Leu Ile Glu Ala Asp																
25 30 35																
gca ctc gac tac acc tcc acc tgc cca gaa tgc tcc caa cct ggg gtg	259															
Ala Leu Asp Tyr Thr Ser Thr Cys Pro. Glu Cys Ser Gln Pro Gly Val																
40 45 50																
ttt cgt cat cac acc cac cgg atg ctc att gat tta ccc atc gtc ggg	307															
Phe Arg His His Thr His Arg Met Leu Ile Asp Leu Pro Ile Val Gly																
55 60 65																
ttt ccc acc aaa ctg ttt atc cgt cta cct cgc tac cgc tgc acc aac	355															
Phe Pro. Thr Lys Leu Phe Ile Arg Leu Pro Arg Tyr Arg Cys Thr Asn																
70 75 80 85																
ccc aca tgt aag caa aag tat ttc caa gca gaa cta agc tgc gct gac	403															
Pro Thr Cys Lys Gln Lys Tyr Phe Gln Ala Glu Leu Ser Cys Ala Asp																
90 95 100																
cac ggt aaa aag gtc acc cac cgg gtc acc cgc tgg att tta caa cgc	451															
His Gly Lys Lys Val Thr His Arg Val Thr Arg Trp Ile Leu Gln Arg																
105 110 115																
ctt gct att gac cgg atg agt gtt cac gca acc gcg aaa gca ctt ggg	499															
Leu Ala Ile Asp Arg Met Ser Val His Ala Thr Ala Lys Ala Leu Gly																
120 125 130																
cta ggg tgg gat tta acc tgc caa cta gcc ctc gat atg tgc cgt gag	547															
Leu Gly Trp Asp Leu Thr Cys Gln Leu Ala Leu Asp Met Cys Arg Glu																
135 140 145																
ctg gtc tat aac gat cct cac cat ctt gat gga gtg tat gtc att ggg	595															
Leu Val Tyr Asn Asp Pro His His Leu Asp Gly Val Tyr Val Ile Gly																
150 155 160 165																
gtg gat gagcat aag tgg tca cat aat agg gct aag cat ggt gat ggg	643															
Val Asp Glu His Lys Trp Ser His Asn Arg Ala Lys His Gly Asp Gly																

170										175					180					
ttt	gtc	acc	gtg	att	gtc	gat	atg	acc	ggg	cat	cgg	tat	gac	tca	cgg	691				
Phe	Val	Thr	Val	Ile	Val	Asp	Met	Thr	Gly	His	Arg	Tyr	Asp	Ser	Arg					
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tgt	cct	gcc	cgg	tta	tta	gat	gtc	gtc	cca	ggg	cgt	agt	gct	gat	gct	739				
Cys	Pro	Ala	Arg	Leu	Leu	Asp	Val	Val	Pro	Gly	Arg	Ser	Ala	Asp	Ala					
		200					205					210								
tta	cgg	tcc	tgg	ctt	ggc	tcc	cgc	ggg	gaa	cag	ttc	cgc	aat	cag	ata	787				
Leu	Arg	Ser	Trp	Leu	Gly	Ser	Arg	Gly	Glu	Gln	Phe	Arg	Asn	Gln	Ile					
	215					220					225									
cgg	atc	gtg	tcc	atg	gat	gga	ttc	caa	ggc	tac	gcc	aca	gca	agt	aaa	835				
Arg	Ile	Val	Ser	Met	Asp	Gly	Phe	Gln	Gly	Tyr	Ala	Thr	Ala	Ser	Lys					
230					235				240						245					
gaa	ctc	att	cct	tct	gct	cgt	cgc	gtg	atg	gat	cca	ttc	cat	gtt	gtg	883				
Glu	Leu	Ile	Pro	Ser	Ala	Arg	Arg	Val	Met	Asp	Pro	Phe	His	Val	Val					
			250					255						260						
cgg	ctt	gct	ggg	gac	aag	ctc	acc	gcc	tgc	cgg	caa	cgc	ctc	cag	cgg	931				
Arg	Leu	Ala	Gly	Asp	Lys	Leu	Thr	Ala	Cys	Arg	Gln	Arg	Leu	Gln	Arg					
			265					270					275							
gag	aaa	tac	cag	cgt	cgt	ggg	tta	agc	cag	gat	ccg	ttg	tat	aaa	aac	979				
Glu	Lys	Tyr	Gln	Arg	Arg	Gly	Leu	Ser	Gln	Asp	Pro	Leu	Tyr	Lys	Asn					
		280					285					290								
cgg	aag	acc	ttg	ttg	acc	acg	cac	aag	tgg	ttg	agt	cct	cgt	cag	caa	1027				
Arg	Lys	Thr	Leu	Leu	Thr	Thr	His	Lys	Trp	Leu	Ser	Pro	Arg	Gln	Gln					
	295					300					305									
gaa	agc	ttg	gag	cag	ttg	tgg	gcg	tat	gac	aaa	gac	tac	ggg	gcg	tta	1075				
Glu	Ser	Leu	Glu	Gln	Leu	Trp	Ala	Tyr	Asp	Lys	Asp	Tyr	Gly	Ala	Leu					
310					315					320					325					
aag	ctt	gcg	tgg	ctt	gcg	tat	cag	gcg	att	att	gat	tgt	tat	cag	atg	1123				
Lys	Leu	Ala	Trp	Leu	Ala	Tyr	Gln	Ala	Ile	Ile	Asp	Cys	Tyr	Gln	Met					
				330					335					340						
ggg	aat	aag	cgt	gaa	gcg	aag	aag	aaa	atg	cgg	acc	att	att	gat	cag	1171				
Gly	Asn	Lys	Arg	Glu	Ala	Lys	Lys	Lys	Met	Arg	Thr	Ile	Ile	Asp	Gln					
			345					350					355							
ctt	cgg	gtg	ttg	aag	ggg	ccg	aat	aag	gaa	ctc	gcg	cag	ttg	ggg	cgt	1219				
Leu	Arg	Val	Leu	Lys	Gly	Pro	Asn	Lys	Glu	Leu	Ala	Gln	Leu	Gly	Arg					
		360					365					370								
agt	ttg	ttt	aaa	cga	ctt	ggg	gat	gtg	ttg	gcg	tat	ttc	gat	gtt	ggg	1267				
Ser	Leu	Phe	Lys	Arg	Leu	Gly	Asp	Val	Leu	Ala	Tyr	Phe	Asp	Val	Gly					
	375					380					385									
gtc	tcc	aac	ggg	ccg	gtc	gaa	gcg	atc	aac	gga	cgg	ttg	gag	cat	ttg	1315				
Val	Ser	Asn	Gly	Pro	Val	Glu	Ala	Ile	Asn	Gly	Arg	Leu	Glu	His	Leu					
390					395					400					405					
cgt	ggg	att	gct	cta	ggg	ttc	cgt	aat	ttg	aac	cac	tac	att	ctg	cgg	1363				
Arg	Gly	Ile	Ala	Leu	Gly	Phe	Arg	Asn	Leu	Asn	His	Tyr	Ile	Leu	Arg					
				410					415					420						

tgc ctt atc cat tca ggg cag ttg gtc cat aag atc aat gca ctc 1408  
 Cys Leu Ile His Ser Gly Gln Leu Val His Lys Ile Asn Ala Leu  
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<211> 436

<212> PRT

<213> Corynebacterium glutamicum

<400> 184

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Glu Leu Gly Leu Thr Ile Thr Gly Ala Ser Asp Ala Gly Asp Tyr Thr  
                   20                                  25                                  30

Leu Ile Glu Ala Asp Ala Leu Asp Tyr Thr Ser Thr Cys Pro Glu Cys  
                   35                                  40                                  45

Ser Gln Pro Gly Val Phe Arg His His Thr His Arg Met Leu Ile Asp  
                   50                                  55                                  60

Leu Pro Ile Val Gly Phe Pro Thr Lys Leu Phe Ile Arg Leu Pro Arg  
                   65                                  70                                  75                                  80

Tyr Arg Cys Thr Asn Pro Thr Cys Lys Gln Lys Tyr Phe Gln Ala Glu  
                                   85                                  90                                  95

Leu Ser Cys Ala Asp His Gly Lys Lys Val Thr His Arg Val Thr Arg  
                   100                                  105                                  110

Trp Ile Leu Gln Arg Leu Ala Ile Asp Arg Met Ser Val His Ala Thr  
                   115                                  120                                  125

Ala Lys Ala Leu Gly Leu Gly Trp Asp Leu Thr Cys Gln Leu Ala Leu  
                   130                                  135                                  140

Asp Met Cys Arg Glu Leu Val Tyr Asn Asp Pro His His Leu Asp Gly  
                   145                                  150                                  155                                  160

Val Tyr Val Ile Gly Val Asp Glu His Lys Trp Ser His Asn Arg Ala  
                                   165                                  170                                  175

Lys His Gly Asp Gly Phe Val Thr Val Ile Val Asp Met Thr Gly His  
                                   180                                  185                                  190

Arg Tyr Asp Ser Arg Cys Pro Ala Arg Leu Leu Asp Val Val Pro Gly  
                   195                                  200                                  205

Arg Ser Ala Asp Ala Leu Arg Ser Trp Leu Gly Ser Arg Gly Glu Gln  
                   210                                  215                                  220

Phe Arg Asn Gln Ile Arg Ile Val Ser Met Asp Gly Phe Gln Gly Tyr  
                   225                                  230                                  235                                  240

Ala Thr Ala Ser Lys Glu Leu Ile Pro Ser Ala Arg Arg Val Met Asp  
                                   245                                  250                                  255

Pro Phe His Val Val Arg Leu Ala Gly Asp Lys Leu Thr Ala Cys Arg  
 260 265 270  
 Gln Arg Leu Gln Arg Glu Lys Tyr Gln Arg Arg Gly Leu Ser Gln Asp  
 275 280 285  
 Pro Leu Tyr Lys Asn Arg Lys Thr Leu Leu Thr Thr His Lys Trp Leu  
 290 295 300  
 Ser Pro Arg Gln Gln Glu Ser Leu Glu Gln Leu Trp Ala Tyr Asp Lys  
 305 310 315 320  
 Asp Tyr Gly Ala Leu Lys Leu Ala Trp Leu Ala Tyr Gln Ala Ile Ile  
 325 330 335  
 Asp Cys Tyr Gln Met Gly Asn Lys Arg Glu Ala Lys Lys Lys Met Arg  
 340 345 350  
 Thr Ile Ile Asp Gln Leu Arg Val Leu Lys Gly Pro Asn Lys Glu Leu  
 355 360 365  
 Ala Gln Leu Gly Arg Ser Leu Phe Lys Arg Leu Gly Asp Val Leu Ala  
 370 375 380  
 Tyr Phe Asp Val Gly Val Ser Asn Gly Pro Val Glu Ala Ile Asn Gly  
 385 390 395 400  
 Arg Leu Glu His Leu Arg Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn  
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 Ile Asn Ala Leu  
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 <213> Corynebacterium glutamicum

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 <223> RXN01541

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 Met Thr Thr Pro His  
 1 5  
 tcc cac cgc gca cca cgt ctg gca tcc acg gtc att att gcc cgc gag 163  
 Ser His Arg Ala Pro Arg Leu Ala Ser Thr Val Ile Ile Ala Arg Glu  
 10 15 20  
 tct gct gac tca ggt acc tta gaa ttc ttt atc cag cag cga caa tcc 211  
 Ser Ala Asp Ser Gly Thr Leu Glu Phe Phe Ile Gln Gln Arg Gln Ser

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Thr	Met	Ala	Tyr	Ala	Ala	Asn	Ala	Val	Val	Phe	Pro	Gly	Gly	Gly	Gly	Val			
				40				45				50							
gag	gac	agc	gat	tat	ccc	ttt	atg	ctc	ccc	cac	cgc	gat	cag	cac	atg		307		
Glu	Asp	Ser	Asp	Tyr	Pro	Phe	Met	Leu	Pro	His	Arg	Asp	Gln	His	Met				
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tcg	cct	gaa	cac	atc	aag	cat	cat	gcc	agc	cga	ctc	cac	atg	gac	tca		355		
Ser	Pro	Glu	His	Ile	Lys	His	His	Ala	Ser	Arg	Leu	His	Met	Asp	Ser				
				70				75				80				85			
gaa	act	atg	gca	gct	cat	att	tcc	gct	gca	cgc	cgg	gaa	gta	tgg	gaa		403		
Glu	Thr	Met	Ala	Ala	His	Ile	Ser	Ala	Ala	Arg	Arg	Glu	Val	Trp	Glu				
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gaa	aca	ggc	gtt	gat	ctc	ggg	aat	tac	aac	cat	gaa	ctc	atc	ccg	atc		451		
Glu	Thr	Gly	Val	Asp	Leu	Gly	Asn	Tyr	Asn	His	Glu	Leu	Ile	Pro	Ile				
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gac	cgc	tgg	atc	aca	cct	gat	att	cct	gct	ttt	agg	cgc	cgt	tac	gac		499		
Asp	Arg	Trp	Ile	Thr	Pro	Asp	Ile	Pro	Ala	Phe	Arg	Arg	Arg	Tyr	Asp				
				120				125				130							
acc	gcc	acc	ttt	gta	ctt	att	cta	agc	aaa	gac	agc	act	aac	gca	gct		547		
Thr	Ala	Thr	Phe	Val	Leu	Ile	Leu	Ser	Lys	Asp	Ser	Thr	Asn	Ala	Ala				
				135				140				145							
ctg	cag	cac	cag	cat	caa	acc	acc	gag	gcc	acc	cat	tct	tat	tgg	gca		595		
Leu	Gln	His	Gln	His	Gln	Thr	Thr	Glu	Ala	Thr	His	Ser	Tyr	Trp	Ala				
				150				155				160				165			
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Thr	Ala	Glu	Glu	Leu	Leu	Thr	Gln	Trp	Ser	Thr	Gly	His	Leu	Asn	Leu				
				170				175				180							
ttg	tta	cca	acg	tgg	tgg	cat	atc	aac	cag	ctc	aat	cac	ctc	cac	acg		691		
Leu	Leu	Pro	Thr	Trp	Trp	His	Ile	Asn	Gln	Leu	Asn	His	Leu	His	Thr				
				185				190				195							
cta	aac	cag	ctg	tat	agc	ttt	gcc	cag	cgt	acc	cat	aat	ccg	cag	cac		739		
Leu	Asn	Gln	Leu	Tyr	Ser	Phe	Ala	Gln	Arg	Thr	His	Asn	Pro	Gln	His				
				200				205				210							
act	cca	ccc	aca	gtg	ttt	gct	aac	tgg	act	gca	ccg	gct	gat	gag	gcc		787		
Thr	Pro	Pro	Thr	Val	Phe	Ala	Asn	Trp	Thr	Ala	Pro	Ala	Asp	Glu	Ala				
				215				220				225							
gcc	atg	cag	cac	tat	ggg	ttc	cct	gat	ccc	gat	gcg	tac	ttt	gac	cat		835		
Ala	Met	Gln	His	Tyr	Gly	Phe	Pro	Asp	Pro	Asp	Ala	Tyr	Phe	Asp	His				
				230				235				240				245			
gcc	act	atc	gca	gga	aaa	cac	cac	aca	ctc	atc	aca	aga	aag				877		
Ala	Thr	Ile																	

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 186  
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 35 40 45  
 Pro Gly Gly Gly Val Glu Asp Ser Asp Tyr Pro Phe Met Leu Pro His  
 50 55 60  
 Arg Asp Gln His Met Ser Pro Glu His Ile Lys His His Ala Ser Arg  
 65 70 75 80  
 Leu His Met Asp Ser Glu Thr Met Ala Ala His Ile Ser Ala Ala Arg  
 85 90 95  
 Arg Glu Val Trp Glu Glu Thr Gly Val Asp Leu Gly Asn Tyr Asn His  
 100 105 110  
 Glu Leu Ile Pro Ile Asp Arg Trp Ile Thr Pro Asp Ile Pro Ala Phe  
 115 120 125  
 Arg Arg Arg Tyr Asp Thr Ala Thr Phe Val Leu Ile Leu Ser Lys Asp  
 130 135 140  
 Ser Thr Asn Ala Ala Leu Gln His Gln His Gln Thr Thr Glu Ala Thr  
 145 150 155 160  
 His Ser Tyr Trp Ala Thr Ala Glu Glu Leu Leu Thr Gln Trp Ser Thr  
 165 170 175  
 Gly His Leu Asn Leu Leu Leu Pro Thr Trp Trp His Ile Asn Gln Leu  
 180 185 190  
 Asn His Leu His Thr Leu Asn Gln Leu Tyr Ser Phe Ala Gln Arg Thr  
 195 200 205  
 His Asn Pro Gln His Thr Pro Pro Thr Val Phe Ala Asn Trp Thr Ala  
 210 215 220  
 Pro Ala Asp Glu Ala Ala Met Gln His Tyr Gly Phe Pro Asp Pro Asp  
 225 230 235 240  
 Ala Tyr Phe Asp His Ala Thr Ile Ala Gly Lys His His Thr Leu Ile  
 245 250 255  
 Thr Arg Lys

<210> 187  
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 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(771)

<223> FRXA01541

<400> 187

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Ala Arg Glu Ser Ala Asp Ser Gly Thr Leu Glu Phe Phe Ile Gln Gln	
20 25 30	
cga caa tcc act atg gct tat gca gca aac gct gtt gtt ttc cca ggc	144
Arg Gln Ser Thr Met Ala Tyr Ala Ala Asn Ala Val Val Phe Pro Gly	
35 40 45	
ggc ggt gtt gag gac agc gat tat ccc ttt atg ctc ccc cac cgc gat	192
Gly Gly Val Glu Asp Ser Asp Tyr Pro Phe Met Leu Pro His Arg Asp	
50 55 60	
cag cac atg tcg cct gaa cac atc aag cat cat gcc agc cga ctc cac	240
Gln His Met Ser Pro Glu His Ile Lys His His Ala Ser Arg Leu His	
65 70 75 80	
atg gac tca gaa act atg gca gct cat att tcc gct gca cgc cgg gaa	288
Met Asp Ser Glu Thr Met Ala Ala His Ile Ser Ala Ala Arg Arg Glu	
85 90 95	
gta tgg gaa gaa aca ggc gtt gat ctc ggt aat tac aac cat gaa ctc	336
Val Trp Glu Glu Thr Gly Val Asp Leu Gly Asn Tyr Asn His Glu Leu	
100 105 110	
atc ccg atc gac cgc tgg atc aca cct gat att cct gct ttt agg cgc	384
Ile Pro Ile Asp Arg Trp Ile Thr Pro Asp Ile Pro Ala Phe Arg Arg	
115 120 125	
cgt tac gac acc gcc acc ttt gta ctt att cta agc aaa gac agc act	432
Arg Tyr Asp Thr Ala Thr Phe Val Leu Ile Leu Ser Lys Asp Ser Thr	
130 135 140	
aac gca gct ctg cag cac cag cat caa acc acc gag gcc acc cat tct	480
Asn Ala Ala Leu Gln His Gln His Gln Thr Thr Glu Ala Thr His Ser	
145 150 155 160	
tat tgg gca act gca gaa gaa ctg ctc act caa tgg tca aca ggt cat	528
Tyr Trp Ala Thr Ala Glu Glu Leu Leu Thr Gln Trp Ser Thr Gly His	
165 170 175	
ctc aac ctg ttg tta cca acg tgg tgg cat atc aac cag ctc aat cac	576
Leu Asn Leu Leu Leu Pro Thr Trp Trp His Ile Asn Gln Leu Asn His	
180 185 190	
ctc cac acg cta aac cag ctg tat agc ttt gcc cag cgt acc cat aat	624
Leu His Thr Leu Asn Gln Leu Tyr Ser Phe Ala Gln Arg Thr His Asn	
195 200 205	
ccg cag cac act cca ccc aca gtg ttt gct aac tgg act gca ccg gct	672

Pro Gln His Thr Pro Pro Thr Val Phe Ala Asn Trp Thr Ala Pro Ala  
 210 215 220

gat gag gcc gcc atg cag cac tat ggg ttc cct gat ccc gat gcg tac 720  
 Asp Glu Ala Ala Met Gln His Tyr Gly Phe Pro Asp Pro Asp Ala Tyr  
 225 230 235 240

ttt gac cat gcc act atc gca gga aaa cac cac aca ctc atc aca aga 768  
 Phe Asp His Ala Thr Ile Ala Gly Lys His His Thr Leu Ile Thr Arg  
 245 250 255

aag taggtctcac catgactttt gca 794  
 Lys

<210> 188  
 <211> 257  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 188  
 Ile Phe Asn Ser His Arg Ala Pro Arg Leu Ala Ser Thr Val Ile Ile  
 1 5 10 15

Ala Arg Glu Ser Ala Asp Ser Gly Thr Leu Glu Phe Phe Ile Gln Gln  
 20 25 30

Arg Gln Ser Thr Met Ala Tyr Ala Ala Asn Ala Val Val Phe Pro Gly  
 35 40 45

Gly Gly Val Glu Asp Ser Asp Tyr Pro Phe Met Leu Pro His Arg Asp  
 50 55 60

Gln His Met Ser Pro Glu His Ile Lys His His Ala Ser Arg Leu His  
 65 70 75 80

Met Asp Ser Glu Thr Met Ala Ala His Ile Ser Ala Ala Arg Arg Glu  
 85 90 95

Val Trp Glu Glu Thr Gly Val Asp Leu Gly Asn Tyr Asn His Glu Leu  
 100 105 110

Ile Pro Ile Asp Arg Trp Ile Thr Pro Asp Ile Pro Ala Phe Arg Arg  
 115 120 125

Arg Tyr Asp Thr Ala Thr Phe Val Leu Ile Leu Ser Lys Asp Ser Thr  
 130 135 140

Asn Ala Ala Leu Gln His Gln His Gln Thr Thr Glu Ala Thr His Ser  
 145 150 155 160

Tyr Trp Ala Thr Ala Glu Glu Leu Leu Thr Gln Trp Ser Thr Gly His  
 165 170 175

Leu Asn Leu Leu Leu Pro Thr Trp Trp His Ile Asn Gln Leu Asn His  
 180 185 190

Leu His Thr Leu Asn Gln Leu Tyr Ser Phe Ala Gln Arg Thr His Asn  
 195 200 205

Pro Gln His Thr Pro Pro Thr Val Phe Ala Asn Trp Thr Ala Pro Ala  
210 215 220

Asp Glu Ala Ala Met Gln His Tyr Gly Phe Pro Asp Pro Asp Ala Tyr  
225 230 235 240

Phe Asp His Ala Thr Ile Ala Gly Lys His His Thr Leu Ile Thr Arg  
245 250 255

Lys

<210> 189

<211> 1059

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1036)

<223> RXA02590

<400> 189

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ggtcttacct ccacctggcc cctcgtgggc tggttccctc atg ggc atc tca ttg 115  
Met Gly Ile Ser Leu  
1 5

ttg tca tca ctg ttg aaa atc cat ggt ttt cca gtc gtc gca gat ttc 163  
Leu Ser Ser Leu Leu Lys Ile His Gly Phe Pro Val Val Ala Asp Phe  
10 15 20

ttc ttc gcg tta gct gtt gtg gtg gca att gtc att att ggc ggt tgg 211  
Phe Phe Ala Leu Ala Val Val Val Ala Ile Val Ile Ile Gly Gly Trp  
25 30 35

cta atc tac cgc tct cct tca ttc aaa act gaa gtc atg ccg gca tgg 259  
Leu Ile Tyr Arg Ser Pro Ser Phe Lys Thr Glu Val Met Pro Ala Trp  
40 45 50

gca atg ctg tcc atg ggt ttg atc gca ttg gga act gca agc ccc gta 307  
Ala Met Leu Ser Met Gly Leu Ile Ala Leu Gly Thr Ala Ser Pro Val  
55 60 65

gtt ttg ggt gat gat ctg tgg gga ttt atg ttt gtg tgc tgg tct att 355  
Val Leu Gly Asp Asp Leu Trp Gly Phe Met Phe Val Cys Trp Ser Ile  
70 75 80 85

ggc aca gcc gtg gga ctt gtt gcc tat tcc tta tat ata acg gcc att 403  
Gly Thr Ala Val Gly Leu Val Ala Tyr Ser Leu Tyr Ile Thr Ala Ile  
90 95 100

ttg cga tct aag gcg ggc aca cca act ttt gcg tgg ggt ctt cct ctt 451  
Leu Arg Ser Lys Ala Gly Thr Pro Thr Phe Ala Trp Gly Leu Pro Leu  
105 110 115

gtc acg ccg atg gtt gct tcc acc tcg gca gca caa ctc cat gag cac 499  
Val Thr Pro Met Val Ala Ser Thr Ser Ala Ala Gln Leu His Glu His  
120 125 130

ttt gaa ctt ccg gcg atg ctg tgg gtt tct ttc ggg ctc ttc ctt tta 547  
 Phe Glu Leu Pro Ala Met Leu Trp Val Ser Phe Gly Leu Phe Leu Leu  
 135 140 145

act ttg gcg tct gca cca gca gtt ttt acc cga gtg tat ttc tac tat 595  
 Thr Leu Ala Ser Ala Pro Ala Val Phe Thr Arg Val Tyr Phe Tyr Tyr  
 150 155 160 165

ttc ggc ccc aag gcg cag ggc atc cca ctg atg gca aca cca aca tca 643  
 Phe Gly Pro Lys Ala Gln Gly Ile Pro Leu Met Ala Thr Pro Thr Ser  
 170 175 180

tgg att cct ttg ggt atg gtg ggc caa tcc act gca gca gct cag ctc 691  
 Trp Ile Pro Leu Gly Met Val Gly Gln Ser Thr Ala Ala Ala Gln Leu  
 185 190 195

atc ggt gcg tcc ttt gga tcc aag aca gca atc aca atg ggc att att 739  
 Ile Gly Ala Ser Phe Gly Ser Lys Thr Ala Ile Thr Met Gly Ile Ile  
 200 205 210

tac ggc atc atc atg gga att ttt acg att cct ctg gga gcc atc gct 787  
 Tyr Gly Ile Ile Met Gly Ile Phe Thr Ile Pro Leu Gly Ala Ile Ala  
 215 220 225

cac ttt gtg ttc tac aga gct gtt ttc aaa ggg gcg aca tac agc ccc 835  
 His Phe Val Phe Tyr Arg Ala Val Phe Lys Gly Ala Thr Tyr Ser Pro  
 230 235 240 245

aca tgg tgg gcc agt acc ttc cca gtt ggc act ttg agt ttg ggt gcg 883  
 Thr Trp Trp Ala Ser Thr Phe Pro Val Gly Thr Leu Ser Leu Gly Ala  
 250 255 260

cat ttt tta tca cag agc acc gga gtg gag tgg ttt aac tac ttc agc 931  
 His Phe Leu Ser Gln Ser Thr Gly Val Glu Trp Phe Asn Tyr Phe Ser  
 265 270 275

ctg tac ttg att gct tta atg ctc ttt cat gtc atc gtg tcc acc atc 979  
 Leu Tyr Leu Ile Ala Leu Met Leu Phe His Val Ile Val Ser Thr Ile  
 280 285 290

gcc ggt acg att gca gta atg aga aga atc gtc gga aag ctt aaa tct 1027  
 Ala Gly Thr Ile Ala Val Met Arg Arg Ile Val Gly Lys Leu Lys Ser  
 295 300 305

caa ctg gcc taaattgcag cgagaggtct aaa 1059  
 Gln Leu Ala  
 310

&lt;210&gt; 190

&lt;211&gt; 312

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 190

Met Gly Ile Ser Leu Leu Ser Ser Leu Leu Lys Ile His Gly Phe Pro  
 1 5 10 15

Val Val Ala Asp Phe Phe Phe Ala Leu Ala Val Val Val Ala Ile Val  
 20 25 30

```

Ile Ile Gly Gly Trp Leu Ile Tyr Arg Ser Pro Ser Phe Lys Thr Glu
      35              40              45

Val Met Pro Ala Trp Ala Met Leu Ser Met Gly Leu Ile Ala Leu Gly
      50              55              60

Thr Ala Ser Pro Val Val Leu Gly Asp Asp Leu Trp Gly Phe Met Phe
      65              70              75              80

Val Cys Trp Ser Ile Gly Thr Ala Val Gly Leu Val Ala Tyr Ser Leu
              85              90              95

Tyr Ile Thr Ala Ile Leu Arg Ser Lys Ala Gly Thr Pro Thr Phe Ala
              100              105              110

Trp Gly Leu Pro Leu Val Thr Pro Met Val Ala Ser Thr Ser Ala Ala
      115              120              125

Gln Leu His Glu His Phe Glu Leu Pro Ala Met Leu Trp Val Ser Phe
      130              135              140

Gly Leu Phe Leu Leu Thr Leu Ala Ser Ala Pro Ala Val Phe Thr Arg
      145              150              155              160

Val Tyr Phe Tyr Tyr Phe Gly Pro Lys Ala Gln Gly Ile Pro Leu Met
              165              170              175

Ala Thr Pro Thr Ser Trp Ile Pro Leu Gly Met Val Gly Gln Ser Thr
              180              185              190

Ala Ala Ala Gln Leu Ile Gly Ala Ser Phe Gly Ser Lys Thr Ala Ile
      195              200              205

Thr Met Gly Ile Ile Tyr Gly Ile Ile Met Gly Ile Phe Thr Ile Pro
      210              215              220

Leu Gly Ala Ile Ala His Phe Val Phe Tyr Arg Ala Val Phe Lys Gly
      225              230              235              240

Ala Thr Tyr Ser Pro Thr Trp Trp Ala Ser Thr Phe Pro Val Gly Thr
              245              250              255

Leu Ser Leu Gly Ala His Phe Leu Ser Gln Ser Thr Gly Val Glu Trp
      260              265              270

Phe Asn Tyr Phe Ser Leu Tyr Leu Ile Ala Leu Met Leu Phe His Val
      275              280              285

Ile Val Ser Thr Ile Ala Gly Thr Ile Ala Val Met Arg Arg Ile Val
      290              295              300

Gly Lys Leu Lys Ser Gln Leu Ala
      305              310

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&lt;210&gt; 191

&lt;211&gt; 1017

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(994)

&lt;223&gt; RXA00016

&lt;400&gt; 191

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ctgaacggat cgcgaactt gaaaaggaaa atgcactcct ccgcgaagag cgtgacatcc 60

tgccgaaaagc ggccaaatat ttcgcggaag agacgaactg gtg atc cgc ttc cga 115
                               Val Ile Arg Phe Arg
                               1           5

ttc gtt gat gac gct cga aag acc tac tcg gtt aag cgg ata tgt gac 163
Phe Val Asp Asp Ala Arg Lys Thr Tyr Ser Val Lys Arg Ile Cys Asp
                        10                15                20

gtg ttg aag ctc aat cgt tcc tca tat tac aaa tgg aaa agc acc gcc 211
Val Leu Lys Leu Asn Arg Ser Ser Tyr Tyr Lys Trp Lys Ser Thr Ala
                        25                30                35

ttc acg cgt gaa aaa cgc ctg ctc agc gac gct att ctt ggg gtc cag 259
Phe Thr Arg Glu Lys Arg Leu Leu Ser Asp Ala Ile Leu Gly Val Gln
                        40                45                50

gtc aag act gta ttc acc act cac agt ggc tgt tat ggg gcc aaa cga 307
Val Lys Thr Val Phe Thr Thr His Ser Gly Cys Tyr Gly Ala Lys Arg
                        55                60                65

atc gcg gct gaa ctc aaa gac cag atc ggc cat gac ctt gcg aac cac 355
Ile Ala Ala Glu Leu Lys Asp Gln Ile Gly His Asp Leu Ala Asn His
                        70                75                80                85

aag cgg gtt gcc cgg atc atg cga tcg ttg aag ctg ttc gga tac aca 403
Lys Arg Val Ala Arg Ile Met Arg Ser Leu Lys Leu Phe Gly Tyr Thr
                        90                95                100

aag aaa cgc aag gtc acc acc acc gtg ccg gac aaa acc aag aca gtg 451
Lys Lys Arg Lys Val Thr Thr Thr Val Pro Asp Lys Thr Lys Thr Val
                        105                110                115

ttc cct gac ctt gtc ggc cgg aag ttc acc gct gac aag ccg aac cag 499
Phe Pro Asp Leu Val Gly Arg Lys Phe Thr Ala Asp Lys Pro Asn Gln
                        120                125                130

ctc tat gtc ggg gat atc acc tat ctg cca att cag gat ggg tcg aat 547
Leu Tyr Val Gly Asp Ile Thr Tyr Leu Pro Ile Gln Asp Gly Ser Asn
                        135                140                145

atg tac ctg gcc acg gtc att gac tgt tac tcc cgc agg ttg gtg ggc 595
Met Tyr Leu Ala Thr Val Ile Asp Cys Tyr Ser Arg Arg Leu Val Gly
                        150                155                160                165

ttt tct atc gca gat cac atg cgc acg agc ttg gtc cag gac gcg ctg 643
Phe Ser Ile Ala Asp His Met Arg Thr Ser Leu Val Gln Asp Ala Leu
                        170                175                180

ctc atg gct aaa gac cag cgt gga aac ctc aaa ggt gcg att ttt cac 691
Leu Met Ala Lys Asp Gln Arg Gly Asn Leu Lys Gly Ala Ile Phe His
                        185                190                195

tcc gac cac ggc agc gtt tac acg tct cat gcg ttt cag gag acg tgt 739

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Ser Asp His Gly Ser Val Tyr Thr Ser His Ala Phe Gln Glu Thr Cys  
 200 205 210

aag aaa cta ggg atc agg cag tcg atg gga tca att ggc acc agt gct 787  
 Lys Lys Leu Gly Ile Arg Gln Ser Met Gly Ser Ile Gly Thr Ser Ala  
 215 220 225

gac aac gct ttg gcg gag tct ttc aat gcc gcg atg aag cgg gaa gtc 835  
 Asp Asn Ala Leu Ala Glu Ser Phe Asn Ala Ala Met Lys Arg Glu Val  
 230 235 240 245

ctg cag gat tcc aag acc ttt gaa aat caa ttg tgc tgt cgc cgg gac 883  
 Leu Gln Asp Ser Lys Thr Phe Glu Asn Gln Leu Cys Cys Arg Arg Asp  
 250 255 260

gtc ttc cgc tgg tgt acc cgt tac aac acg gtt cgc cgg cat tcc tgg 931  
 Val Phe Arg Trp Cys Thr Arg Tyr Asn Thr Val Arg Arg His Ser Trp  
 265 270 275

tgt aga tat ctg gct ccg gtc gtg ttt gag gag cgc ggt cct gct atc 979  
 Cys Arg Tyr Leu Ala Pro Val Val Phe Glu Glu Arg Gly Pro Ala Ile  
 280 285 290

ctg aga tct gct tcc tgatcaaata ctccgtgtcc acc 1017  
 Leu Arg Ser Ala Ser  
 295

&lt;210&gt; 192

&lt;211&gt; 298

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 192

Val Ile Arg Phe Arg Phe Val Asp Asp Ala Arg Lys Thr Tyr Ser Val  
 1 5 10 15

Lys Arg Ile Cys Asp Val Leu Lys Leu Asn Arg Ser Ser Tyr Tyr Lys  
 20 25 30

Trp Lys Ser Thr Ala Phe Thr Arg Glu Lys Arg Leu Leu Ser Asp Ala  
 35 40 45

Ile Leu Gly Val Gln Val Lys Thr Val Phe Thr Thr His Ser Gly Cys  
 50 55 60

Tyr Gly Ala Lys Arg Ile Ala Ala Glu Leu Lys Asp Gln Ile Gly His  
 65 70 75 80

Asp Leu Ala Asn His Lys Arg Val Ala Arg Ile Met Arg Ser Leu Lys  
 85 90 95

Leu Phe Gly Tyr Thr Lys Lys Arg Lys Val Thr Thr Thr Val Pro Asp  
 100 105 110

Lys Thr Lys Thr Val Phe Pro Asp Leu Val Gly Arg Lys Phe Thr Ala  
 115 120 125

Asp Lys Pro Asn Gln Leu Tyr Val Gly Asp Ile Thr Tyr Leu Pro Ile  
 130 135 140

Gln Asp Gly Ser Asn Met Tyr Leu Ala Thr Val Ile Asp Cys Tyr Ser  
 145 150 155 160  
 Arg Arg Leu Val Gly Phe Ser Ile Ala Asp His Met Arg Thr Ser Leu  
 165 170 175  
 Val Gln Asp Ala Leu Leu Met Ala Lys Asp Gln Arg Gly Asn Leu Lys  
 180 185 190  
 Gly Ala Ile Phe His Ser Asp His Gly Ser Val Tyr Thr Ser His Ala  
 195 200 205  
 Phe Gln Glu Thr Cys Lys Lys Leu Gly Ile Arg Gln Ser Met Gly Ser  
 210 215 220  
 Ile Gly Thr Ser Ala Asp Asn Ala Leu Ala Glu Ser Phe Asn Ala Ala  
 225 230 235 240  
 Met Lys Arg Glu Val Leu Gln Asp Ser Lys Thr Phe Glu Asn Gln Leu  
 245 250 255  
 Cys Cys Arg Arg Asp Val Phe Arg Trp Cys Thr Arg Tyr Asn Thr Val  
 260 265 270  
 Arg Arg His Ser Trp Cys Arg Tyr Leu Ala Pro Val Val Phe Glu Glu  
 275 280 285  
 Arg Gly Pro Ala Ile Leu Arg Ser Ala Ser  
 290 295

<210> 193

<211> 573

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(550)

<223> RXA00265

<400> 193

tgggctcacc aggcttcag caccgcgagct tcccaacgct gctatcaagg cacgtaaaaa 60

cccagcacca actgcacgac cagaaacgag aattgattaa atg cgc tcc gct cac 115  
 Met Arg Ser Ala His  
 1 5

ggc cca tac att gat aag ttc ttc ccc gag cca tac aag aac atg ctc 163  
 Gly Pro Tyr Ile Asp Lys Phe Phe Pro Glu Pro Tyr Lys Asn Met Leu  
 10 15 20

gag ctc acc aag act ctg cga aag atc tac ccg gac gtt gat ctg cct 211  
 Glu Leu Thr Lys Thr Leu Arg Lys Ile Tyr Pro Asp Val Asp Leu Pro  
 25 30 35

acc tca ttg att gag ctg gtc aat gtc cgc gtt tct caa atc aac gga 259  
 Thr Ser Leu Ile Glu Leu Val Asn Val Arg Val Ser Gln Ile Asn Gly  
 40 45 50

tgt ggc acc tgc tta agt tta cat gtt ccc gct gct cgc cgt gcc ggc 307

Cys Gly Thr Cys Leu Ser Leu His Val Pro Ala Ala Arg Arg Ala Gly  
           55                                60                                65  
 gtt cca gag aag aaa ctc gat gct ctg gca gcg tgg caa atg gtg gat 355  
 Val Pro Glu Lys Lys Leu Asp Ala Leu Ala Ala Trp Gln Met Val Asp  
       70                                75                                80                                85  
 gaa ttc acc gtg gag gaa aag gca gca cta cag cta gca gaa tcc tta 403  
 Glu Phe Thr Val Glu Glu Lys Ala Ala Leu Gln Leu Ala Glu Ser Leu  
                                 90                                95                                100  
 acc ttg ctg gaa tcc cgc gaa ggt cac ctg gct gca cgc aca gcc tgc 451  
 Thr Leu Leu Glu Ser Arg Glu Gly His Leu Ala Ala Arg Thr Ala Cys  
                                 105                                110                                115  
 agt gtg ttt gcc gaa gag cag gta gct gcc ctg gaa tgg gct atc att 499  
 Ser Val Phe Ala Glu Glu Gln Val Ala Ala Leu Glu Trp Ala Ile Ile  
                                 120                                125                                130  
 gcg atc aat gct ttc aac cgc att tct att gcc agt ggg cac cca ctg 547  
 Ala Ile Asn Ala Phe Asn Arg Ile Ser Ile Ala Ser Gly His Pro Leu  
                                 135                                140                                145  
 ctc tagtaatcag gcagcaaaaa act 573  
 Leu  
 150

&lt;210&gt; 194

&lt;211&gt; 150

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 194

Met Arg Ser Ala His Gly Pro Tyr Ile Asp Lys Phe Phe Pro Glu Pro  
       1                                5                                10                                15  
 Tyr Lys Asn Met Leu Glu Leu Thr Lys Thr Leu Arg Lys Ile Tyr Pro  
                                 20                                25                                30  
 Asp Val Asp Leu Pro Thr Ser Leu Ile Glu Leu Val Asn Val Arg Val  
                                 35                                40                                45  
 Ser Gln Ile Asn Gly Cys Gly Thr Cys Leu Ser Leu His Val Pro Ala  
       50                                55                                60  
 Ala Arg Arg Ala Gly Val Pro Glu Lys Lys Leu Asp Ala Leu Ala Ala  
       65                                70                                75                                80  
 Trp Gln Met Val Asp Glu Phe Thr Val Glu Glu Lys Ala Ala Leu Gln  
                                 85                                90                                95  
 Leu Ala Glu Ser Leu Thr Leu Leu Glu Ser Arg Glu Gly His Leu Ala  
                                 100                                105                                110  
 Ala Arg Thr Ala Cys Ser Val Phe Ala Glu Glu Gln Val Ala Ala Leu  
                                 115                                120                                125  
 Glu Trp Ala Ile Ile Ala Ile Asn Ala Phe Asn Arg Ile Ser Ile Ala  
       130                                135                                140

Ser Gly His Pro Leu Leu  
145 150

<210> 195  
<211> 381  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(358)  
<223> RXA00938

<400> 195  
atgatctacc gctgggtcca gaaatacgcc cctgagctgg acaagcaaac acggtggtac 60  
  
cggcaggtgc ctgactggca ggccagttcc tggcgggtgg atg aga cct ata tcc 115  
Met Arg Pro Ile Ser  
1 5  
  
ggg tcg gcg gca ggt ggt gct acc tct gat ctg gcg atc acc gcc ggt 163  
Gly Ser Ala Ala Gly Gly Ala Thr Ser Asp Leu Ala Ile Thr Ala Gly  
10 15 20  
  
ggc cag acc ctg gac ttt tac ctc tct ccg aag cgg aac gtg gcc gca 211  
Gly Gln Thr Leu Asp Phe Tyr Leu Ser Pro Lys Arg Asn Val Ala Ala  
25 30 35  
  
gcg aag cgt ttc ctg gcc aag gcc ctc aga tcc aat gcg tca gcc ggg 259  
Ala Lys Arg Phe Leu Ala Lys Ala Leu Arg Ser Asn Ala Ser Ala Gly  
40 45 50  
  
tat ccc aga gtg atc aac acc gat aaa gca ccc tcc cta gcc agg gca 307  
Tyr Pro Arg Val Ile Asn Thr Asp Lys Ala Pro Ser Leu Ala Arg Ala  
55 60 65  
  
atc acc gag ttg aag tca gag gga atc tgc ccg cca aca gtg gaa cac 355  
Ile Thr Glu Leu Lys Ser Glu Gly Ile Cys Pro Pro Thr Val Glu His  
70 75 80 85  
  
cgg tagtgaaat acctcaacaa cat 381  
Arg

<210> 196  
<211> 86  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 196  
Met Arg Pro Ile Ser Gly Ser Ala Ala Gly Gly Ala Thr Ser Asp Leu  
1 5 10 15  
  
Ala Ile Thr Ala Gly Gly Gln Thr Leu Asp Phe Tyr Leu Ser Pro Lys  
20 25 30  
  
Arg Asn Val Ala Ala Ala Lys Arg Phe Leu Ala Lys Ala Leu Arg Ser  
35 40 45

Asn Ala Ser Ala Gly Tyr Pro Arg Val Ile Asn Thr Asp Lys Ala Pro  
 50 55 60

Ser Leu Ala Arg Ala Ile Thr Glu Leu Lys Ser Glu Gly Ile Cys Pro  
 65 70 75 80

Pro Thr Val Glu His Arg  
 85

<210> 197  
 <211> 339  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(316)  
 <223> RXA01264

<400> 197  
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gaaggggatc aacagcctgc gcaaaggcct accagcgaga atg gac gag ctt gcc 115  
 Met Asp Glu Leu Ala  
 1 5

caa ctg ggg cac acc ttg tgg cgt cgg cgt aag aac gtg ttg gcg tcc 163  
 Gln Leu Gly His Thr Leu Trp Arg Arg Arg Lys Asn Val Leu Ala Ser  
 10 15 20

ttc aat atc ggt gca tcc aac gga cct gtc gag gcc atc aac ggc aga 211  
 Phe Asn Ile Gly Ala Ser Asn Gly Pro Val Glu Ala Ile Asn Gly Arg  
 25 30 35

ctt gag cac ctg cgc ggg atc acc ttg ggg ttc agg aac ctc aac cac 259  
 Leu Glu His Leu Arg Gly Ile Thr Leu Gly Phe Arg Asn Leu Asn His  
 40 45 50

tac atc ttg cgg tgc ttg atc caa gcc gga caa ctg cag agg aag atc 307  
 Tyr Ile Leu Arg Cys Leu Ile Gln Ala Gly Gln Leu Gln Arg Lys Ile  
 55 60 65

aat gta ctc taaatccgaa gagttggcaa aga 339  
 Asn Val Leu  
 70

<210> 198  
 <211> 72  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 198  
 Met Asp Glu Leu Ala Gln Leu Gly His Thr Leu Trp Arg Arg Arg Lys  
 1 5 10 15

Asn Val Leu Ala Ser Phe Asn Ile Gly Ala Ser Asn Gly Pro Val Glu  
 20 25 30

Ala Ile Asn Gly Arg Leu Glu His Leu Arg Gly Ile Thr Leu Gly Phe

35 40 45  
 Arg Asn Leu Asn His Tyr Ile Leu Arg Cys Leu Ile Gln Ala Gly Gln  
 50 55 60  
 Leu Gln Arg Lys Ile Asn Val Leu  
 65 70

<210> 199  
 <211> 273  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(250)  
 <223> RXA01265

<400> 199  
 tacgaggaag atcttcacaa aatcctgtac tgcgcggatg actgatccaa gttcaaccac 60  
 cggggcactg ctagatcttg cagcgccttg tgattgacgg atg agt gtg tct gcc 115  
 Met Ser Val Ser Ala  
 1 5  
 acg gct aaa gca ctg aag atc ggc tgg gaa cta gtc aac cag gtt gca 163  
 Thr Ala Lys Ala Leu Lys Ile Gly Trp Glu Leu Val Asn Gln Val Ala  
 10 15 20  
 ctc gat gct tgc cga cag ctc att tac aac gac ccg cgc cac ctt gaa 211  
 Leu Asp Ala Cys Arg Gln Leu Ile Tyr Asn Asp Pro Arg His Leu Glu  
 25 30 35  
 gtc gat gaa cat gta tgg aag tat act cga aag cca ggt tagccgtcga 260  
 Val Asp Glu His Val Trp Lys Tyr Thr Arg Lys Pro Gly  
 40 45 50  
 acctggtgac cat 273

<210> 200  
 <211> 50  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 200  
 Met Ser Val Ser Ala Thr Ala Lys Ala Leu Lys Ile Gly Trp Glu Leu  
 1 5 10 15  
 Val Asn Gln Val Ala Leu Asp Ala Cys Arg Gln Leu Ile Tyr Asn Asp  
 20 25 30  
 Pro Arg His Leu Glu Val Asp Glu His Val Trp Lys Tyr Thr Arg Lys  
 35 40 45  
 Pro Gly  
 50

<210> 201

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<211> 267
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101) .. (244)  
<223> RXA01327
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<400> 201
gaaatccaaa tatcctctac gaacgcaatg gtcacacagt ttctaaactc gaaatcgcct 60

tattcgacaa catcgattgt aacgcctcga catcgaccgt atg agt atc gca gca 115
Met Ser Ile Ala Ala
1 5

acc gcg aaa gcc ctc ggt cta ggc tgg gat ctc acc tgc caa cta gcc 163
Thr Ala Lys Ala Leu Gly Leu Gly Trp Asp Leu Thr Cys Gln Leu Ala
10 15 20

cta gat atg tgc cac gaa ctc atc tac tac gac ccc acc cac cta gaa 211
Leu Asp Met Cys His Glu Leu Ile Tyr Tyr Asp Pro Thr His Leu Glu
25 30 35

att gtg cac gtt att ggc gtc gat gag cac aaa tgatctcata accgattaaa 264
Ile Val His Val Ile Gly Val Asp Glu His Lys
40 45

aca 267

```

```
<210> 202
<211> 48
<212> PRT
<213> Corynebacterium glutamicum
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```

<400> 202
Met Ser Ile Ala Ala Thr Ala Lys Ala Leu Gly Leu Gly Trp Asp Leu
  1             5             10             15
Thr Cys Gln Leu Ala Leu Asp Met Cys His Glu Leu Ile Tyr Tyr Asp
          20             25             30
Pro Thr His Leu Glu Ile Val His Val Ile Gly Val Asp Glu His Lys
      35             40             45

```

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<210> 203
<211> 498
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(475)
<223> RXA01328
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<400> 203
cacaaatgat ctcataaccg attaaaacat ggtgatggct atgtcaccgt cattgttaat 60
atgaccagcc ttccaccgcg atgccacgtc cccagcgagg ttg ctt gat gta gtc 115
```

Leu Leu Asp Val Val  
1 5

gaa ggc cgc agt gct gat gcg ttg cgg gcg tgg ctt gca cgc cga agc 163  
Glu Gly Arg Ser Ala Asp Ala Leu Arg Ala Trp Leu Ala Arg Arg Ser  
10 15 20

cca gca ttt cga cac caa gta cgc att gta act atg gat gga ttc caa 211  
Pro Ala Phe Arg His Gln Val Arg Ile Val Thr Met Asp Gly Phe Gln  
25 30 35

ggc tat gcc aca acc agc aaa caa ctt ctg ccc gcc gca cgc cga gtc 259  
Gly Tyr Ala Thr Thr Ser Lys Gln Leu Leu Pro Ala Ala Arg Arg Val  
40 45 50

atg gat cct ttc cac gtg gta ctc ctc gcc ggc gat aaa ctc acc cga 307  
Met Asp Pro Phe His Val Val Leu Leu Ala Gly Asp Lys Leu Thr Arg  
55 60 65

tgc cga caa cgt ttg cag cag gaa aaa tac cac cgg cgg ggt ttg cat 355  
Cys Arg Gln Arg Leu Gln Gln Glu Lys Tyr His Arg Arg Gly Leu His  
70 75 80 85

gat gac ccg ttg tat aag aac cgg aaa acc ttg ctg acc acg caa aaa 403  
Asp Asp Pro Leu Tyr Lys Asn Arg Lys Thr Leu Leu Thr Thr Gln Lys  
90 95 100

tgg ttg agt aag aaa aag caa agc gtc ttg atg agt tgt tta gct ttg 451  
Trp Leu Ser Lys Lys Lys Gln Ser Val Leu Met Ser Cys Leu Ala Leu  
105 110 115

ata aag act acg cgg cac tgc aac tgatgtggca ggcgtatcaa ggc 498  
Ile Lys Thr Thr Arg His Cys Asn  
120 125

&lt;210&gt; 204

&lt;211&gt; 125

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 204

Leu Leu Asp Val Val Glu Gly Arg Ser Ala Asp Ala Leu Arg Ala Trp  
1 5 10 15

Leu Ala Arg Arg Ser Pro Ala Phe Arg His Gln Val Arg Ile Val Thr  
20 25 30

Met Asp Gly Phe Gln Gly Tyr Ala Thr Thr Ser Lys Gln Leu Leu Pro  
35 40 45

Ala Ala Arg Arg Val Met Asp Pro Phe His Val Val Leu Leu Ala Gly  
50 55 60

Asp Lys Leu Thr Arg Cys Arg Gln Arg Leu Gln Gln Glu Lys Tyr His  
65 70 75 80

Arg Arg Gly Leu His Asp Asp Pro Leu Tyr Lys Asn Arg Lys Thr Leu  
85 90 95

Leu Thr Thr Gln Lys Trp Leu Ser Lys Lys Lys Gln Ser Val Leu Met

100 105 110

Ser Cys Leu Ala Leu Ile Lys Thr Thr Arg His Cys Asn  
115 120 125

<210> 205  
<211> 414  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(391)  
<223> RXA01329

<400> 205  
aaaagcaaag cgtcttgatg agttgttttag ctttgataaa gactacgcgg cactgcaact 60  
gatgtggcag gcgtatcaag gcattattga ctgatacaac atg gcc gat aaa cgc 115  
Met Ala Asp Lys Arg  
1 5  
cgc gca aag acc atg atg cgc gag att gtt gac cag atg cgg cta ctg 163  
Arg Ala Lys Thr Met Met Arg Glu Ile Val Asp Gln Met Arg Leu Leu  
10 15 20  
aaa gga caa gcg aat cga gaa ctt gca caa cta ggc cgc agc cta cac 211  
Lys Gly Gln Ala Asn Arg Glu Leu Ala Gln Leu Gly Arg Ser Leu His  
25 30 35  
aaa cgc ctc ggt gac atc ctg gcg tat ttc gat gtc gga atc tct aac 259  
Lys Arg Leu Gly Asp Ile Leu Ala Tyr Phe Asp Val Gly Ile Ser Asn  
40 45 50  
gga ccc gta gaa gca atc aac gga cga ctc gaa cac ctc cgc gga atc 307  
Gly Pro Val Glu Ala Ile Asn Gly Arg Leu Glu His Leu Arg Gly Ile  
55 60 65  
gcc cta gga ttt cgc aac ctc aac cac tac atc ctg cac tgt ctc atc 355  
Ala Leu Gly Phe Arg Asn Leu Asn His Tyr Ile Leu His Cys Leu Ile  
70 75 80 85  
cac tcc gga caa ctc acc cac aaa atc aac gca ctc taaaaccgga 401  
His Ser Gly Gln Leu Thr His Lys Ile Asn Ala Leu  
90 95  
agagcccgat tgc 414

<210> 206  
<211> 97  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 206  
Met Ala Asp Lys Arg Arg Ala Lys Thr Met Met Arg Glu Ile Val Asp  
1 5 10 15  
Gln Met Arg Leu Leu Lys Gly Gln Ala Asn Arg Glu Leu Ala Gln Leu  
20 25 30

Gly Arg Ser Leu His Lys Arg Leu Gly Asp Ile Leu Ala Tyr Phe Asp  
                   35                                  40                                  45  
 Val Gly Ile Ser Asn Gly Pro Val Glu Ala Ile Asn Gly Arg Leu Glu  
           50                                  55                                  60  
 His Leu Arg Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn His Tyr Ile  
   65                                  70                                  75                                  80  
 Leu His Cys Leu Ile His Ser Gly Gln Leu Thr His Lys Ile Asn Ala  
                                   85                                  90                                  95  
 Leu

<210> 207  
 <211> 954  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(931)  
 <223> RXA01443

<400> 207  
 gaaagctgct aaatattttcc cggcaagaga caaactggtg agctgcttcc ggtttggtga 60  
  
 cgacgtgcga aaaacctatc cgggtaagcg gttatgcgaa gtg ttg aaa atc aac 115  
   Val Leu Lys Ile Asn  
   1                                  5  
  
 cgc tcc tcg tac tac aaa tgg aaa aag act gcc ccg acc agg agc aac 163  
 Arg Ser Ser Tyr Tyr Lys Trp Lys Lys Thr Ala Pro Thr Arg Ser Asn  
                                   10                                  15                                  20  
  
 cgc ctg ctc agc gac gca gtc tta gga gcg aag atc aag tcc atc ttc 211  
 Arg Leu Leu Ser Asp Ala Val Leu Gly Ala Lys Ile Lys Ser Ile Phe  
                                   25                                  30                                  35  
  
 acg aaa gaa cgc ggc tgc tac ggc tca aaa cgc atc acg gct gag ctc 259  
 Thr Lys Glu Arg Gly Cys Tyr Gly Ser Lys Arg Ile Thr Ala Glu Leu  
                   40                                  45                                  50  
  
 aac gat gat cct ggc agc act ccg gtt aac cat aaa cga gtc gcc cgg 307  
 Asn Asp Asp Pro Gly Ser Thr Pro Val Asn His Lys Arg Val Ala Arg  
   55                                  60                                  65  
  
 atc atg gca tca tta aag ctg ttt ggt ttc acg aag aaa cgc agg gtc 355  
 Ile Met Ala Ser Leu Lys Leu Phe Gly Phe Thr Lys Lys Arg Arg Val  
   70                                  75                                  80                                  85  
  
 atc acg acc gtg tct gat aaa aag aag cct gtc ttc cct gac ctg gtc 403  
 Ile Thr Thr Val Ser Asp Lys Lys Lys Pro Val Phe Pro Asp Leu Val  
                                   90                                  95                                  100  
  
 aaa cgt cat ttt aac gca cta gca gca aat gaa gtt tac gtc ggg gat 451  
 Lys Arg His Phe Asn Ala Leu Ala Ala Asn Glu Val Tyr Val Gly Asp  
                   105                                  110                                  115

att act tac cta ccg atc gca gat ggc acg aac atg tat ctg gct acg 499  
 Ile Thr Tyr Leu Pro Ile Ala Asp Gly Thr Asn Met Tyr Leu Ala Thr  
 120 125 130

gtc att gat tgc tat tcc cgt agg ctg gtg ggt ttt gcg att gcg gat 547  
 Val Ile Asp Cys Tyr Ser Arg Arg Leu Val Gly Phe Ala Ile Ala Asp  
 135 140 145

cat atg cgc acg tca ttg gtg cag gag gca ttg ctg atg gcg aag agt 595  
 His Met Arg Thr Ser Leu Val Gln Glu Ala Leu Leu Met Ala Lys Ser  
 150 155 160 165

cag cga ggc agc ctg aag ggt gcg gtg ttt cat tcg gat cac ggc agt 643  
 Gln Arg Gly Ser Leu Lys Gly Ala Val Phe His Ser Asp His Gly Ser  
 170 175 180

gtg tac acc tcg cag gcg ttt cag gac act tgt aaa aag ttg ggt gtt 691  
 Val Tyr Thr Ser Gln Ala Phe Gln Asp Thr Cys Lys Lys Leu Gly Val  
 185 190 195

cgt cag tcg atg ggt gct gtt ggt acc agt gcg gat aat tcg ctg gcg 739  
 Arg Gln Ser Met Gly Ala Val Gly Thr Ser Ala Asp Asn Ser Leu Ala  
 200 205 210

gag tcg ttt aat gcc gcc ctc aag cga gag gtg ctg cag gat tcc aag 787  
 Glu Ser Phe Asn Ala Ala Leu Lys Arg Glu Val Leu Gln Asp Ser Lys  
 215 220 225

acg ttt gcc aat cag ttg gtg tgc cgc cgg gag gta ttt cgc tgg tgt 835  
 Thr Phe Ala Asn Gln Leu Val Cys Arg Arg Glu Val Phe Arg Trp Cys  
 230 235 240 245

acc agg tac agc aca aat cgc agg cat tct tgg tgt ggc tat gtg gtg 883  
 Thr Arg Tyr Ser Thr Asn Arg Arg His Ser Trp Cys Gly Tyr Val Val  
 250 255 260

cct gcg gtg ttc gag agt aga aat tta gct att ctg aaa tct gtt tcc 931  
 Pro Ala Val Phe Glu Ser Arg Asn Leu Ala Ile Leu Lys Ser Val Ser  
 265 270 275

tgattaaatc gcctgtgttt cca 954

&lt;210&gt; 208

&lt;211&gt; 277

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 208

Val Leu Lys Ile Asn Arg Ser Ser Tyr Tyr Lys Trp Lys Lys Thr Ala  
 1 5 10 15

Pro Thr Arg Ser Asn Arg Leu Leu Ser Asp Ala Val Leu Gly Ala Lys  
 20 25 30

Ile Lys Ser Ile Phe Thr Lys Glu Arg Gly Cys Tyr Gly Ser Lys Arg  
 35 40 45

Ile Thr Ala Glu Leu Asn Asp Asp Pro Gly Ser Thr Pro Val Asn His  
 50 55 60

Lys Arg Val Ala Arg Ile Met Ala Ser Leu Lys Leu Phe Gly Phe Thr  
 65 70 75 80  
 Lys Lys Arg Arg Val Ile Thr Thr Val Ser Asp Lys Lys Lys Pro Val  
 85 90 95  
 Phe Pro Asp Leu Val Lys Arg His Phe Asn Ala Leu Ala Ala Asn Glu  
 100 105 110  
 Val Tyr Val Gly Asp Ile Thr Tyr Leu Pro Ile Ala Asp Gly Thr Asn  
 115 120 125  
 Met Tyr Leu Ala Thr Val Ile Asp Cys Tyr Ser Arg Arg Leu Val Gly  
 130 135 140  
 Phe Ala Ile Ala Asp His Met Arg Thr Ser Leu Val Gln Glu Ala Leu  
 145 150 155 160  
 Leu Met Ala Lys Ser Gln Arg Gly Ser Leu Lys Gly Ala Val Phe His  
 165 170 175  
 Ser Asp His Gly Ser Val Tyr Thr Ser Gln Ala Phe Gln Asp Thr Cys  
 180 185 190  
 Lys Lys Leu Gly Val Arg Gln Ser Met Gly Ala Val Gly Thr Ser Ala  
 195 200 205  
 Asp Asn Ser Leu Ala Glu Ser Phe Asn Ala Ala Leu Lys Arg Glu Val  
 210 215 220  
 Leu Gln Asp Ser Lys Thr Phe Ala Asn Gln Leu Val Cys Arg Arg Glu  
 225 230 235 240  
 Val Phe Arg Trp Cys Thr Arg Tyr Ser Thr Asn Arg Arg His Ser Trp  
 245 250 255  
 Cys Gly Tyr Val Val Pro Ala Val Phe Glu Ser Arg Asn Leu Ala Ile  
 260 265 270  
 Leu Lys Ser Val Ser  
 275

<210> 209  
 <211> 390  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(367)  
 <223> RXA01444

<400> 209  
 ttttaccac cttccctgtt tgctggttaa gggacctggc ccctgtttgg tagacaccta 60  
 acatcccaac attctgggat agaaaggtaa cctaccgatc atg cca acc aag acc 115  
 Met Pro Thr Lys Thr  
 1 5

```

tat tcc gag gag ttc aaa cgc gac gcc gtt gct ttg tac gag aac tcc 163
Tyr Ser Glu Glu Phe Lys Arg Asp Ala Val Ala Leu Tyr Glu Asn Ser
      10                      15                      20

gac ggg gcc tca ctc caa cag atc gcc aac gat ctc ggc atc aac cga 211
Asp Gly Ala Ser Leu Gln Gln Ile Ala Asn Asp Leu Gly Ile Asn Arg
      25                      30                      35

gta acc ctg aaa aac tgg atc atc aaa tac gga tcc aac cac aac gta 259
Val Thr Leu Lys Asn Trp Ile Ile Lys Tyr Gly Ser Asn His Asn Val
      40                      45                      50

caa ggg aca acc cca tct gcg gca gtc tct gaa gct gaa caa atc cgg 307
Gln Gly Thr Thr Pro Ser Ala Ala Val Ser Glu Ala Glu Gln Ile Arg
      55                      60                      65

cag ctg aag aag gaa aac gcg cta caa cgc gca aga acg cga cat cct 355
Gln Leu Lys Lys Glu Asn Ala Leu Gln Arg Ala Arg Thr Arg His Pro
      70                      75                      80

gcg gaa agc tgc taaatatttc ccggcaagag aca 390
Ala Glu Ser Cys

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<210> 210  
 <211> 89  
 <212> PRT  
 <213> Corynebacterium glutamicum

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<400> 210
Met Pro Thr Lys Thr Tyr Ser Glu Glu Phe Lys Arg Asp Ala Val Ala
  1                      5                      10                      15

Leu Tyr Glu Asn Ser Asp Gly Ala Ser Leu Gln Gln Ile Ala Asn Asp
      20                      25                      30

Leu Gly Ile Asn Arg Val Thr Leu Lys Asn Trp Ile Ile Lys Tyr Gly
      35                      40                      45

Ser Asn His Asn Val Gln Gly Thr Thr Pro Ser Ala Ala Val Ser Glu
      50                      55                      60

Ala Glu Gln Ile Arg Gln Leu Lys Lys Glu Asn Ala Leu Gln Arg Ala
      65                      70                      75                      80

Arg Thr Arg His Pro Ala Glu Ser Cys
      85

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<210> 211  
 <211> 492  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(469)  
 <223> RXA01648

<400> 211

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ccaatgaagt ttacgtcggg gatattactt atctgccgat tgctgatggg tcgaatatgt 60
atttgacgac ggtcattgat tgctattctt agcacggttg gtg ggt ttt gcc ttt 115
                               Val Gly Phe Ala Phe
                               1           5

gcg gat cat atg cgc acg tca ttg gtg cag gag gcg ttg atg atg gcg 163
Ala Asp His Met Arg Thr Ser Leu Val Gln Glu Ala Leu Met Met Ala
                10                15                20

aag agt cag cga ggc agt cta cag ggt gct gtt ttt cat tcg gat cac 211
Lys Ser Gln Arg Gly Ser Leu Gln Gly Ala Val Phe His Ser Asp His
                25                30                35

ggc agt gtg tac acc tcg cag gcg ttt cag gac act tgt aaa aag ttg 259
Gly Ser Val Tyr Thr Ser Gln Ala Phe Gln Asp Thr Cys Lys Lys Leu
                40                45                50

ggt gtt cgt cag tcg atg ggt gct gtt ggt acc agt gcg gat aat tcg 307
Gly Val Arg Gln Ser Met Gly Ala Val Gly Thr Ser Ala Asp Asn Ser
                55                60                65

cta gcg gag tcg ttt aat gcc gcg ctc aag cgg gaa gtg ctg cag gat 355
Leu Ala Glu Ser Phe Asn Ala Ala Leu Lys Arg Glu Val Leu Gln Asp
                70                75                80                85

tcc aag acg ttt gct aat cag ttg gtg tgc cgt cgg gag gta ttt cgg 403
Ser Lys Thr Phe Ala Asn Gln Leu Val Cys Arg Arg Glu Val Phe Arg
                90                95                100

tgg tgt gac cta gta caa cac ggt gcg cag aca ttc ttg gtg tgg cta 451
Trp Cys Asp Leu Val Gln His Gly Ala Gln Thr Phe Leu Val Trp Leu
                105                110                115

tgt ggc gcc tgc ggt gtt tgaggtccag gggtctgcta ttc 492
Cys Gly Ala Cys Gly Val
                120

```

&lt;210&gt; 212

&lt;211&gt; 123

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 212

```

Val Gly Phe Ala Phe Ala Asp His Met Arg Thr Ser Leu Val Gln Glu
 1           5           10           15

Ala Leu Met Met Ala Lys Ser Gln Arg Gly Ser Leu Gln Gly Ala Val
 20                25                30

Phe His Ser Asp His Gly Ser Val Tyr Thr Ser Gln Ala Phe Gln Asp
 35                40                45

Thr Cys Lys Lys Leu Gly Val Arg Gln Ser Met Gly Ala Val Gly Thr
 50                55                60

Ser Ala Asp Asn Ser Leu Ala Glu Ser Phe Asn Ala Ala Leu Lys Arg
 65                70                75                80

Glu Val Leu Gln Asp Ser Lys Thr Phe Ala Asn Gln Leu Val Cys Arg

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[illegible]

<210> 214  
 <211> 140  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 214  
 Val Leu Lys Ile Asn Arg Ser Ser Tyr Tyr Lys Trp Lys Lys Thr Ala  
     1                    5                    10                    15  
 Leu Thr Arg Lys Lys Leu Leu Leu Ser Asp Ala Val Leu Gly Ala Lys  
             20                    25                    30  
 Ile Lys Ser Ile Phe Thr Lys Glu Arg Gly Cys Tyr Gly Ala Lys Arg  
             35                    40                    45  
 Ile Thr Ala Glu Leu Asn Asp Gly Pro Gly Thr Thr Thr Pro Val Asn  
             50                    55                    60  
 His Lys Arg Val Ala Arg Val Met Ser Ser Met Lys Leu Val Gly Phe  
       65                    70                    75                    80  
 Thr Lys Lys Arg Lys Val Ile Thr Thr Ile Pro Ala Ala Val Lys Pro  
             85                    90                    95  
 Val Phe Pro Asp Leu Val Lys Arg Gln Phe Asn Ala Leu Ala Ala Asn  
             100                    105                    110  
 Glu Val Tyr Val Gly Asp Ile Thr Tyr Leu Pro Ile Ala Asp Gly Ser  
             115                    120                    125  
 Asn Met Tyr Leu Thr Thr Val Ile Asp Cys Tyr Ser  
       130                    135                    140

<210> 215  
 <211> 237  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(214)  
 <223> RXA01650

<400> 215  
 cagatcgcca acgatctcgg catcaaccga gtaaccctga aaaacttcga tcaataaata 60  
 cggtgcgcat gcctcaacca acaccaaaga agcaacagca atg tcg gaa gct gaa 115  
   Met Ser Glu Ala Glu  
   1                    5  
 caa atc aga cag cta aag aag gaa aac gca cta ctg cgt gaa gaa cgc 163  
 Gln Ile Arg Gln Leu Lys Lys Glu Asn Ala Leu Leu Arg Glu Glu Arg  
                     10                    15                    20  
 gac att ttg cgc aag gct gct aaa tat ttt ccc ggc aag agg caa gac 211  
 Asp Ile Leu Arg Lys Ala Ala Lys Tyr Phe Pro Gly Lys Arg Gln Asp  
             25                    30                    35

tta tgacccgctt ctggtttggt gac  
Leu

237

<210> 216  
<211> 38  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 216  
Met Ser Glu Ala Glu Gln Ile Arg Gln Leu Lys Lys Glu Asn Ala Leu  
1 5 10 15  
Leu Arg Glu Glu Arg Asp Ile Leu Arg Lys Ala Ala Lys Tyr Phe Pro  
20 25 30  
Gly Lys Arg Gln Asp Leu  
35

<210> 217  
<211> 258  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(235)  
<223> RXA01651

<400> 217  
caatctctaa ggagaaagtt tatgacaaat aggacctgac ccctgtttgg tagacaccta 60  
acatcccaac attctgggac agaaaggtaa cctacctatc atg cca acc aag acc 115  
Met Pro Thr Lys Thr  
1 5  
tac tcc gag gag ttc aaa cgc gac gcc gtt gct ttg tac gag aac tcc 163  
Tyr Ser Glu Glu Phe Lys Arg Asp Ala Val Ala Leu Tyr Glu Asn Ser  
10 15 20  
gat ggg gcc tca ctc caa cag atc gcc aac gat ctc ggc atc aac cga 211  
Asp Gly Ala Ser Leu Gln Gln Ile Ala Asn Asp Leu Gly Ile Asn Arg  
25 30 35  
gta acc ctg aaa aac ttc gat caa taaatacggg gcgcatgcct caa 258  
Val Thr Leu Lys Asn Phe Asp Gln  
40 45

<210> 218  
<211> 45  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 218  
Met Pro Thr Lys Thr Tyr Ser Glu Glu Phe Lys Arg Asp Ala Val Ala  
1 5 10 15  
Leu Tyr Glu Asn Ser Asp Gly Ala Ser Leu Gln Gln Ile Ala Asn Asp

<210> 220

<211> 137  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 220

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Met Ala Gly His Thr His Lys Thr His Arg Thr Ala Tyr Lys Gln Leu
  1              5              10              15

Glu Ala Leu Ala Arg Asn Gly His Leu Phe Thr Tyr Ile Asp Pro Pro
          20              25              30

Ala Glu Val Asp Gly Val Val Lys Ser Thr Thr Asn Cys Leu Glu Gly
          35              40              45

Gly Ile Asn Ala Gln Ile Lys Ala Leu Ala Arg Asn His Arg Gly Met
  50              55              60

Phe Asp Glu His Gln Arg Ile Ala Val Asp Trp Trp Leu Leu Met His
  65              70              75              80

Thr Gln Leu Pro Gly Asp Pro Val Glu Ile Ala Arg Gln Gln Asn Trp
          85              90              95

Gly Gln Asp Gly Leu Ala Asn Val Pro Asp Leu Ile Gln Gln Glu Gln
          100             105             110

Pro His Asp His Tyr Gly Arg Pro Val Thr Tyr Asp Thr Gly Ile Asp
          115             120             125

Ala Thr Thr Thr Arg Arg Lys Ser Lys
  130              135
  
```

<210> 221  
 <211> 534  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(511)  
 <223> FRXA01680

<400> 221

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aagagttcta cctcacctac ggggactggc ttaacgaacg cacctaccgc gctgatgtac 60

cagcacatgc catcccgaaa catatccgcc ccaatcagaa atg gca ggt cac acc 115
                               Met Ala Gly His Thr
                               1              5

cac aaa acc cac cgg act gct tat aag cag ttg gaa gcc ttg gcc cgc 163
His Lys Thr His Arg Thr Ala Tyr Lys Gln Leu Glu Ala Leu Ala Arg
          10              15              20

aat ggg cat ttg ttt acc tat att gat cca cca gca gag gtt gac ggg 211
Asn Gly His Leu Phe Thr Tyr Ile Asp Pro Pro Ala Glu Val Asp Gly
          25              30              35

gtg gtg aaa tca aca acg aac tgt ttg gaa ggt ggt atc aac gct cag 259
Val Val Lys Ser Thr Thr Asn Cys Leu Glu Gly Gly Ile Asn Ala Gln
          40              45              50
  
```

att aaa gcg ttg gcg aga aac cat cgg ggg atg ttt gat gaa cat caa 307  
 Ile Lys Ala Leu Ala Arg Asn His Arg Gly Met Phe Asp Glu His Gln  
 55 60 65  
  
 cgt atc gcg gtg gat tgg tgg tta ttg atg cat acg cag ttg cct ggc 355  
 Arg Ile Ala Val Asp Trp Trp Leu Leu Met His Thr Gln Leu Pro Gly  
 70 75 80 85  
  
 gat ccg gat gag atc gcc agg caa caa aac tgg ggt caa gac gga ctc 403  
 Asp Pro Asp Glu Ile Ala Arg Gln Gln Asn Trp Gly Gln Asp Gly Leu  
 90 95 100  
  
 gcc aac gtc ccc gac ttg atc caa caa gaa caa cca cac gac cac tac 451  
 Ala Asn Val Pro Asp Leu Ile Gln Gln Glu Gln Pro His Asp His Tyr  
 105 110 115  
  
 ggg cgc ccg gtt acc tat gac acc gga atc gat gcc aca acg aca cgc 499  
 Gly Arg Pro Val Thr Tyr Asp Thr Gly Ile Asp Ala Thr Thr Thr Arg  
 120 125 130  
  
 cgt aaa agc aag taaaaatccc ggcccaccaa caa 534  
 Arg Lys Ser Lys  
 135

<210> 222  
 <211> 137  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 222  
 Met Ala Gly His Thr His Lys Thr His Arg Thr Ala Tyr Lys Gln Leu  
 1 5 10 15  
  
 Glu Ala Leu Ala Arg Asn Gly His Leu Phe Thr Tyr Ile Asp Pro Pro  
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 Ala Glu Val Asp Gly Val Val Lys Ser Thr Thr Asn Cys Leu Glu Gly  
 35 40 45  
  
 Gly Ile Asn Ala Gln Ile Lys Ala Leu Ala Arg Asn His Arg Gly Met  
 50 55 60  
  
 Phe Asp Glu His Gln Arg Ile Ala Val Asp Trp Trp Leu Leu Met His  
 65 70 75 80  
  
 Thr Gln Leu Pro Gly Asp Pro Asp Glu Ile Ala Arg Gln Gln Asn Trp  
 85 90 95  
  
 Gly Gln Asp Gly Leu Ala Asn Val Pro Asp Leu Ile Gln Gln Glu Gln  
 100 105 110  
  
 Pro His Asp His Tyr Gly Arg Pro Val Thr Tyr Asp Thr Gly Ile Asp  
 115 120 125  
  
 Ala Thr Thr Thr Arg Arg Lys Ser Lys  
 130 135

<210> 223

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<220>
<221> CDS
<222> (101)..(682)
<223> RXN01784
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acg atg ttt gac ctc acg ggc acc cga acc cag acg cgg tgatcgtcag 692

Thr Met Phe Asp Leu Thr Gly Thr Arg Thr Gln Thr Arg  
                   185                  190

ccggatattc gag

705

<210> 224  
 <211> 194  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 224  
 Met Met Thr Glu Arg Gly Val Pro Val Asp His Thr Thr Ile Tyr Arg  
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 Trp Val Gln Lys Tyr Ala Leu Glu Leu Asp Lys Gln Thr Arg Trp Tyr  
                   20                  25                  30  
 Arg Gln Val Pro Asp Trp Gln Ala Ser Ser Trp Arg Val Asp Glu Thr  
                   35                  40                  45  
 Tyr Ile Arg Val Gly Gly Thr Trp Cys Tyr Leu Tyr Arg Ala Ile Thr  
   50                  55                  60  
 Ala Gly Gly Gln Thr Leu Glu Phe Tyr Leu Ser Pro Lys Arg Asn Val  
   65                  70                  75                  80  
 Ala Ala Ala Lys Arg Phe Leu Ala Lys Thr Leu Arg Ser Asn Thr Thr  
                   85                  90                  95  
 Ala Gly Ser Pro Arg Val Ile Asn Thr Asp Lys Ala Pro Ala Leu Ala  
                   100                  105                  110  
 Lys Ala Ile Ser Glu Leu Lys Ala Glu Gly Ile Cys Pro Gln Thr Val  
   115                  120                  125  
 Glu His Arg Gln Val Lys Tyr Leu Asn Asn Val Ile Glu Gly Asp His  
   130                  135                  140  
 Gly Arg Leu Lys Arg Ile Leu Gly Pro Lys Gly Ala Phe Lys Asn Arg  
   145                  150                  155                  160  
 Ile Ser Ala Tyr Arg Thr Leu Lys Gly Met Glu Ala Met His Ser Leu  
                   165                  170                  175  
 Arg Lys Gly Gln Gly Thr Met Phe Asp Leu Thr Gly Thr Arg Thr Gln  
                   180                  185                  190  
 Thr Arg

<210> 225  
 <211> 572  
 <212> DNA  
 <213> Corynebacterium glutamicum  
 <220>  
 <221> CDS  
 <222> (1)..(549)  
 <223> FRXA01784

&lt;400&gt; 225

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acc acc atc tac cgc tgg gtc cag aaa tac gcc ctt gag ctg gat aag      48
Thr Thr Ile Tyr Arg Trp Val Gln Lys Tyr Ala Leu Glu Leu Asp Lys
  1              5              10              15

cag act cgc tgg tac cgg cag gtt cct gac tgg cag gcc agt tcc tgg      96
Gln Thr Arg Trp Tyr Arg Gln Val Pro Asp Trp Gln Ala Ser Ser Trp
              20              25              30

cgg gtg gat gag acc tat atc cgg gtc ggc ggc acg tgg tgc tat ctc      144
Arg Val Asp Glu Thr Tyr Ile Arg Val Gly Gly Thr Trp Cys Tyr Leu
              35              40              45

tac cgg gct att acc gcg ggt ggg cag acc ctg gag ttt tat ctc tca      192
Tyr Arg Ala Ile Thr Ala Gly Gln Thr Leu Glu Phe Tyr Leu Ser
              50              55              60

cca aaa cgg aat gtg gct gcg gcc aag cgt ttc ctg gcc aag acg ctg      240
Pro Lys Arg Asn Val Ala Ala Ala Lys Arg Phe Leu Ala Lys Thr Leu
  65              70              75              80

cga tcg aat acg aca gcc ggg tcc ccg cgg gtc atc aac acc gac aag      288
Arg Ser Asn Thr Thr Ala Gly Ser Pro Arg Val Ile Asn Thr Asp Lys
              85              90              95

gca cca gct ctg gcc aag gca ata tcc gag ctg aag gcg gag gga atc      336
Ala Pro Ala Leu Ala Lys Ala Ile Ser Glu Leu Lys Ala Glu Gly Ile
              100              105              110

tgc cct cag acg gtg gag cac cgg cag gtg aaa tac ctc aac aac gtt      384
Cys Pro Gln Thr Val Glu His Arg Gln Val Lys Tyr Leu Asn Asn Val
              115              120              125

atc gag gga gat cat ggc cga ctt aaa aga atc ctg ggg ccg aag gga      432
Ile Glu Gly Asp His Gly Arg Leu Lys Arg Ile Leu Gly Pro Lys Gly
              130              135              140

gcg ttc aaa aac cga att tcc gcc tac cgg acg ttg aaa ggg atg gaa      480
Ala Phe Lys Asn Arg Ile Ser Ala Tyr Arg Thr Leu Lys Gly Met Glu
  145              150              155              160

gcg atg cat tca tta cgg aaa ggc cag ggc acg atg ttt gac ctc acg      528
Ala Met His Ser Leu Arg Lys Gly Gln Gly Thr Met Phe Asp Leu Thr
              165              170              175

ggc acc cga acc cag acg cgg tgatcgtcag ccggatattc gag      572
Gly Thr Arg Thr Gln Thr Arg
              180

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&lt;210&gt; 226

&lt;211&gt; 183

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 226

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Thr Thr Ile Tyr Arg Trp Val Gln Lys Tyr Ala Leu Glu Leu Asp Lys
  1              5              10              15

Gln Thr Arg Trp Tyr Arg Gln Val Pro Asp Trp Gln Ala Ser Ser Trp

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20					25					30						
Arg	Val	Asp	Glu	Thr	Tyr	Ile	Arg	Val	Gly	Gly	Thr	Trp	Cys	Tyr	Leu	
35					40					45						
Tyr	Arg	Ala	Ile	Thr	Ala	Gly	Gly	Gln	Thr	Leu	Glu	Phe	Tyr	Leu	Ser	
50					55					60						
Pro	Lys	Arg	Asn	Val	Ala	Ala	Ala	Lys	Arg	Phe	Leu	Ala	Lys	Thr	Leu	
65					70					75					80	
Arg	Ser	Asn	Thr	Thr	Ala	Gly	Ser	Pro	Arg	Val	Ile	Asn	Thr	Asp	Lys	
85					90					95						
Ala	Pro	Ala	Leu	Ala	Lys	Ala	Ile	Ser	Glu	Leu	Lys	Ala	Glu	Gly	Ile	
100					105					110						
Cys	Pro	Gln	Thr	Val	Glu	His	Arg	Gln	Val	Lys	Tyr	Leu	Asn	Asn	Val	
115					120					125						
Ile	Glu	Gly	Asp	His	Gly	Arg	Leu	Lys	Arg	Ile	Leu	Gly	Pro	Lys	Gly	
130					135					140						
Ala	Phe	Lys	Asn	Arg	Ile	Ser	Ala	Tyr	Arg	Thr	Leu	Lys	Gly	Met	Glu	
145					150					155					160	
Ala	Met	His	Ser	Leu	Arg	Lys	Gly	Gln	Gly	Thr	Met	Phe	Asp	Leu	Thr	
165					170					175						
Gly	Thr	Arg	Thr	Gln	Thr	Arg										
180																

&lt;210&gt; 227

&lt;211&gt; 1329

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1306)

&lt;223&gt; RXA01862

&lt;400&gt; 227

tctcacagta atgtggatgc cagcacaagt atgtccgacc accccagcga tgaagcgtaa 60

ataatccaac	tcctactca	tcgctaggag	gcacagactc	atg gcc tat gac ttc	115
				Met Ala Tyr Asp Phe	
				1 5	

gtc att gga atg gac gtc ggc aaa tac ttc cac cac gcc tgc gtc ctc	163
Val Ile Gly Met Asp Val Gly Lys Tyr Phe His His Ala Cys Val Leu	
10 15 20	

gat ccc cag ggc aga caa gtc cta tcc aaa cgc atc aac caa cac gaa	211
Asp Pro Gln Gly Arg Gln Val Leu Ser Lys Arg Ile Asn Gln His Glu	
25 30 35	

ggc tcg cta cgc aag ctc ttc gac aaa ttc ctg gcc aat gac gcc gag	259
Gly Ser Leu Arg Lys Leu Phe Asp Lys Phe Leu Ala Asn Asp Ala Glu	
40 45 50	

gtc ctt gtc gtc gtc gat cag ccc aac aac atc ggc agg cta acc gtc	307
Val Leu Val Val Val Asp Gln Pro Asn Asn Ile Gly Arg Leu Thr Val	
55 60 65	
gca gtc gcc caa gca atg gga gcc gac gtt cgc tac ctc ccc ggg ctt	355
Ala Val Ala Gln Ala Met Gly Ala Asp Val Arg Tyr Leu Pro Gly Leu	
70 75 80 85	
gcc atg cga caa ctt tca cgt atc cac gtc ggc aac tcc aag acc gat	403
Ala Met Arg Gln Leu Ser Arg Ile His Val Gly Asn Ser Lys Thr Asp	
90 95 100	
gta cgg gac gct tat gtc atc gcc cat gcc ggc ctc aac ctt ccg gat	451
Val Arg Asp Ala Tyr Val Ile Ala His Ala Gly Leu Asn Leu Pro Asp	
105 110 115	
gcc ctg cgt agc gtc gac cgc gtt gag gaa gtc ttc ctc cag ctg aaa	499
Ala Leu Arg Ser Val Asp Arg Val Glu Glu Val Phe Leu Gln Leu Lys	
120 125 130	
gtc ctc aac ggt atc gac gaa gac ctc gcc cgc gcc tac aca cgc ctg	547
Val Leu Asn Gly Ile Asp Glu Asp Leu Ala Arg Ala Tyr Thr Arg Leu	
135 140 145	
atc aac cag atg caa tcc gcg ctc gtg ggc acc tac ccc gca ttc gaa	595
Ile Asn Gln Met Gln Ser Ala Leu Val Gly Thr Tyr Pro Ala Phe Glu	
150 155 160 165	
cat gtc ctg cgt ggg cag atg att cac cgc aag tgg att ctc cac ctt	643
His Val Leu Arg Gly Gln Met Ile His Arg Lys Trp Ile Leu His Leu	
170 175 180	
ctg gcg aaa tac ggt ggc ccc acc aag att cga cgc gtc ggc aaa gca	691
Leu Ala Lys Tyr Gly Gly Pro Thr Lys Ile Arg Arg Val Gly Lys Ala	
185 190 195	
cgg ctg gca gct ttc gca cgt ggt cac agg gca cgt aat cct gag cca	739
Arg Leu Ala Ala Phe Ala Arg Gly His Arg Ala Arg Asn Pro Glu Pro	
200 205 210	
gtt atc gat gcc atg ctt gct gcg atc cac ggc cag acg gta tcc atc	787
Val Ile Asp Ala Met Leu Ala Ala Ile His Gly Gln Thr Val Ser Ile	
215 220 225	
gcc ggc gca gaa tac gcg gaa ctt ggc gta gca atg tcc gcc aaa gat	835
Ala Gly Ala Glu Tyr Ala Glu Leu Gly Val Ala Met Ser Ala Lys Asp	
230 235 240 245	
gca cta gcc aag ctg gag cac cgc aaa gag att gaa ggc cag gta ctc	883
Ala Leu Ala Lys Leu Glu His Arg Lys Glu Ile Glu Gly Gln Val Leu	
250 255 260	
gag ctg atc cag gac att cct cag acc gag att ctc ttg tcc atg ccc	931
Glu Leu Ile Gln Asp Ile Pro Gln Thr Glu Ile Leu Leu Ser Met Pro	
265 270 275	
ggc atc ggc cca cgt agc gcc gcg caa atc ctt atg acc gtc ggc gat	979
Gly Ile Gly Pro Arg Ser Ala Ala Gln Ile Leu Met Thr Val Gly Asp	
280 285 290	

atg tcc gac ttt ccc gat gca gcg cac ctg gcg tcc tat gca ggc ctg 1027  
 Met Ser Asp Phe Pro Asp Ala Ala His Leu Ala Ser Tyr Ala Gly Leu  
 295 300 305  
  
 tcg ccg cag aca aat cag tcg gga acg tcg atc atg tcg aat tcg ccc 1075  
 Ser Pro Gln Thr Asn Gln Ser Gly Thr Ser Ile Met Ser Asn Ser Pro  
 310 315 320 325  
  
 aac cgg gcc ggc aac aag aaa ttg aag aac gcc cta tgg cag tcg tct 1123  
 Asn Arg Ala Gly Asn Lys Lys Leu Lys Asn Ala Leu Trp Gln Ser Ser  
 330 335 340  
  
 ttt gca tcg atc aga ttc cac gag cgt tcc cgg caa ttc tat gaa cga 1171  
 Phe Ala Ser Ile Arg Phe His Glu Arg Ser Arg Gln Phe Tyr Glu Arg  
 345 350 355  
  
 aaa cgc aac gaa ggc aaa aga cac aac gcc gca gtc gtc gcg ctc gca 1219  
 Lys Arg Asn Glu Gly Lys Arg His Asn Ala Ala Val Val Ala Leu Ala  
 360 365 370  
  
 cgc cga cgc ctc aac gtc ctc ttc gcc atg atg cgc agc gga gag ctc 1267  
 Arg Arg Arg Leu Asn Val Leu Phe Ala Met Met Arg Ser Gly Glu Leu  
 375 380 385  
  
 tac aga gac atc ccc aca gcc cag gag gcc gca gcg gcc tagccccctac 1316  
 Tyr Arg Asp Ile Pro Thr Ala Gln Glu Ala Ala Ala  
 390 395 400  
  
 aagccccgaa gcc 1329

&lt;210&gt; 228

&lt;211&gt; 402

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 228

Met Ala Tyr Asp Phe Val Ile Gly Met Asp Val Gly Lys Tyr Phe His  
 1 5 10 15  
  
 His Ala Cys Val Leu Asp Pro Gln Gly Arg Gln Val Leu Ser Lys Arg  
 20 25 30  
  
 Ile Asn Gln His Glu Gly Ser Leu Arg Lys Leu Phe Asp Lys Phe Leu  
 35 40 45  
  
 Ala Asn Asp Ala Glu Val Leu Val Val Val Asp Gln Pro Asn Asn Ile  
 50 55 60  
  
 Gly Arg Leu Thr Val Ala Val Ala Gln Ala Met Gly Ala Asp Val Arg  
 65 70 75 80  
  
 Tyr Leu Pro Gly Leu Ala Met Arg Gln Leu Ser Arg Ile His Val Gly  
 85 90 95  
  
 Asn Ser Lys Thr Asp Val Arg Asp Ala Tyr Val Ile Ala His Ala Gly  
 100 105 110  
  
 Leu Asn Leu Pro Asp Ala Leu Arg Ser Val Asp Arg Val Glu Glu Val  
 115 120 125

Phe Leu Gln Leu Lys Val Leu Asn Gly Ile Asp Glu Asp Leu Ala Arg  
 130 135 140  
 Ala Tyr Thr Arg Leu Ile Asn Gln Met Gln Ser Ala Leu Val Gly Thr  
 145 150 155 160  
 Tyr Pro Ala Phe Glu His Val Leu Arg Gly Gln Met Ile His Arg Lys  
 165 170 175  
 Trp Ile Leu His Leu Leu Ala Lys Tyr Gly Gly Pro Thr Lys Ile Arg  
 180 185 190  
 Arg Val Gly Lys Ala Arg Leu Ala Ala Phe Ala Arg Gly His Arg Ala  
 195 200 205  
 Arg Asn Pro Glu Pro Val Ile Asp Ala Met Leu Ala Ala Ile His Gly  
 210 215 220  
 Gln Thr Val Ser Ile Ala Gly Ala Glu Tyr Ala Glu Leu Gly Val Ala  
 225 230 235 240  
 Met Ser Ala Lys Asp Ala Leu Ala Lys Leu Glu His Arg Lys Glu Ile  
 245 250 255  
 Glu Gly Gln Val Leu Glu Leu Ile Gln Asp Ile Pro Gln Thr Glu Ile  
 260 265 270  
 Leu Leu Ser Met Pro Gly Ile Gly Pro Arg Ser Ala Ala Gln Ile Leu  
 275 280 285  
 Met Thr Val Gly Asp Met Ser Asp Phe Pro Asp Ala Ala His Leu Ala  
 290 295 300  
 Ser Tyr Ala Gly Leu Ser Pro Gln Thr Asn Gln Ser Gly Thr Ser Ile  
 305 310 315 320  
 Met Ser Asn Ser Pro Asn Arg Ala Gly Asn Lys Lys Leu Lys Asn Ala  
 325 330 335  
 Leu Trp Gln Ser Ser Phe Ala Ser Ile Arg Phe His Glu Arg Ser Arg  
 340 345 350  
 Gln Phe Tyr Glu Arg Lys Arg Asn Glu Gly Lys Arg His Asn Ala Ala  
 355 360 365  
 Val Val Ala Leu Ala Arg Arg Arg Leu Asn Val Leu Phe Ala Met Met  
 370 375 380  
 Arg Ser Gly Glu Leu Tyr Arg Asp Ile Pro Thr Ala Gln Glu Ala Ala  
 385 390 395 400  
 Ala Ala

&lt;210&gt; 229

&lt;211&gt; 504

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

<400> 229

caaaaacttg acgagcgcaa cctgggggat ctaccagcgg atg atc gcg gcc tac 115  
Met Ile Ala Ala Tyr  
1 5

cgc gag aag gac cga tcc ctc ggc cgc gcg gcg atg gag gcg ctc atc 163  
 Arg Glu Lys Asp Arg Ser Leu Gly Arg Ala Ala Met Glu Ala Leu Ile  
 10 15 20

gac gcc gtc agc caa gac gtc ccc gcc ggg ctg gac gag ttg cgc aag 211  
Asp Ala Val Ser Gln Asp Val Pro Ala Gly Leu Asp Glu Leu Arg Lys  
25 30 35

ctc ggt cgg acc ctg aag gct cgc gcc acc gac gtg ctg gcc tac ttc 259  
Leu Gly Arg Thr Leu Lys Ala Arg Ala Thr Asp Val Leu Ala Tyr Phe  
40 45 50

gag cgg cct ggc acc agc aat ggc ccc aca gag gcg atc aac gga cgc 307  
Glu Arg Pro Gly Thr Ser Asn Gly Pro Thr Glu Ala Ile Asn Gly Arg  
55 60 65

ctg gag cac ctg cgc ggc tgc gcc ctg ggc ttc cgc aac ctg acc aac 355  
Leu Glu His Leu Arg Gly Ser Ala Leu Gly Phe Arg Asn Leu Thr Asn  
70 75 80 85

tac atc gcc aga tcc ctg ctc gag ttc cgg cgg att cag acc tca act 403  
 Tyr Ile Ala Arg Ser Leu Leu Glu Phe Arg Arg Ile Gln Thr Ser Thr  
 90 95 100

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aca ccc tca tct gtg aag agc cgc ttt aga cat ccc tca tcg tca cgg      451
Thr Pro Ser Ser Val Lys Ser Arg Phe Arg His Pro Ser Ser Ser Arg
          105                      110                      115

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acc act atg aac gat gtc ccg act cac cta tgaacgatgt cctgaacctc cac 504  
Thr Thr Met Asn Asp Val Pro Thr His Leu  
120 125

$\langle 210 \rangle$  230

<211> 127

&lt;212&gt; PRT

<213> Corynebacterium glutamicum

<400> 230

Met Ile Ala Ala Tyr Arg Glu Lys Asp Arg Ser Leu Gly Arg Ala Ala  
1 5 10 15

Met Glu Ala Leu Ile Asp Ala Val Ser Gln Asp Val Pro Ala Gly Leu  
20 25 30

Asp Glu Leu Arg Lys Leu Gly Arg Thr Leu Lys Ala Arg Ala Thr Asp  
35 40 45

Val Leu Ala Tyr Phe Glu Arg Pro Gly Thr Ser Asn Gly Pro Thr Glu  
50 55 60

Ala Ile Asn Gly Arg Leu Glu His Leu Arg Gly Ser Ala Leu Gly Phe  
65 70 75 80

Arg Asn Leu Thr Asn Tyr Ile Ala Arg Ser Leu Leu Glu Phe Arg Arg  
85 90 95

Ile Gln Thr Ser Thr Thr Pro Ser Ser Val Lys Ser Arg Phe Arg His  
100 105 110

Pro Ser Ser Ser Arg Thr Thr Met Asn Asp Val Pro Thr His Leu  
115 120 125

<210> 231

<211> 831

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(808)

<223> RXA01998

<400> 231

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gttggggcag taggaagacc ggcgtggaat aatcaggtcc atg ggc atc ttc tcc 115  
Met Gly Ile Phe Ser  
1 5

ggt cgg cag ttc cct cgt gaa atc atc ctg tgg gcg gtg cgg tgg tac 163  
Gly Arg Gln Phe Pro Arg Glu Ile Ile Leu Trp Ala Val Arg Trp Tyr  
10 15 20

tgc cgc tac ggc gtg agc tat cgc gac ctc gaa gag atg atg acc gag 211  
Cys Arg Tyr Gly Val Ser Tyr Arg Asp Leu Glu Glu Met Met Thr Glu  
25 30 35

cgg gga gtg ccg gtc gat cac acc acg atc tac cgc tgg gtc cag aaa 259  
Arg Gly Val Pro Val Asp His Thr Thr Ile Tyr Arg Trp Val Gln Lys  
40 45 50

tat gct cct gag ctg gat aag aag acc cgg tgg tat cgg caa gtt cct 307  
Tyr Ala Pro Glu Leu Asp Lys Lys Thr Arg Trp Tyr Arg Gln Val Pro  
55 60 65

gac tgg cag gcc agg tcc tgg cgg gtg gat gag acc tat atc cgg gtc 355  
Asp Trp Gln Ala Arg Ser Trp Arg Val Asp Glu Thr Tyr Ile Arg Val  
70 75 80 85

ggg gga aag tgg tgc tac ctc tat cgg gca atc acc gcc ggt agc cag 403  
Gly Gly Lys Trp Cys Tyr Leu Tyr Arg Ala Ile Thr Ala Gly Ser Gln  
90 95 100

acc ctg gac ttc tac ctc tcc ccg aag aga aac gtc gcg gcg gcg aag 451  
Thr Leu Asp Phe Tyr Leu Ser Pro Lys Arg Asn Val Ala Ala Ala Lys  
105 110 115

cgt ttc ctg gcg aag acg ctg cgg tcg aat aaa tcg gca ggc tat ccg 499  
Arg Phe Leu Ala Lys Thr Leu Arg Ser Asn Lys Ser Ala Gly Tyr Pro

120	125	130	
cgg gtg atc agc acc gac aag gcc ccc tca ctc gcc agg gca atc tct			547
Arg Val Ile Ser Thr Asp Lys Ala Pro Ser Leu Ala Arg Ala Ile Ser			
135	140	145	
gag ctg aag gcg gaa ggc gtc tgt cca tcg acg gtc gag cat cgt cgg			595
Glu Leu Lys Ala Glu Gly Val Cys Pro Ser Thr Val Glu His Arg Arg			
150	155	160	165
gtg aaa tac ctc aac aac gtc att gaa ggc gac cat ggt cgg tta aag			643
Val Lys Tyr Leu Asn Asn Val Ile Glu Gly Asp His Gly Arg Leu Lys			
	170	175	180
cgg atc ctg ggg ccg aaa ggc gca ttc aaa aac cga acg tct gcc tac			691
Arg Ile Leu Gly Pro Lys Gly Ala Phe Lys Asn Arg Thr Ser Ala Tyr			
	185	190	195
cgg acg ttg aaa ggg atg gag gcg atg cac tca ttg cgg aag ggg cag			739
Arg Thr Leu Lys Gly Met Glu Ala Met His Ser Leu Arg Lys Gly Gln			
	200	205	210
ggc acg atg ttt gcc tat ggt cac ccg aat ccg gat gca gtg att gtt			787
Gly Thr Met Phe Ala Tyr Gly His Pro Asn Pro Asp Ala Val Ile Val			
	215	220	225
agc cgg gta ttc gag acg gcc tgacaacaca ggcacatagc gtt			831
Ser Arg Val Phe Glu Thr Ala			
230	235		

&lt;210&gt; 232

&lt;211&gt; 236

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 232

Met Gly Ile Phe Ser Gly Arg Gln Phe Pro Arg Glu Ile Ile Leu Trp	
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Ala Val Arg Trp Tyr Cys Arg Tyr Gly Val Ser Tyr Arg Asp Leu Glu	
	20 25 30
Glu Met Met Thr Glu Arg Gly Val Pro Val Asp His Thr Thr Ile Tyr	
	35 40 45
Arg Trp Val Gln Lys Tyr Ala Pro Glu Leu Asp Lys Lys Thr Arg Trp	
	50 55 60
Tyr Arg Gln Val Pro Asp Trp Gln Ala Arg Ser Trp Arg Val Asp Glu	
	65 70 75 80
Thr Tyr Ile Arg Val Gly Gly Lys Trp Cys Tyr Leu Tyr Arg Ala Ile	
	85 90 95
Thr Ala Gly Ser Gln Thr Leu Asp Phe Tyr Leu Ser Pro Lys Arg Asn	
	100 105 110
Val Ala Ala Ala Lys Arg Phe Leu Ala Lys Thr Leu Arg Ser Asn Lys	
	115 120 125

Ser Ala Gly Tyr Pro Arg Val Ile Ser Thr Asp Lys Ala Pro Ser Leu  
 130 135 140

Ala Arg Ala Ile Ser Glu Leu Lys Ala Glu Gly Val Cys Pro Ser Thr  
 145 150 155 160

Val Glu His Arg Arg Val Lys Tyr Leu Asn Asn Val Ile Glu Gly Asp  
 165 170 175

His Gly Arg Leu Lys Arg Ile Leu Gly Pro Lys Gly Ala Phe Lys Asn  
 180 185 190

Arg Thr Ser Ala Tyr Arg Thr Leu Lys Gly Met Glu Ala Met His Ser  
 195 200 205

Leu Arg Lys Gly Gln Gly Thr Met Phe Ala Tyr Gly His Pro Asn Pro  
 210 215 220

Asp Ala Val Ile Val Ser Arg Val Phe Glu Thr Ala  
 225 230 235

<210> 233  
 <211> 274  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(274)  
 <223> RXA02837

<400> 233  
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agagggggcga ggtcgccctga ttggtcggac gaagggtgaa atg aac acc aag ctc 115  
 Met Asn Thr Lys Leu  
 1 5

cat gct gtg acc gat gcg acg ggg cgt cca atc cgc ttc ttc atg acc 163  
 His Ala Val Thr Asp Ala Thr Gly Arg Pro Ile Arg Phe Phe Met Thr  
 10 15 20

gcc gga aag gtc agc gac tac atc gga gct atg gct ttg cta ggc agc 211  
 Ala Gly Lys Val Ser Asp Tyr Ile Gly Ala Met Ala Leu Leu Gly Ser  
 25 30 35

ctg ccc aag gcc ggc tgg ctt cta gcg gat cgg ggc tat gac gcg gac 259  
 Leu Pro Lys Ala Gly Trp Leu Leu Ala Asp Arg Gly Tyr Asp Ala Asp  
 40 45 50

tgg ttc aga gat gca 274  
 Trp Phe Arg Asp Ala  
 55

<210> 234  
 <211> 58  
 <212> PRT  
 <213> Corynebacterium glutamicum

&lt;400&gt; 234

Met Asn Thr Lys Leu His Ala Val Thr Asp Ala Thr Gly Arg Pro Ile  
 1 5 10 15

Arg Phe Phe Met Thr Ala Gly Lys Val Ser Asp Tyr Ile Gly Ala Met  
 20 25 30

Ala Leu Leu Gly Ser Leu Pro Lys Ala Gly Trp Leu Leu Ala Asp Arg  
 35 40 45

Gly Tyr Asp Ala Asp Trp Phe Arg Asp Ala  
 50 55

&lt;210&gt; 235

&lt;211&gt; 1731

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1708)

&lt;223&gt; RXA00005

&lt;400&gt; 235

gtggaagccc agttcacctc tcccctgctc aacaatgggc aaacctgttt ccttggtacc 60

cgaatccttg ctccaaaatc acggcggggtt caggggggtga atg cac cac gag caa 115  
 Met His His Glu Gln  
 1 5

ccc gaa ggg tgc gaa gtg ggc att cgt aga aca atc cca gag gaa agc 163  
 Pro Glu Gly Cys Glu Val Gly Ile Arg Arg Thr Ile Pro Glu Glu Ser  
 10 15 20

cgt acg gct ttc ctc gac atg atc aat caa ggt atg tca ggt ctt gct 211  
 Arg Thr Ala Phe Leu Asp Met Ile Asn Gln Gly Met Ser Gly Leu Ala  
 25 30 35

gcg tct aca gcg gtc ggg gtc agt gaa ttc acc ggg cga aag tgg gcg 259  
 Ala Ser Thr Ala Val Gly Val Ser Glu Phe Thr Gly Arg Lys Trp Ala  
 40 45 50

aag gcc gcc ggg gtg aaa ctg acc cgc ggc ccg cga ggt ggc aat gct 307  
 Lys Ala Ala Gly Val Lys Leu Thr Arg Gly Pro Arg Gly Gly Asn Ala  
 55 60 65

ttt gac acc gcc gag aaa ctt gag att gca gcc agc atg cta gag aaa 355  
 Phe Asp Thr Ala Glu Lys Leu Glu Ile Ala Ala Ser Met Leu Glu Lys  
 70 75 80 85

gga tgc cta ccc cga gaa atc ggc gag tat gtc ggc atg act cgg gcc 403  
 Gly Cys Leu Pro Arg Glu Ile Gly Glu Tyr Val Gly Met Thr Arg Ala  
 90 95 100

aat ata tcc cta tgg cgc aaa caa ggc cca gac aag ctt cgc caa cgc 451  
 Asn Ile Ser Leu Trp Arg Lys Gln Gly Pro Asp Lys Leu Arg Gln Arg  
 105 110 115

gca gcc acc ttg cgc acc ggc aag cga gca gct gaa ttc atc cac gcc 499  
 Ala Ala Thr Leu Arg Thr Gly Lys Arg Ala Ala Glu Phe Ile His Ala

120					125					130						
ccg	gtg	atg	ggc	cct	tat	tat	ggg	cca	cgc	aca	ctc	cat	caa	gtg	ttg	547
Pro	Val	Met	Gly	Pro	Tyr	Tyr	Gly	Pro	Arg	Thr	Leu	His	Gln	Val	Leu	
	135						140					145				
cgt	gag	gac	tac	aca	aca	ctg	ttt	gac	gag	tta	tct	gcg	ttg	ggg	ttg	595
Arg	Glu	Asp	Tyr	Thr	Thr	Leu	Phe	Asp	Glu	Leu	Ser	Ala	Leu	Gly	Leu	
150					155					160					165	
cca	gca	cag	gtg	tgt	ggg	gcc	tta	ctt	cat	ctt	gct	cca	cca	cca	tca	643
Pro	Ala	Gln	Val	Cys	Gly	Ala	Leu	Leu	His	Leu	Ala	Pro	Pro	Pro	Ser	
				170					175					180		
tta	cgc	ttt	tct	tat	atg	tcg	tgt	gta	gtg	ccg	tta	ttt	gct	gat	gaa	691
Leu	Arg	Phe	Ser	Tyr	Met	Ser	Cys	Val	Val	Pro	Leu	Phe	Ala	Asp	Glu	
			185					190					195			
atc	aaa	gtc	gta	gga	caa	ggc	aca	cga	tta	tcg	tta	gaa	gag	aaa	atg	739
Ile	Lys	Val	Val	Gly	Gln	Gly	Thr	Arg	Leu	Ser	Leu	Glu	Glu	Lys	Met	
		200					205					210				
atg	atc	caa	cgt	ttc	cat	gac	acc	ggg	gtc	agt	gca	gca	gaa	atc	ggt	787
Met	Ile	Gln	Arg	Phe	His	Asp	Thr	Gly	Val	Ser	Ala	Ala	Glu	Ile	Gly	
	215					220					225					
cga	cgc	ctg	ggt	cgg	tgt	cgg	caa	aca	att	tcc	agg	gaa	ctt	cga	cgt	835
Arg	Arg	Leu	Gly	Arg	Cys	Arg	Gln	Thr	Ile	Ser	Arg	Glu	Leu	Arg	Arg	
230					235					240					245	
ggt	caa	gat	gat	gat	gga	cgt	tat	cgt	gca	cgc	gac	tcc	tat	gaa	ggt	883
Gly	Gln	Asp	Asp	Asp	Gly	Arg	Tyr	Arg	Ala	Arg	Asp	Ser	Tyr	Glu	Gly	
				250					255					260		
gcg	atc	agg	aaa	cta	gcg	cgt	ccg	aaa	aca	ccg	aaa	ctt	gat	gcc	aat	931
Ala	Ile	Arg	Lys	Leu	Ala	Arg	Pro	Lys	Thr	Pro	Lys	Leu	Asp	Ala	Asn	
			265					270					275			
cgt	agg	ctt	cgg	gct	gtg	gtg	gtc	gag	gcg	ttg	aat	aat	aaa	tta	tct	979
Arg	Arg	Leu	Arg	Ala	Val	Val	Val	Glu	Ala	Leu	Asn	Asn	Lys	Leu	Ser	
		280					285					290				
ccg	gag	cag	att	tct	ggt	ctt	tta	gcc	acc	gag	cat	gct	aac	gat	agc	1027
Pro	Glu	Gln	Ile	Ser	Gly	Leu	Leu	Ala	Thr	Glu	His	Ala	Asn	Asp	Ser	
	295					300					305					
tct	atg	cag	att	agt	cat	gaa	act	att	tac	cag	gcg	tta	tat	gtt	caa	1075
Ser	Met	Gln	Ile	Ser	His	Glu	Thr	Ile	Tyr	Gln	Ala	Leu	Tyr	Val	Gln	
310					315					320					325	
ggt	aaa	ggg	gcg	ttg	cgt	gat	gaa	ttg	aag	gtg	gag	aaa	ttt	ctt	cgt	1123
Gly	Lys	Gly	Ala	Leu	Arg	Asp	Glu	Leu	Lys	Val	Glu	Lys	Phe	Leu	Arg	
				330					335					340		
acc	ggt	cgg	aag	gga	cgt	aaa	ccg	cag	tcg	aag	ttg	cca	tcg	aga	ggt	1171
Thr	Gly	Arg	Lys	Gly	Arg	Lys	Pro	Gln	Ser	Lys	Leu	Pro	Ser	Arg	Gly	
			345					350					355			
aag	ccg	tgg	gtg	gag	ggt	gcg	ttg	att	agt	caa	cgc	cca	gca	gaa	gtt	1219
Lys	Pro	Trp	Val	Glu	Gly	Ala	Leu	Ile	Ser	Gln	Arg	Pro	Ala	Glu	Val	
		360					365					370				

gct gat cgt gct gtg cct ggg cac tgg gag ggc gat tta gta att ggt 1267  
 Ala Asp Arg Ala Val Pro Gly His Trp Glu Gly Asp Leu Val Ile Gly  
 375 380 385

ggt gaa aac caa gcg aca gcg ttg gtg acg ttg gtg gag cgc acg agc 1315  
 Gly Glu Asn Gln Ala Thr Ala Leu Val Thr Leu Val Glu Arg Thr Ser  
 390 395 400 405

cgg ttg acg ttg att aag cgg ttg ggg gtt aat cat gag gcg tcg act 1363  
 Arg Leu Thr Leu Ile Lys Arg Leu Gly Val Asn His Glu Ala Ser Thr  
 410 415 420

gtg acg gat gcg ttg gtg gag atg atg ggt gat ttg ccg cag gcg ttg 1411  
 Val Thr Asp Ala Leu Val Glu Met Met Gly Asp Leu Pro Gln Ala Leu  
 425 430 435

cgt cgg agt ttg acg tgg gat cag ggt gtg gag atg gca gag cat gcg 1459  
 Arg Arg Ser Leu Thr Trp Asp Gln Gly Val Glu Met Ala Glu His Ala  
 440 445 450

cgg ttt agc gtg gtg acc aag tgt ccg gtg ttt ttc tgt gat cct cat 1507  
 Arg Phe Ser Val Val Thr Lys Cys Pro Val Phe Phe Cys Asp Pro His  
 455 460 465

tcg ccg tgg cag cgt ggg tcg aat gag aat acg aat gga ttg gtc agg 1555  
 Ser Pro Trp Gln Arg Gly Ser Asn Glu Asn Thr Asn Gly Leu Val Arg  
 470 475 480 485

gat ttt ttc ccg aag ggc act aat ttt gct aaa gta agt gac gaa gaa 1603  
 Asp Phe Phe Pro Lys Gly Thr Asn Phe Ala Lys Val Ser Asp Glu Glu  
 490 495 500

gtt cag cgg gca cag gat ctg ctg aat tac cgg ccg cgg aaa atg cat 1651  
 Val Gln Arg Ala Gln Asp Leu Leu Asn Tyr Arg Pro Arg Lys Met His  
 505 510 515

ggt ttt aaa agc gcg acg cag gta tat gaa aaa atc gta gtt ggt gca 1699  
 Gly Phe Lys Ser Ala Thr Gln Val Tyr Glu Lys Ile Val Val Gly Ala  
 520 525 530

tcc acc gat tgaattcgcc ctaggttgga tgc 1731  
 Ser Thr Asp  
 535

&lt;210&gt; 236

&lt;211&gt; 536

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 236

Met His His Glu Gln Pro Glu Gly Cys Glu Val Gly Ile Arg Arg Thr  
 1 5 10 15

Ile Pro Glu Glu Ser Arg Thr Ala Phe Leu Asp Met Ile Asn Gln Gly  
 20 25 30

Met Ser Gly Leu Ala Ala Ser Thr Ala Val Gly Val Ser Glu Phe Thr  
 35 40 45

Gly Arg Lys Trp Ala Lys Ala Ala Gly Val Lys Leu Thr Arg Gly Pro  
 50 55 60  
 Arg Gly Gly Asn Ala Phe Asp Thr Ala Glu Lys Leu Glu Ile Ala Ala  
 65 70 75 80  
 Ser Met Leu Glu Lys Gly Cys Leu Pro Arg Glu Ile Gly Glu Tyr Val  
 85 90 95  
 Gly Met Thr Arg Ala Asn Ile Ser Leu Trp Arg Lys Gln Gly Pro Asp  
 100 105 110  
 Lys Leu Arg Gln Arg Ala Ala Thr Leu Arg Thr Gly Lys Arg Ala Ala  
 115 120 125  
 Glu Phe Ile His Ala Pro Val Met Gly Pro Tyr Tyr Gly Pro Arg Thr  
 130 135 140  
 Leu His Gln Val Leu Arg Glu Asp Tyr Thr Thr Leu Phe Asp Glu Leu  
 145 150 155 160  
 Ser Ala Leu Gly Leu Pro Ala Gln Val Cys Gly Ala Leu Leu His Leu  
 165 170 175  
 Ala Pro Pro Pro Ser Leu Arg Phe Ser Tyr Met Ser Cys Val Val Pro  
 180 185 190  
 Leu Phe Ala Asp Glu Ile Lys Val Val Gly Gln Gly Thr Arg Leu Ser  
 195 200 205  
 Leu Glu Glu Lys Met Met Ile Gln Arg Phe His Asp Thr Gly Val Ser  
 210 215 220  
 Ala Ala Glu Ile Gly Arg Arg Leu Gly Arg Cys Arg Gln Thr Ile Ser  
 225 230 235 240  
 Arg Glu Leu Arg Arg Gly Gln Asp Asp Asp Gly Arg Tyr Arg Ala Arg  
 245 250 255  
 Asp Ser Tyr Glu Gly Ala Ile Arg Lys Leu Ala Arg Pro Lys Thr Pro  
 260 265 270  
 Lys Leu Asp Ala Asn Arg Arg Leu Arg Ala Val Val Val Glu Ala Leu  
 275 280 285  
 Asn Asn Lys Leu Ser Pro Glu Gln Ile Ser Gly Leu Leu Ala Thr Glu  
 290 295 300  
 His Ala Asn Asp Ser Ser Met Gln Ile Ser His Glu Thr Ile Tyr Gln  
 305 310 315 320  
 Ala Leu Tyr Val Gln Gly Lys Gly Ala Leu Arg Asp Glu Leu Lys Val  
 325 330 335  
 Glu Lys Phe Leu Arg Thr Gly Arg Lys Gly Arg Lys Pro Gln Ser Lys  
 340 345 350  
 Leu Pro Ser Arg Gly Lys Pro Trp Val Glu Gly Ala Leu Ile Ser Gln  
 355 360 365  
 Arg Pro Ala Glu Val Ala Asp Arg Ala Val Pro Gly His Trp Glu Gly

370	375	380
Asp Leu Val Ile Gly Gly Glu Asn Gln Ala Thr Ala Leu Val Thr Leu		
385	390	395 400
Val Glu Arg Thr Ser Arg Leu Thr Leu Ile Lys Arg Leu Gly Val Asn		
	405	410 415
His Glu Ala Ser Thr Val Thr Asp Ala Leu Val Glu Met Met Gly Asp		
	420	425 430
Leu Pro Gln Ala Leu Arg Arg Ser Leu Thr Trp Asp Gln Gly Val Glu		
	435	440 445
Met Ala Glu His Ala Arg Phe Ser Val Val Thr Lys Cys Pro Val Phe		
	450	455 460
Phe Cys Asp Pro His Ser Pro Trp Gln Arg Gly Ser Asn Glu Asn Thr		
	465	470 475 480
Asn Gly Leu Val Arg Asp Phe Phe Pro Lys Gly Thr Asn Phe Ala Lys		
	485	490 495
Val Ser Asp Glu Glu Val Gln Arg Ala Gln Asp Leu Leu Asn Tyr Arg		
	500	505 510
Pro Arg Lys Met His Gly Phe Lys Ser Ala Thr Gln Val Tyr Glu Lys		
	515	520 525
Ile Val Val Gly Ala Ser Thr Asp		
	530	535

&lt;210&gt; 237

&lt;211&gt; 417

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(394)

&lt;223&gt; RXA00017

&lt;400&gt; 237

tcattccaatg tggagaagtt caaaagctga agctggacct gacccccgga tgggtggacac 60

cttgaaacaa gcatgatgct gggaaaggta atctgccacc	atg cca cgc aag acc	115
	Met Pro Arg Lys Thr	
	1 5	

tac aca gag gag ttc aag cgc gac gct gtc gcg ctc tac gag aac tcc	163
Tyr Thr Glu Glu Phe Lys Arg Asp Ala Val Ala Leu Tyr Glu Asn Ser	
10 15 20	

gcc ggc acc tcg atc cag aag atc gcc aat gat ctc gga atc aac cga	211
Ala Gly Thr Ser Ile Gln Lys Ile Ala Asn Asp Leu Gly Ile Asn Arg	
25 30 35	

atg acc ctt aaa aac tgg att act aaa tac ggg gcc aac tca act cca	259
Met Thr Leu Lys Asn Trp Ile Thr Lys Tyr Gly Ala Asn Ser Thr Pro	
40 45 50	

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cat ggc gct aac acg gcc acc gcg ctg tcc gaa gct gaa cgg atc cgc 307
His Gly Ala Asn Thr Ala Thr Ala Leu Ser Glu Ala Glu Arg Ile Arg
   55                60                65

caa ctt gaa aag gaa aat gca ctc ctc cgc gaa gag cgt gac atc ctg 355
Gln Leu Glu Lys Glu Asn Ala Leu Leu Arg Glu Glu Arg Asp Ile Leu
   70                75                80                85

cgg aaa gcg gcc aaa tat ttc gcg gaa gag acg aac tgg tgatccgctt 404
Arg Lys Ala Ala Lys Tyr Phe Ala Glu Glu Thr Asn Trp
           90                95

ccgattcggtt gat 417

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<210> 238
<211> 98
<212> PRT
<213> Corynebacterium glutamicum

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<400> 238
Met Pro Arg Lys Thr Tyr Thr Glu Glu Phe Lys Arg Asp Ala Val Ala
  1                5                10                15

Leu Tyr Glu Asn Ser Ala Gly Thr Ser Ile Gln Lys Ile Ala Asn Asp
           20                25                30

Leu Gly Ile Asn Arg Met Thr Leu Lys Asn Trp Ile Thr Lys Tyr Gly
   35                40                45

Ala Asn Ser Thr Pro His Gly Ala Asn Thr Ala Thr Ala Leu Ser Glu
   50                55                60

Ala Glu Arg Ile Arg Gln Leu Glu Lys Glu Asn Ala Leu Leu Arg Glu
   65                70                75                80

Glu Arg Asp Ile Leu Arg Lys Ala Ala Lys Tyr Phe Ala Glu Glu Thr
           85                90                95

Asn Trp

```

```

<210> 239
<211> 222
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(199)
<223> RXA00057

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<400> 239
tcgcgtcgac gctttcgaac aggtgctgtt ttagaaggga aatagacaac aaatataacc 60

ctacaaatat tatatagaca gcctcggaat gaggcagtca ttg gga tca att ggc 115
Leu Gly Ser Ile Gly
           1                5

```

acc agt gct gac aac gcg tta gcg gag tcg ttc aac gcc gca ctc agg 163  
 Thr Ser Ala Asp Asn Ala Leu Ala Glu Ser Phe Asn Ala Ala Leu Arg  
                   10                  15                  20

cgg gaa gtc ctc caa gat tct aag act ttt gcg aac tagttgatct 209  
 Arg Glu Val Leu Gln Asp Ser Lys Thr Phe Ala Asn  
                   25                  30

gccgccggga tgt 222

<210> 240

<211> 33

<212> PRT

<213> Corynebacterium glutamicum

<400> 240

Leu Gly Ser Ile Gly Thr Ser Ala Asp Asn Ala Leu Ala Glu Ser Phe  
   1                  5                  10                  15

Asn Ala Ala Leu Arg Arg Glu Val Leu Gln Asp Ser Lys Thr Phe Ala  
                   20                  25                  30

Asn

<210> 241

<211> 921

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(898)

<223> RXA00227

<400> 241

tgggtttgct tcggatgggg ctttaacaag cttcacagat gttggttttt cataggcaag 60

ctatccagaa gtaggcttta cagaaagtca ggggtgtggca atg gtg atg cag ggc 115  
   Met Val Met Gln Gly  
   1                  5

att ggt ggt agg aag ctg gcg gcg acg gtg ctg ttg gtt cgg gat ggg 163  
 Ile Gly Gly Arg Lys Leu Ala Ala Thr Val Leu Leu Val Arg Asp Gly  
                   10                  15                  20

atc atc aat ggg cgt cct gat gtg gag gtt tac att cag gag cgt gtg 211  
 Ile Ile Asn Gly Arg Pro Asp Val Glu Val Tyr Ile Gln Glu Arg Val  
                   25                  30                  35

tct act atg gct aat ttt cct cgg gcg acg gtg ttt ccg ggt ggg ggt 259  
 Ser Thr Met Ala Asn Phe Pro Arg Ala Thr Val Phe Pro Gly Gly Gly  
                   40                  45                  50

gtt gat tct cgg gat ttt gcg gat ggt cac ggt aag gaa gtg tgg agg 307  
 Val Asp Ser Arg Asp Phe Ala Asp Gly His Gly Lys Glu Val Trp Arg  
                   55                  60                  65

gga cct agc gcg gag gag tgg ggt gtg cgt tta ggc gtg gag cct cat 355

Gly 70	Pro	Ser	Ala	Glu	Glu 75	Trp	Gly	Val	Arg	Leu 80	Gly	Val	Glu	Pro	His 85	
ggt	gcg	tat	gcg	ttg	ggt	ttt	gct	gcg	gtt	cgt	gag	ttg	ttt	gaa	gag	403
Val	Ala	Tyr	Ala	Leu	Val	Phe	Ala	Ala	Val	Arg	Glu	Leu	Phe	Glu	Glu	
				90					95					100		
gcc	ggt	acg	ttg	ctt	gcg	gag	cat	acg	gat	ggg	tct	ggg	ttg	gtg	aag	451
Ala	Gly	Thr	Leu	Leu	Ala	Glu	His	Thr	Asp	Gly	Ser	Gly	Leu	Val	Lys	
			105					110					115			
aat	gct	ggg	cag	tat	cac	gga	tat	cgg	gag	ttg	ttg	gag	act	cat	gag	499
Asn	Ala	Gly	Gln	Tyr	His	Gly	Tyr	Arg	Glu	Leu	Leu	Glu	Thr	His	Glu	
		120					125					130				
atg	tcg	ctg	acg	gat	atg	ttg	cag	agt	gag	aat	ttg	gcg	att	cgt	agt	547
Met	Ser	Leu	Thr	Asp	Met	Leu	Gln	Ser	Glu	Asn	Leu	Ala	Ile	Arg	Ser	
						140					145					
gat	ttg	att	gtg	cct	ttt	gcc	agg	tgg	gcg	agc	cct	gag	ggg	aat	agg	595
Asp	Leu	Ile	Val	Pro	Phe	Ala	Arg	Trp	Ala	Ser	Pro	Glu	Gly	Asn	Arg	
150					155				160						165	
gag	cag	ttt	gat	acg	ttt	tct	ttt	gtt	gct	gtg	gag	ccg	gag	ggg	cag	643
Glu	Gln	Phe	Asp	Thr	Phe	Ser	Phe	Val	Ala	Val	Glu	Pro	Glu	Gly	Gln	
				170				175						180		
tgt	gcg	gat	ggg	aat	acg	tcg	gag	gcg	tct	tcg	acg	ggg	tat	ttt	cct	691
Cys	Ala	Asp	Gly	Asn	Thr	Ser	Glu	Ala	Ser	Ser	Thr	Gly	Tyr	Phe	Pro	
			185					190					195			
gca	cgg	ctg	att	ttg	gat	ggg	tgg	cgc	gcc	ggg	ttg	ttg	agg	ttg	gtt	739
Ala	Arg	Leu	Ile	Leu	Asp	Gly	Trp	Arg	Ala	Gly	Leu	Leu	Arg	Leu	Val	
		200					205				210					
att	ccg	acg	tgg	gcg	tcg	ttg	ttt	gag	ttg	tcg	cag	ttt	aag	act	gtg	787
Ile	Pro	Thr	Trp	Ala	Ser	Leu	Phe	Glu	Leu	Ser	Gln	Phe	Lys	Thr	Val	
	215					220					225					
gag	gaa	ttg	ctg	gag	tac	agc	gcg	cag	gtt	gat	atg	tct	cct	gtg	ttg	835
Glu	Glu	Leu	Leu	Glu	Tyr	Ser	Ala	Gln	Val	Asp	Met	Ser	Pro	Val	Leu	
230					235					240				245		
gat	gat	gcg	gtg	gat	aat	ccg	agg	tat	gcg	gag	ttt	tat	cag	gcg	atg	883
Asp	Asp	Ala	Val	Asp	Asn	Pro	Arg	Tyr	Ala	Glu	Phe	Tyr	Gln	Ala	Met	
				250					255					260		
cgc	acg	gaa	cgg	ttt	tgatcattta	aggttcattc	atg									921
Arg	Thr	Glu	Arg	Phe												
				265												

&lt;210&gt; 242

&lt;211&gt; 266

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 242

Met	Val	Met	Gln	Gly	Ile	Gly	Gly	Arg	Lys	Leu	Ala	Ala	Thr	Val	Leu
1				5					10					15	

Leu Val Arg Asp Gly Ile Ile Asn Gly Arg Pro Asp Val Glu Val Tyr  
                   20                  25                  30  
 Ile Gln Glu Arg Val Ser Thr Met Ala Asn Phe Pro Arg Ala Thr Val  
                   35                  40                  45  
 Phe Pro Gly Gly Gly Val Asp Ser Arg Asp Phe Ala Asp Gly His Gly  
           50                  55                  60  
 Lys Glu Val Trp Arg Gly Pro Ser Ala Glu Glu Trp Gly Val Arg Leu  
   65                  70                  75                  80  
 Gly Val Glu Pro His Val Ala Tyr Ala Leu Val Phe Ala Ala Val Arg  
                   85                  90                  95  
 Glu Leu Phe Glu Glu Ala Gly Thr Leu Leu Ala Glu His Thr Asp Gly  
           100                  105                  110  
 Ser Gly Leu Val Lys Asn Ala Gly Gln Tyr His Gly Tyr Arg Glu Leu  
           115                  120                  125  
 Leu Glu Thr His Glu Met Ser Leu Thr Asp Met Leu Gln Ser Glu Asn  
   130                  135                  140  
 Leu Ala Ile Arg Ser Asp Leu Ile Val Pro Phe Ala Arg Trp Ala Ser  
 145                  150                  155                  160  
 Pro Glu Gly Asn Arg Glu Gln Phe Asp Thr Phe Ser Phe Val Ala Val  
                   165                  170                  175  
 Glu Pro Glu Gly Gln Cys Ala Asp Gly Asn Thr Ser Glu Ala Ser Ser  
           180                  185                  190  
 Thr Gly Tyr Phe Pro Ala Arg Leu Ile Leu Asp Gly Trp Arg Ala Gly  
   195                  200                  205  
 Leu Leu Arg Leu Val Ile Pro Thr Trp Ala Ser Leu Phe Glu Leu Ser  
   210                  215                  220  
 Gln Phe Lys Thr Val Glu Glu Leu Leu Glu Tyr Ser Ala Gln Val Asp  
 225                  230                  235                  240  
 Met Ser Pro Val Leu Asp Asp Ala Val Asp Asn Pro Arg Tyr Ala Glu  
           245                  250                  255  
 Phe Tyr Gln Ala Met Arg Thr Glu Arg Phe  
           260                  265

<210> 243

<211> 570

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(547)

<223> RXA01819

<400> 243

ggttgggggtc atcaaaggat gcggacatcg ctgtgggggtt gtgtaataat tgcacctgtg 60



His Pro Arg Phe His Met His Phe Thr Pro Thr Tyr Ser Ser Trp Ile  
 65 70 75 80  
 Asn Gln Val Glu Arg Leu Phe Ala Glu Val Thr Arg Glu Leu Leu Gln  
 85 90 95  
 Arg Ser Asp His Arg Ser Val Gln Ala Leu Glu Lys Asp Leu Arg Asn  
 100 105 110  
 Trp Val Lys Ala Trp Asn Glu Asp Pro Lys Pro Phe Ile Trp Thr Lys  
 115 120 125  
 Thr Ala Glu Glu Ile Leu Ser Ser Ile Ala Arg Tyr Leu Lys Arg Ile  
 130 135 140  
 Asn Gly Ala Gly His  
 145

<210> 245  
 <211> 879  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(856)  
 <223> RXN03052

<400> 245  
 ccgctttatc tactacggcc tcagccatag cgtgggttggc gaagttgtgt ttgcaatagt 60  
 tttttaaata tccccagcct tcattcctgt aacggtcata atg ccc ttt tct cac 115  
 Met Pro Phe Ser His  
 1 5  
 gac aaa tct gaa ctc ggt ggg gaa acc ccc tac ggg ctt gta cat gtt 163  
 Asp Lys Ser Glu Leu Gly Gly Glu Thr Pro Tyr Gly Leu Val His Val  
 10 15 20  
 aac cct atg gct gaa gtg cga cct gta aaa gca caa acc aac gag ccc 211  
 Asn Pro Met Ala Glu Val Arg Pro Val Lys Ala Gln Thr Asn Glu Pro  
 25 30 35  
 caa gca ctg cag gtt gct gac att caa ccc ttt cac gct gtt att gcg 259  
 Gln Ala Leu Gln Val Ala Asp Ile Gln Pro Phe His Ala Val Ile Ala  
 40 45 50  
 gcc tca aaa caa ttg act ctc atc gac gtt gtc gat gtc tgc ctt gga 307  
 Ala Ser Lys Gln Leu Thr Leu Ile Asp Val Val Asp Val Cys Leu Gly  
 55 60 65  
 aca gtg ttg cga gca tgg gaa gca ctg agc ctg cga tgg gta gac gtg 355  
 Thr Val Leu Arg Ala Trp Glu Ala Leu Ser Leu Arg Trp Val Asp Val  
 70 75 80 85  
 gtg ctt gac gag gag cat cca aga atc ttt atc cga ggc acc att gtc 403  
 Val Leu Asp Glu Glu His Pro Arg Ile Phe Ile Arg Gly Thr Ile Val  
 90 95 100

tac aac aaa gaa aaa ggt aac cac aga caa gat aaa aca aaa acg acc 451  
 Tyr Asn Lys Glu Lys Gly Asn His Arg Gln Asp Lys Thr Lys Thr Thr  
 105 110 115  
  
 agc agt agg cgt gtc att cag ttg cca gaa att gcc tca gac gtc tta 499  
 Ser Ser Arg Arg Val Ile Gln Leu Pro Glu Ile Ala Ser Asp Val Leu  
 120 125 130  
  
 cgc aaa aga cat gca ctc tac gcc gaa cat ctc gaa atg gtg ttc cct 547  
 Arg Lys Arg His Ala Leu Tyr Ala Glu His Leu Glu Met Val Phe Pro  
 135 140 145  
  
 tcc gct aga ggc aca tat att tat gag tcc aat ttc aac aaa ttg ttg 595  
 Ser Ala Arg Gly Thr Tyr Ile Tyr Glu Ser Asn Phe Asn Lys Leu Leu  
 150 155 160 165  
  
 cga aaa cac cga aag ggt act gca tat gat tgg gtg acc gtg cac agc 643  
 Arg Lys His Arg Lys Gly Thr Ala Tyr Asp Trp Val Thr Val His Ser  
 170 175 180  
  
 atc agg aaa acc ctt gca tca att gtc tct gag aac ctt gat tcc aag 691  
 Ile Arg Lys Thr Leu Ala Ser Ile Val Ser Glu Asn Leu Asp Ser Lys  
 185 190 195  
  
 gcc gca tca gac gta ctc ggc cat gct gac tca cga ctc aca gaa cgg 739  
 Ala Ala Ser Asp Val Leu Gly His Ala Asp Ser Arg Leu Thr Glu Arg  
 200 205 210  
  
 gtc tac atc gct aaa act gac aaa gac gtt ccg att ggt gat gtc gtc 787  
 Val Tyr Ile Ala Lys Thr Asp Lys Asp Val Pro Ile Gly Asp Val Val  
 215 220 225  
  
 aac caa gcg ctc aaa gag gca cga aaa gtc tcc aaa aag tct cca aat 835  
 Asn Gln Ala Leu Lys Glu Ala Arg Lys Val Ser Lys Lys Ser Pro Asn  
 230 235 240 245  
  
 aaa gaa gct aaa gaa gaa gaa tagacgcaat agttgcattt tta 879  
 Lys Glu Ala Lys Glu Glu Glu  
 250

&lt;210&gt; 246

&lt;211&gt; 252

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 246

Met Pro Phe Ser His Asp Lys Ser Glu Leu Gly Gly Glu Thr Pro Tyr  
 1 5 10 15  
  
 Gly Leu Val His Val Asn Pro Met Ala Glu Val Arg Pro Val Lys Ala  
 20 25 30  
  
 Gln Thr Asn Glu Pro Gln Ala Leu Gln Val Ala Asp Ile Gln Pro Phe  
 35 40 45  
  
 His Ala Val Ile Ala Ala Ser Lys Gln Leu Thr Leu Ile Asp Val Val  
 50 55 60  
  
 Asp Val Cys Leu Gly Thr Val Leu Arg Ala Trp Glu Ala Leu Ser Leu  
 65 70 75 80

Arg Trp Val Asp Val Val Leu Asp Glu Glu His Pro Arg Ile Phe Ile  
85 90 95

Arg Gly Thr Ile Val Tyr Asn Lys Glu Lys Gly Asn His Arg Gln Asp  
100 105 110

Lys Thr Lys Thr Thr Ser Ser Arg Arg Val Ile Gln Leu Pro Glu Ile  
115 120 125

Ala Ser Asp Val Leu Arg Lys Arg His Ala Leu Tyr Ala Glu His Leu  
130 135 140

Glu Met Val Phe Pro Ser Ala Arg Gly Thr Tyr Ile Tyr Glu Ser Asn  
145 150 155 160

Phe Asn Lys Leu Leu Arg Lys His Arg Lys Gly Thr Ala Tyr Asp Trp  
165 170 175

Val Thr Val His Ser Ile Arg Lys Thr Leu Ala Ser Ile Val Ser Glu  
180 185 190

Asn Leu Asp Ser Lys Ala Ala Ser Asp Val Leu Gly His Ala Asp Ser  
195 200 205

Arg Leu Thr Glu Arg Val Tyr Ile Ala Lys Thr Asp Lys Asp Val Pro  
210 215 220

Ile Gly Asp Val Val Asn Gln Ala Leu Lys Glu Ala Arg Lys Val Ser  
225 230 235 240

Lys Lys Ser Pro Asn Lys Glu Ala Lys Glu Glu Glu  
245 250

&lt;210&gt; 247

&lt;211&gt; 478

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(478)

&lt;223&gt; RXN02915

&lt;400&gt; 247

cacttaatgc catgaccttg tgcattgcata gtgtcatgac cttgtgcaca cccagacct 60

acaccacagg catagtccta ggctgctcac aattgacatc atg cct aaa ccc cta 115  
Met Pro Lys Pro Leu  
1 5

ccc cca gaa acc cga cgc aag atc atc gat ttc gat ccg ttc gca ccg 163  
Pro Pro Glu Thr Arg Arg Lys Ile Ile Asp Phe Asp Pro Phe Ala Pro  
10 15 20

aac agc ccc tcg atc gaa gag ttc tgc agt cgg cta aaa ata tcg cgg 211  
Asn Ser Pro Ser Ile Glu Glu Phe Cys Ser Arg Leu Lys Ile Ser Arg  
25 30 35

cgc agc ttc tac aac atc cgc aac cga tac caa caa gac gcc aac gca 259

Arg Ser Phe Tyr Asn Ile Arg Asn Arg Tyr Gln Gln Asp Ala Asn Ala  
                   40                                  45                                  50  
 gca ctg cat tca cac tcc agc gcc cca atc acc gcc cgg cga acg tac 307  
 Ala Leu His Ser His Ser Ser Ala Pro Ile Thr Ala Arg Arg Thr Tyr  
           55                                  60                                  65  
 gat gaa tcc atc acc agc acc ttg ctg tcc atc cgc gca cgc ctg aaa 355  
 Asp Glu Ser Ile Thr Ser Thr Leu Leu Ser Ile Arg Ala Arg Leu Lys  
       70                                  75                                  80                                  85  
 gcc caa gga tgg gag tac ggc ccg atc tct att cga ttc gaa ggc atc 403  
 Ala Gln Gly Trp Glu Tyr Gly Pro Ile Ser Ile Arg Phe Glu Gly Ile  
                                   90                                  95                                  100  
 ttc acc cgg gaa ctg act gca ccg att cca tct gtt tca acc att gct 451  
 Phe Thr Arg Glu Leu Thr Ala Pro Ile Pro Ser Val Ser Thr Ile Ala  
                                   105                                  110                                  115  
 cgt ttg tta cgc gcc gca gga gct gtt 478  
 Arg Leu Leu Arg Ala Ala Gly Ala Val  
           120                                  125

&lt;210&gt; 248

&lt;211&gt; 126

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 248

Met Pro Lys Pro Leu Pro Pro Glu Thr Arg Arg Lys Ile Ile Asp Phe  
   1                                  5                                  10                                  15  
 Asp Pro Phe Ala Pro Asn Ser Pro Ser Ile Glu Glu Phe Cys Ser Arg  
                   20                                  25                                  30  
 Leu Lys Ile Ser Arg Arg Ser Phe Tyr Asn Ile Arg Asn Arg Tyr Gln  
           35                                  40                                  45  
 Gln Asp Ala Asn Ala Ala Leu His Ser His Ser Ser Ala Pro Ile Thr  
       50                                  55                                  60  
 Ala Arg Arg Thr Tyr Asp Glu Ser Ile Thr Ser Thr Leu Leu Ser Ile  
       65                                  70                                  75                                  80  
 Arg Ala Arg Leu Lys Ala Gln Gly Trp Glu Tyr Gly Pro Ile Ser Ile  
                   85                                  90                                  95  
 Arg Phe Glu Gly Ile Phe Thr Arg Glu Leu Thr Ala Pro Ile Pro Ser  
           100                                  105                                  110  
 Val Ser Thr Ile Ala Arg Leu Leu Arg Ala Ala Gly Ala Val  
       115                                  120                                  125

&lt;210&gt; 249

&lt;211&gt; 657

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(634)

&lt;223&gt; RXN02919

&lt;400&gt; 249

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atttccctcg cgagatccat cctgtgggcg gtgcacaggt cactgccgct acgggctcag 60

ctgacctaag atctcgagga aatgatgact tcagcgcgga  gtg ccg gtc gat cac 115
                                         Val Pro Val Asp His
                                         1                               5

acc acc atc tac cgc tgg gtc cag aaa tac gcc cct gag ctg gat aag 163
Thr Thr Ile Tyr Arg Trp Val Gln Lys Tyr Ala Pro Glu Leu Asp Lys
                        10                               15                               20

cag act cgc tgg tac cgg cag gtt cct gac tgg cag gcc agt tcc tgg 211
Gln Thr Arg Trp Tyr Arg Gln Val Pro Asp Trp Gln Ala Ser Ser Trp
                        25                               30                               35

cgg gtg gat gag acc tat atc cgg gtc ggc ggc acg tgg tgc tat ctc 259
Arg Val Asp Glu Thr Tyr Ile Arg Val Gly Gly Thr Trp Cys Tyr Leu
                        40                               45                               50

tac cgg gct att acc gcg ggt ggg cag acc ctg gag ttt tat ctc tca 307
Tyr Arg Ala Ile Thr Ala Gly Gln Thr Leu Glu Phe Tyr Leu Ser
                        55                               60                               65

cca aaa cgg aat gtg gct gcg gcc aag cgt ttc ctg gcc aag acg ctg 355
Pro Lys Arg Asn Val Ala Ala Ala Lys Arg Phe Leu Ala Lys Thr Leu
                        70                               75                               80                               85

cga tcg aat acg aca gcc ggg tcc ccg cgg gtc atc aac acc gac aag 403
Arg Ser Asn Thr Thr Ala Gly Ser Pro Arg Val Ile Asn Thr Asp Lys
                        90                               95                               100

gca cca gct ctg gcc aag gca ata tcc gag ctg aag gcg gag gga atc 451
Ala Pro Ala Leu Ala Lys Ala Ile Ser Glu Leu Lys Ala Glu Gly Ile
                        105                               110                               115

tgc cct cag acg gtg gag cac cgg cag gtg aaa tac ctc aac aac gtt 499
Cys Pro Gln Thr Val Glu His Arg Gln Val Lys Tyr Leu Asn Asn Val
                        120                               125                               130

atc gag gga gat cat ggc cga ctc aaa aga atc ctg ggg ccg aag gga 547
Ile Glu Gly Asp His Gly Arg Leu Lys Arg Ile Leu Gly Pro Lys Gly
                        135                               140                               145

gcg ttc aaa aac cga att tcc gcc tac cgg acg ttg aaa ggg atg gag 595
Ala Phe Lys Asn Arg Ile Ser Ala Tyr Arg Thr Leu Lys Gly Met Glu
                        150                               155                               160                               165

gcg atg cat tca ttg cgg aaa ggg tca ggg aac gat gtt tgacctcacg 644
Ala Met His Ser Leu Arg Lys Gly Ser Gly Asn Asp Val
                        170                               175

ggcacccgaa ccc 657

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&lt;210&gt; 250

&lt;211&gt; 178

&lt;212&gt; PRT

<213> Corynebacterium glutamicum

<400> 250

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Val Pro Val Asp His Thr Thr Ile Tyr Arg Trp Val Gln Lys Tyr Ala
 1             5             10             15

Pro Glu Leu Asp Lys Gln Thr Arg Trp Tyr Arg Gln Val Pro Asp Trp
          20             25             30

Gln Ala Ser Ser Trp Arg Val Asp Glu Thr Tyr Ile Arg Val Gly Gly
          35             40             45

Thr Trp Cys Tyr Leu Tyr Arg Ala Ile Thr Ala Gly Gly Gln Thr Leu
          50             55             60

Glu Phe Tyr Leu Ser Pro Lys Arg Asn Val Ala Ala Ala Lys Arg Phe
          65             70             75             80

Leu Ala Lys Thr Leu Arg Ser Asn Thr Thr Ala Gly Ser Pro Arg Val
          85             90             95

Ile Asn Thr Asp Lys Ala Pro Ala Leu Ala Lys Ala Ile Ser Glu Leu
          100            105            110

Lys Ala Glu Gly Ile Cys Pro Gln Thr Val Glu His Arg Gln Val Lys
          115            120            125

Tyr Leu Asn Asn Val Ile Glu Gly Asp His Gly Arg Leu Lys Arg Ile
          130            135            140

Leu Gly Pro Lys Gly Ala Phe Lys Asn Arg Ile Ser Ala Tyr Arg Thr
          145            150            155            160

Leu Lys Gly Met Glu Ala Met His Ser Leu Arg Lys Gly Ser Gly Asn
          165            170            175

Asp Val

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<210> 251

<211> 1281

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1258)

<223> RXN03033

<400> 251

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aagaccatca gaatcaaatg gtgatcgata tcttgggaaa agctattggg accaggccca 60

atcctggcga gggcttagac gaggaggacg ccacctaaac gtg gat gag caa cgc      115
                               Val Asp Glu Gln Arg
                               1             5

gcc ttt gat caa gga ctc aag gaa gaa aac acc ttg atc aca gat ctc      163
Ala Phe Asp Gln Gly Leu Lys Glu Glu Asn Thr Leu Ile Thr Asp Leu
          10             15             20

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acc acc tgt gcc agg ctg agc cat aac aag gca tta cgg ctg atc aag	211
Thr Thr Cys Ala Arg Leu Ser His Asn Lys Ala Leu Arg Leu Ile Lys	
25 30 35	
ctg tcg aaa tca acg gcg tat tac cgc aac aag ccg cgt ccc cgt cct	259
Leu Ser Lys Ser Thr Ala Tyr Tyr Arg Asn Lys Pro Arg Pro Arg Pro	
40 45 50	
gca ccg aaa cct gtc ctg cag gcc gtg cca gca cca aca gca cct ggt	307
Ala Pro Lys Pro Val Leu Gln Ala Val Pro Ala Pro Thr Ala Pro Gly	
55 60 65	
gtg gaa ccc aca cca gag cct tgg cag ggg aag gag cca gca gtg tcg	355
Val Glu Pro Thr Pro Glu Pro Trp Gln Gly Lys Glu Pro Ala Val Ser	
70 75 80 85	
tcg gtg cgt caa gcg ttg gca gaa cac gaa cgc cag ttc att gtt gat	403
Ser Val Arg Gln Ala Leu Ala Glu His Glu Arg Gln Phe Ile Val Asp	
90 95 100	
gcg atc acc gcg tac cca caa ctg agc gtt agt ggg gtg ttt aac atg	451
Ala Ile Thr Ala Tyr Pro Gln Leu Ser Val Ser Gly Val Phe Asn Met	
105 110 115	
ttg ttt aac aaa ggc atc tac cgc gca tca cta cgt aca tgg tgg cgt	499
Leu Phe Asn Lys Gly Ile Tyr Arg Ala Ser Leu Arg Thr Trp Trp Arg	
120 125 130	
gtt gcc aag cag cac aag ttg tta cac aaa gac cga gtc agt gcc ctg	547
Val Ala Lys Gln His Lys Leu Leu His Lys Asp Arg Val Ser Ala Leu	
135 140 145	
tcc ccg ggg aaa cga tca cca acg cca ccg gtt aag ccg agg ttg gaa	595
Ser Pro Gly Lys Arg Ser Pro Thr Pro Arg Val Lys Pro Arg Leu Glu	
150 155 160 165	
gca aca cag cct ggt cag gtg gtg tgt tgg gat gtg acg ttc ttg ccg	643
Ala Thr Gln Pro Gly Gln Val Val Cys Trp Asp Val Thr Phe Leu Pro	
170 175 180	
tcg ctg gta cgt ggt aag acc tat gcg ttg cat ctg gcg att gat ttg	691
Ser Leu Val Arg Gly Lys Thr Tyr Ala Leu His Leu Ala Ile Asp Leu	
185 190 195	
ttt tcc cgc aag att gtt ggg gcg aag gtc gcg ccg acg gaa aat acc	739
Phe Ser Arg Lys Ile Val Gly Ala Lys Val Ala Pro Thr Glu Asn Thr	
200 205 210	
tcc acc gcg gtg gag ttg tta acg cag gtg tta gcg gat aat ccg ggt	787
Ser Thr Ala Val Glu Leu Leu Thr Gln Val Leu Ala Asp Asn Pro Gly	
215 220 225	
gtg gtg acg gtg cat tcg gat aat ggg tcg gcg atg aca tcg acg agg	835
Val Val Thr Val His Ser Asp Asn Gly Ser Ala Met Thr Ser Thr Arg	
230 235 240 245	
gtg ccg ccg ttg tta gcg gat cat ggt gtg gcg ttg tcg ttg att ccg	883
Val Arg Arg Leu Leu Ala Asp His Gly Val Ala Leu Ser Leu Ile Arg	
250 255 260	
ccg ccg gtg agt gat gat aat gcg ttt gtg gag tcg gtg ttt cat acg	931

Pro Arg Val Ser Asp Asp Asn Ala Phe Val Glu Ser Val Phe His Thr  
 265 270 275

ttg aag tat cgg ccg ttt tat ccg aag gtg ttt gca tcg atg gat cag 979  
 Leu Lys Tyr Arg Pro Phe Tyr Pro Lys Val Phe Ala Ser Met Asp Gln  
 280 285 290

gcc cgg gtg tgg gtg gag gag ttt gtg gtg tat tac aac acg gtt cat 1027  
 Ala Arg Val Trp Val Glu Glu Phe Val Val Tyr Tyr Asn Thr Val His  
 295 300 305

ccg cat tct ggt gtg gct ggg cat act ccg cag tcg gtg ttt gat ggt 1075  
 Pro His Ser Gly Val Ala Gly His Thr Pro Gln Ser Val Phe Asp Gly  
 310 315 320 325

agt tgg agg gcg gct cat agg ttg cgt gtg cag gcg ttg gat gcc cat 1123  
 Ser Trp Arg Ala Ala His Arg Leu Arg Val Gln Ala Leu Asp Ala His  
 330 335 340

tac cgg cag ttc ccg cag cgg tat gtg ggg cgg ccg gtg gtt cag gaa 1171  
 Tyr Arg Gln Phe Pro Gln Arg Tyr Val Gly Arg Pro Val Val Gln Glu  
 345 350 355

gtt gct ggt gtg gtg cgt ctt aat ggt gcg cgt gat gat ggg tct gta 1219  
 Val Ala Gly Val Val Arg Leu Asn Gly Ala Arg Asp Asp Gly Ser Val  
 360 365 370

cag gag agg gtt ggt ggt gta gcg tcg ctg tta agt gct tgagtttagca 1268  
 Gln Glu Arg Val Gly Gly Val Ala Ser Leu Leu Ser Ala  
 375 380 385

tgtgttctta tcg 1281

&lt;210&gt; 252

&lt;211&gt; 386

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 252

Val Asp Glu Gln Arg Ala Phe Asp Gln Gly Leu Lys Glu Glu Asn Thr  
 1 5 10 15

Leu Ile Thr Asp Leu Thr Thr Cys Ala Arg Leu Ser His Asn Lys Ala  
 20 25 30

Leu Arg Leu Ile Lys Leu Ser Lys Ser Thr Ala Tyr Tyr Arg Asn Lys  
 35 40 45

Pro Arg Pro Arg Pro Ala Pro Lys Pro Val Leu Gln Ala Val Pro Ala  
 50 55 60

Pro Thr Ala Pro Gly Val Glu Pro Thr Pro Glu Pro Trp Gln Gly Lys  
 65 70 75 80

Glu Pro Ala Val Ser Ser Val Arg Gln Ala Leu Ala Glu His Glu Arg  
 85 90 95

Gln Phe Ile Val Asp Ala Ile Thr Ala Tyr Pro Gln Leu Ser Val Ser  
 100 105 110

Gly Val Phe Asn Met Leu Phe Asn Lys Gly Ile Tyr Arg Ala Ser Leu  
 115 120 125  
 Arg Thr Trp Trp Arg Val Ala Lys Gln His Lys Leu Leu His Lys Asp  
 130 135 140  
 Arg Val Ser Ala Leu Ser Pro Gly Lys Arg Ser Pro Thr Pro Arg Val  
 145 150 155 160  
 Lys Pro Arg Leu Glu Ala Thr Gln Pro Gly Gln Val Val Cys Trp Asp  
 165 170 175  
 Val Thr Phe Leu Pro Ser Leu Val Arg Gly Lys Thr Tyr Ala Leu His  
 180 185 190  
 Leu Ala Ile Asp Leu Phe Ser Arg Lys Ile Val Gly Ala Lys Val Ala  
 195 200 205  
 Pro Thr Glu Asn Thr Ser Thr Ala Val Glu Leu Leu Thr Gln Val Leu  
 210 215 220  
 Ala Asp Asn Pro Gly Val Val Thr Val His Ser Asp Asn Gly Ser Ala  
 225 230 235 240  
 Met Thr Ser Thr Arg Val Arg Arg Leu Leu Ala Asp His Gly Val Ala  
 245 250 255  
 Leu Ser Leu Ile Arg Pro Arg Val Ser Asp Asp Asn Ala Phe Val Glu  
 260 265 270  
 Ser Val Phe His Thr Leu Lys Tyr Arg Pro Phe Tyr Pro Lys Val Phe  
 275 280 285  
 Ala Ser Met Asp Gln Ala Arg Val Trp Val Glu Glu Phe Val Val Tyr  
 290 295 300  
 Tyr Asn Thr Val His Pro His Ser Gly Val Ala Gly His Thr Pro Gln  
 305 310 315 320  
 Ser Val Phe Asp Gly Ser Trp Arg Ala Ala His Arg Leu Arg Val Gln  
 325 330 335  
 Ala Leu Asp Ala His Tyr Arg Gln Phe Pro Gln Arg Tyr Val Gly Arg  
 340 345 350  
 Pro Val Val Gln Glu Val Ala Gly Val Val Arg Leu Asn Gly Ala Arg  
 355 360 365  
 Asp Asp Gly Ser Val Gln Glu Arg Val Gly Gly Val Ala Ser Leu Leu  
 370 375 380  
 Ser Ala  
 385

&lt;210&gt; 253

&lt;211&gt; 1281

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1258)

&lt;223&gt; RXN03035

&lt;400&gt; 253

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aagaccatca gaatcaaatg gtgatcgata tcttgggaaa agctattggg accaggccca 60

atcctggcga gggcttagac gaggaggacg ccacctaaac gtg gat gag caa cgc 115
Val Asp Glu Gln Arg
1 5

gcc ttt gat caa gga ctc aag gaa gaa aac acc ttg atc aca gat ctc 163
Ala Phe Asp Gln Gly Leu Lys Glu Glu Asn Thr Leu Ile Thr Asp Leu
10 15 20

acc acc tgt gcc agg ctg agc cat aac aag gca tta cgg ctg atc aag 211
Thr Thr Cys Ala Arg Leu Ser His Asn Lys Ala Leu Arg Leu Ile Lys
25 30 35

ctg tcg aaa tca acg gcg tat tac cgc aac aag ccg cgt ccc cgt cct 259
Leu Ser Lys Ser Thr Ala Tyr Tyr Arg Asn Lys Pro Arg Pro Arg Pro
40 45 50

gca ccg aaa cct gtc ctg cag gcc gtg cca gca cca aca gca cct ggt 307
Ala Pro Lys Pro Val Leu Gln Ala Val Pro Ala Pro Thr Ala Pro Gly
55 60 65

gtg gaa ccc aca cca gag cct tgg cag ggg aag gag cca gca gtg tcg 355
Val Glu Pro Thr Pro Glu Pro Trp Gln Gly Lys Glu Pro Ala Val Ser
70 75 80 85

tcg gtg cgt caa gcg ttg gca gaa cac gaa cgc cag ttc att gtt gat 403
Ser Val Arg Gln Ala Leu Ala Glu His Glu Arg Gln Phe Ile Val Asp
90 95 100

gcg atc acc gcg tac cca caa ctg agc gtt agt ggg gtg ttt aac atg 451
Ala Ile Thr Ala Tyr Pro Gln Leu Ser Val Ser Gly Val Phe Asn Met
105 110 115

ttg ttt aac aaa ggc atc tac cgc gca tca cta cgt aca tgg tgg cgt 499
Leu Phe Asn Lys Gly Ile Tyr Arg Ala Ser Leu Arg Thr Trp Trp Arg
120 125 130

gtt gcc aag cag cac aag ttg tta cac aaa gac cga gtc agt gcc ctg 547
Val Ala Lys Gln His Lys Leu Leu His Lys Asp Arg Val Ser Ala Leu
135 140 145

tcc ccg ggg aaa cga tca cca acg cca ccg gtt aag ccg agg ttg gaa 595
Ser Pro Gly Lys Arg Ser Pro Thr Pro Arg Val Lys Pro Arg Leu Glu
150 155 160 165

gca aca cag cct ggt cag gtg gtg tgt tgg gat gtg acg ttc ttg ccg 643
Ala Thr Gln Pro Gly Gln Val Val Cys Trp Asp Val Thr Phe Leu Pro
170 175 180

tcg ctg gta cgt ggt aag acc tat gcg ttg cat ctg gcg att gat ttg 691
Ser Leu Val Arg Gly Lys Thr Tyr Ala Leu His Leu Ala Ile Asp Leu
185 190 195

ttt tcc cgc aag att gtt ggg gcg aag gtc gcg ccg acg gaa aat acc 739
Phe Ser Arg Lys Ile Val Gly Ala Lys Val Ala Pro Thr Glu Asn Thr

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200	205	210	
tcc acc gcg gtg gag ttg tta acg cag gtg tta gcg gat aat ccg ggt Ser Thr Ala Val Glu Leu Leu Thr Gln Val Leu Ala Asp Asn Pro Gly 215 220 225			787
gtg gtg acg gtg cat tcg gat aat ggg tcg gcg atg aca tcg acg agg Val Val Thr Val His Ser Asp Asn Gly Ser Ala Met Thr Ser Thr Arg 230 235 240 245			835
gtg cgg cgg ttg tta gcg gat cat ggt gtg gcg ttg tcg ttg att cgg Val Arg Arg Leu Leu Ala Asp His Gly Val Ala Leu Ser Leu Ile Arg 250 255 260			883
ccg cgg gtg agt gat gat aat gcg ttt gtg gag tcg gtg ttt cat acg Pro Arg Val Ser Asp Asp Asn Ala Phe Val Glu Ser Val Phe His Thr 265 270 275			931
ttg aag tat cgg ccg ttt tat ccg aag gtg ttt gca tcg atg gat cag Leu Lys Tyr Arg Pro Phe Tyr Pro Lys Val Phe Ala Ser Met Asp Gln 280 285 290			979
gcc cgg gtg tgg gtg gag gag ttt gtg gtg tat tac aac acg gtt cat Ala Arg Val Trp Val Glu Glu Phe Val Val Tyr Tyr Asn Thr Val His 295 300 305			1027
ccg cat tct ggt gtg gct ggg cat act ccg cag tcg gtg ttt gat ggt Pro His Ser Gly Val Ala Gly His Thr Pro Gln Ser Val Phe Asp Gly 310 315 320 325			1075
agt tgg agg gcg gct cat agg ttg cgt gtg cag gcg ttg gat gcc cat Ser Trp Arg Ala Ala His Arg Leu Arg Val Gln Ala Leu Asp Ala His 330 335 340			1123
tac cgg cag ttc ccg cag cgg tat gtg ggg cgg ccg gtg gtt cag gaa Tyr Arg Gln Phe Pro Gln Arg Tyr Val Gly Arg Pro Val Val Gln Glu 345 350 355			1171
gtt gct ggt gtg gtg cgt ctt aat ggt gcg cgt gat gat ggg tct gta Val Ala Gly Val Val Arg Leu Asn Gly Ala Arg Asp Asp Gly Ser Val 360 365 370			1219
cag gag agg gtt ggt ggt gta gcg tcg ctg tta agt gct tgagtttagca Gln Glu Arg Val Gly Gly Val Ala Ser Leu Leu Ser Ala 375 380 385			1268
tgtgttctta tcg			1281

&lt;210&gt; 254

&lt;211&gt; 386

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 254

Val	Asp	Glu	Gln	Arg	Ala	Phe	Asp	Gln	Gly	Leu	Lys	Glu	Glu	Asn	Thr
1				5					10					15	

Leu	Ile	Thr	Asp	Leu	Thr	Thr	Cys	Ala	Arg	Leu	Ser	His	Asn	Lys	Ala
			20					25					30		

Leu Arg Leu Ile Lys Leu Ser Lys Ser Thr Ala Tyr Tyr Arg Asn Lys  
                   35                                  40                                  45  
 Pro Arg Pro Arg Pro Ala Pro Lys Pro Val Leu Gln Ala Val Pro Ala  
           50  55                                  60  
 Pro Thr Ala Pro Gly Val Glu Pro Thr Pro Glu Pro Trp Gln Gly Lys  
   65                                  70                                  75                                  80  
 Glu Pro Ala Val Ser Ser Val Arg Gln Ala Leu Ala Glu His Glu Arg  
                                   85                                  90                                  95  
 Gln Phe Ile Val Asp Ala Ile Thr Ala Tyr Pro Gln Leu Ser Val Ser  
                   100                                  105                                  110  
 Gly Val Phe Asn Met Leu Phe Asn Lys Gly Ile Tyr Arg Ala Ser Leu  
           115                                  120                                  125  
 Arg Thr Trp Trp Arg Val Ala Lys Gln His Lys Leu Leu His Lys Asp  
   130                                  135                                  140  
 Arg Val Ser Ala Leu Ser Pro Gly Lys Arg Ser Pro Thr Pro Arg Val  
   145                                  150                                  155                                  160  
 Lys Pro Arg Leu Glu Ala Thr Gln Pro Gly Gln Val Val Cys Trp Asp  
                   165                                  170                                  175  
 Val Thr Phe Leu Pro Ser Leu Val Arg Gly Lys Thr Tyr Ala Leu His  
                   180                                  185                                  190  
 Leu Ala Ile Asp Leu Phe Ser Arg Lys Ile Val Gly Ala Lys Val Ala  
           195                                  200                                  205  
 Pro Thr Glu Asn Thr Ser Thr Ala Val Glu Leu Leu Thr Gln Val Leu  
   210                                  215                                  220  
 Ala Asp Asn Pro Gly Val Val Thr Val His Ser Asp Asn Gly Ser Ala  
   225                                  230                                  235                                  240  
 Met Thr Ser Thr Arg Val Arg Arg Leu Leu Ala Asp His Gly Val Ala  
                   245                                  250                                  255  
 Leu Ser Leu Ile Arg Pro Arg Val Ser Asp Asp Asn Ala Phe Val Glu  
                   260                                  265                                  270  
 Ser Val Phe His Thr Leu Lys Tyr Arg Pro Phe Tyr Pro Lys Val Phe  
           275                                  280                                  285  
 Ala Ser Met Asp Gln Ala Arg Val Trp Val Glu Glu Phe Val Val Tyr  
   290                                  295                                  300  
 Tyr Asn Thr Val His Pro His Ser Gly Val Ala Gly His Thr Pro Gln  
   305                                  310                                  315                                  320  
 Ser Val Phe Asp Gly Ser Trp Arg Ala Ala His Arg Leu Arg Val Gln  
                   325                                  330                                  335  
 Ala Leu Asp Ala His Tyr Arg Gln Phe Pro Gln Arg Tyr Val Gly Arg  
                   340                                  345                                  350  
 Pro Val Val Gln Glu Val Ala Gly Val Val Arg Leu Asn Gly Ala Arg

	355						360						365					
Asp	Asp	Gly	Ser	Val	Gln	Glu	Arg	Val	Gly	Gly	Val	Ala	Ser	Leu	Leu			
	370					375					380							
 Ser Ala 385																		
<210> 255																		
<211> 1065																		
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<213> Corynebacterium glutamicum																		
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tgcacgtcgg	cctgggttttt	tggtccatgg	cgactacaac	atg gtc cac atg gtc	115													
				Met Val His Met Val														
				1	5													
ttc gcc gat atg aac act gac cgt gcg gcg cag gcc tac atc atc gtg	163																	
Phe Gly Asp Met Asn Thr Asp Arg Ala Ala Gln Ala Tyr Ile Ile Val																		
	10		15		20													
atc acc acc atc gtc atg gtg gtg ttg ttc tgg atc gtg ctc aga tat	211																	
Ile Thr Thr Ile Val Met Val Val Leu Phe Trp Ile Val Leu Arg Tyr																		
	25		30		35													
tgg tcg ctg gct gac cgg gcc cgc gcc cag cgg ttc acc gcc agc atc	259																	
Trp Ser Leu Ala Asp Arg Ala Arg Ala Gln Arg Phe Thr Ala Ser Ile																		
	40		45		50													
acg gag atc gga cgc aaa atc ttc ctc aac cgg ctg cgt ccc cgg atg	307																	
Thr Glu Ile Gly Arg Lys Ile Phe Leu Asn Arg Leu Arg Pro Arg Met																		
	55		60		65													
agc agg cag aac acc tac acg gac aag gac atc tcg cag ttc cac tgg	355																	
Ser Arg Gln Asn Thr Tyr Thr Asp Lys Asp Ile Ser Gln Phe His Trp																		
	70		75		80		85											
acc aat ggc ctg ccg ccg acc gat gat gaa tcc ccc gag tgg atc gcc	403																	
Thr Asn Gly Leu Pro Pro Thr Asp Asp Glu Ser Pro Glu Trp Ile Ala																		
	90		95		100													
gcc cgc gac aac gag tgg gag gga tac acc atc acc ctc ggc gac gat	451																	
Ala Arg Asp Asn Glu Trp Glu Gly Tyr Thr Ile Thr Leu Gly Asp Asp																		
	105		110		115													
ccc aac ggc acc gag aaa acc atc acc ctc gac gat ctg cgg gag ctg	499																	
Pro Asn Gly Thr Glu Lys Thr Ile Thr Leu Asp Asp Leu Arg Glu Leu																		
	120		125		130													

ccg cag acc tcg tat gtc gcc gtc cac acg tgc atg cag ggc tgg tca 547  
 Pro Gln Thr Ser Tyr Val Ala Val His Thr Cys Met Gln Gly Trp Ser  
 135 140 145  
  
 gct acc gcc cgg tgg aca ggg gtg cgg tta cgt gat gtt ttg tgt cat 595  
 Ala Thr Ala Arg Trp Thr Gly Val Arg Leu Arg Asp Val Leu Cys His  
 150 155 160 165  
  
 gac ctt gtg cac acc cta gac ctt cac cac agg cat agt cct cgg ctg 643  
 Asp Leu Val His Thr Leu Asp Leu His His Arg His Ser Pro Arg Leu  
 170 175 180  
  
 ctc aca att gag atc ata cct aaa ccc ctg ccc cca gaa acc cga tgc 691  
 Leu Thr Ile Glu Ile Ile Pro Lys Pro Leu Pro Pro Glu Thr Arg Cys  
 185 190 195  
  
 aag atc atc gat ttc gat ctg ttc gca ccg aac agt ccc tcg atc gaa 739  
 Lys Ile Ile Asp Phe Asp Leu Phe Ala Pro Asn Ser Pro Ser Ile Glu  
 200 205 210  
  
 gag ttc tgc agt cgg ctt aaa ata tcg cgg cgc agc ttc tac aac atc 787  
 Glu Phe Cys Ser Arg Leu Lys Ile Ser Arg Arg Ser Phe Tyr Asn Ile  
 215 220 225  
  
 cgc aac cga tac caa caa gat gcc agt gca gcg ctg cat cca cgc tcc 835  
 Arg Asn Arg Tyr Gln Gln Asp Ala Ser Ala Ala Leu His Pro Arg Ser  
 230 235 240 245  
  
 agc gcc cag atc acc tcc cgg cga aca tac gat gaa tcc atc acc agt 883  
 Ser Ala Gln Ile Thr Ser Arg Arg Thr Tyr Asp Glu Ser Ile Thr Ser  
 250 255 260  
  
 atc ttg ttg gcc atc cgc gca ccg cct gaa agc cca agg atg gga rta 931  
 Ile Leu Leu Ala Ile Arg Ala Pro Pro Glu Ser Pro Arg Met Gly Xaa  
 265 270 275  
  
 cgg ycc gat ctc tat ycg att cga agg cat ckc cac cgg gga act gac 979  
 Arg Xaa Asp Leu Tyr Xaa Ile Arg Arg His Xaa His Arg Gly Thr Asp  
 280 285 290  
  
 tgc acc gat tcc atc cgt ctc aac tat cgc ttg ctt gtt acg cgc tgc 1027  
 Cys Thr Asp Ser Ile Arg Leu Asn Tyr Arg Leu Val Thr Arg Cys  
 295 300 305  
  
 agg agc agt cga aag taaccctaag aagcgaccaa agt 1065  
 Arg Ser Ser Arg Lys  
 310

&lt;210&gt; 256

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;223&gt; All occurrences of Xaa = any amino acid

&lt;400&gt; 256

Met Val His Met Val Phe Gly Asp Met Asn Thr Asp Arg Ala Ala Gln  
 1 5 10 15

Ala Tyr Ile Ile Val Ile Thr Thr Ile Val Met Val Val Leu Phe Trp  
                             20                            25                            30  
 Ile Val Leu Arg Tyr Trp Ser Leu Ala Asp Arg Ala Arg Ala Gln Arg  
                             35                            40                            45  
 Phe Thr Ala Ser Ile Thr Glu Ile Gly Arg Lys Ile Phe Leu Asn Arg  
                             50                            55                            60  
 Leu Arg Pro Arg Met Ser Arg Gln Asn Thr Tyr Thr Asp Lys Asp Ile  
                             65                            70                            75                            80  
 Ser Gln Phe His Trp Thr Asn Gly Leu Pro Pro Thr Asp Asp Glu Ser  
                             85                            90                            95  
 Pro Glu Trp Ile Ala Ala Arg Asp Asn Glu Trp Glu Gly Tyr Thr Ile  
                             100                            105                            110  
 Thr Leu Gly Asp Asp Pro Asn Gly Thr Glu Lys Thr Ile Thr Leu Asp  
                             115                            120                            125  
 Asp Leu Arg Glu Leu Pro Gln Thr Ser Tyr Val Ala Val His Thr Cys  
                             130                            135                            140  
 Met Gln Gly Trp Ser Ala Thr Ala Arg Trp Thr Gly Val Arg Leu Arg  
                             145                            150                            155                            160  
 Asp Val Leu Cys His Asp Leu Val His Thr Leu Asp Leu His His Arg  
                             165                            170                            175  
 His Ser Pro Arg Leu Leu Thr Ile Glu Ile Ile Pro Lys Pro Leu Pro  
                             180                            185                            190  
 Pro Glu Thr Arg Cys Lys Ile Ile Asp Phe Asp Leu Phe Ala Pro Asn  
                             195                            200                            205  
 Ser Pro Ser Ile Glu Glu Phe Cys Ser Arg Leu Lys Ile Ser Arg Arg  
                             210                            215                            220  
 Ser Phe Tyr Asn Ile Arg Asn Arg Tyr Gln Gln Asp Ala Ser Ala Ala  
                             225                            230                            235                            240  
 Leu His Pro Arg Ser Ser Ala Gln Ile Thr Ser Arg Arg Thr Tyr Asp  
                             245                            250                            255  
 Glu Ser Ile Thr Ser Ile Leu Leu Ala Ile Arg Ala Pro Pro Glu Ser  
                             260                            265                            270  
 Pro Arg Met Gly Xaa Arg Xaa Asp Leu Tyr Xaa Ile Arg Arg His Xaa  
                             275                            280                            285  
 His Arg Gly Thr Asp Cys Thr Asp Ser Ile Arg Leu Asn Tyr Arg Leu  
                             290                            295                            300  
 Leu Val Thr Arg Cys Arg Ser Ser Arg Lys  
                             305                            310

&lt;210&gt; 257

&lt;211&gt; 951

&lt;212&gt; DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(928)

<223> RXN03070

<400> 257

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gtggataaaa gggaaaacat aggggtcatg aaatagaaca agcacgaggc ctggtaaata 60

cgaattcgac caagaaaacg taaacaccccc aggagtactc gtg cct gcc ctt cca 115
                               Val Pro Ala Leu Pro
                               1 5

tca tct atc atc gac ccc ctc tgg cgc cag ttc tcc gcc tta atc cca 163
Ser Ser Ile Ile Asp Pro Leu Trp Arg Gln Phe Ser Ala Leu Ile Pro
                               10 15 20

ccg gtt atc atc acc cac cca cta ggg tgc cac cgt gca cgc att gct 211
Pro Val Ile Ile Thr His Pro Leu Gly Cys His Arg Ala Arg Ile Ala
                               25 30 35

gac cgg atc atc gtc gac aaa ctc atc gca gtg ctt gtc ctc ggt gtc 259
Asp Arg Ile Ile Val Asp Lys Leu Ile Ala Val Leu Val Leu Gly Val
                               40 45 50

tcc tat atc aag att tcc gat tcc acc tgc tca gcc acc acg ata cgc 307
Ser Tyr Ile Lys Ile Ser Asp Ser Thr Cys Ser Ala Thr Thr Ile Arg
                               55 60 65

acc cgc cga gac gag tgg atc act gcc ggg att ttc aag aat tta gaa 355
Thr Arg Arg Asp Glu Trp Ile Thr Ala Gly Ile Phe Lys Asn Leu Glu
                               70 75 80 85

cag atc tgt ctg gag tcc tac gac cgt ttc atc ggg tta gac cta gaa 403
Gln Ile Cys Leu Glu Ser Tyr Asp Arg Phe Ile Gly Leu Asp Leu Glu
                               90 95 100

aac tta aat gtt gat ggc tgc att gtt aaa gct ccc tgc ggc gga gag 451
Asn Leu Asn Val Asp Gly Cys Ile Val Lys Ala Pro Cys Gly Gly Glu
                               105 110 115

gta gcc ggc aga ttc ccg gtt gac cgg gaa aaa ggc acc aaa cgc tcg 499
Val Ala Gly Arg Phe Pro Val Asp Arg Glu Lys Gly Thr Lys Arg Ser
                               120 125 130

tta atg gtc gat gga cat gga atc ccg atc ggg tgc gtg gtc gcc gga 547
Leu Met Val Asp Gly His Gly Ile Pro Ile Gly Cys Val Val Ala Gly
                               135 140 145

gcc aat cgg cat gat tta ccg ttg tta gct gca acc ttg gac acg ctc 595
Ala Asn Arg His Asp Leu Pro Leu Leu Ala Ala Thr Leu Asp Thr Leu
                               150 155 160 165

ggc cgg ttt ggg ggc tct ctt ccc gat cag atc acg gtg cat ctc gat 643
Gly Arg Phe Gly Gly Ser Leu Pro Asp Gln Ile Thr Val His Leu Asp
                               170 175 180

gct ggg tat gac tcg aag aaa acc cgc agg cta ctc agc gaa ttt ggt 691
Ala Gly Tyr Asp Ser Lys Lys Thr Arg Arg Leu Leu Ser Glu Phe Gly
                               185 190 195

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tat agc tgg gtg atc agc att aaa ggt gag ccg ctg cag gct ggg act 739  
 Tyr Ser Trp Val Ile Ser Ile Lys Gly Glu Pro Leu Gln Ala Gly Thr  
 200 205 210  
  
 cgg tgg gtg gtg gag cgt act aac tct tgg cat aac cgg ggt ttt aag 787  
 Arg Trp Val Val Glu Arg Thr Asn Ser Trp His Asn Arg Gly Phe Lys  
 215 220 225  
  
 aaa ctt agt atc tgc acc gaa cgt tgt acc cgg gtt gtg gaa gcg ttt 835  
 Lys Leu Ser Ile Cys Thr Glu Arg Cys Thr Arg Val Val Glu Ala Phe  
 230 235 240 245  
  
 atc gct tta gcc aac gcg gtg att att ctg cgt cgg ctt atc aaa cag 883  
 Ile Ala Leu Ala Asn Ala Val Ile Ile Leu Arg Arg Leu Ile Lys Gln  
 250 255 260  
  
 gcc tgg act agt tac cgc tgg gac acc cga ccg ggc cac aga cct 928  
 Ala Trp Thr Ser Tyr Arg Trp Asp Thr Arg Pro Gly His Arg Pro  
 265 270 275  
  
 taatctatcc gcgcaatctc taa 951

<210> 258  
 <211> 276  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 258  
 Val Pro Ala Leu Pro Ser Ser Ile Ile Asp Pro Leu Trp Arg Gln Phe  
 1 5 10 15  
  
 Ser Ala Leu Ile Pro Pro Val Ile Ile Thr His Pro Leu Gly Cys His  
 20 25 30  
  
 Arg Ala Arg Ile Ala Asp Arg Ile Ile Val Asp Lys Leu Ile Ala Val  
 35 40 45  
  
 Leu Val Leu Gly Val Ser Tyr Ile Lys Ile Ser Asp Ser Thr Cys Ser  
 50 55 60  
  
 Ala Thr Thr Ile Arg Thr Arg Arg Asp Glu Trp Ile Thr Ala Gly Ile  
 65 70 75 80  
  
 Phe Lys Asn Leu Glu Gln Ile Cys Leu Glu Ser Tyr Asp Arg Phe Ile  
 85 90 95  
  
 Gly Leu Asp Leu Glu Asn Leu Asn Val Asp Gly Cys Ile Val Lys Ala  
 100 105 110  
  
 Pro Cys Gly Gly Glu Val Ala Gly Arg Phe Pro Val Asp Arg Glu Lys  
 115 120 125  
  
 Gly Thr Lys Arg Ser Leu Met Val Asp Gly His Gly Ile Pro Ile Gly  
 130 135 140  
  
 Cys Val Val Ala Gly Ala Asn Arg His Asp Leu Pro Leu Leu Ala Ala  
 145 150 155 160  
  
 Thr Leu Asp Thr Leu Gly Arg Phe Gly Gly Ser Leu Pro Asp Gln Ile

165										170					175				
Thr	Val	His	Leu	Asp	Ala	Gly	Tyr	Asp	Ser	Lys	Lys	Thr	Arg	Arg	Leu				
			180					185					190						
Leu	Ser	Glu	Phe	Gly	Tyr	Ser	Trp	Val	Ile	Ser	Ile	Lys	Gly	Glu	Pro				
		195					200					205							
Leu	Gln	Ala	Gly	Thr	Arg	Trp	Val	Val	Glu	Arg	Thr	Asn	Ser	Trp	His				
	210					215					220								
Asn	Arg	Gly	Phe	Lys	Lys	Leu	Ser	Ile	Cys	Thr	Glu	Arg	Cys	Thr	Arg				
225					230					235					240				
Val	Val	Glu	Ala	Phe	Ile	Ala	Leu	Ala	Asn	Ala	Val	Ile	Ile	Leu	Arg				
			245					250						255					
Arg	Leu	Ile	Lys	Gln	Ala	Trp	Thr	Ser	Tyr	Arg	Trp	Asp	Thr	Arg	Pro				
			260					265					270						
Gly	His	Arg	Pro																
		275																	

&lt;210&gt; 259

&lt;211&gt; 742

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(742)

&lt;223&gt; RXN03121

&lt;400&gt; 259

ctaggggtgg cgggattgca aaaatccgtc cccgggttcgc catgaaatgc tgattttgat 60

cgaatctttg	cgctaactgt	agggcggggtt	caggggggtga	atg	cac	cac	gag	caa	115
				Met	His	His	Glu	Gln	
				1				5	

ccc	gaa	ggg	tgc	gaa	gtg	ggc	att	cgt	aga	aca	atc	cca	gag	gaa	agc	163
Pro	Glu	Gly	Cys	Glu	Val	Gly	Ile	Arg	Arg	Thr	Ile	Pro	Glu	Glu	Ser	
			10					15						20		

cgt	acg	gct	ttc	ctc	gac	atg	atc	aat	caa	ggg	atg	tca	ggg	ctt	gct	211
Arg	Thr	Ala	Phe	Leu	Asp	Met	Ile	Asn	Gln	Gly	Met	Ser	Gly	Leu	Ala	
		25						30					35			

gcg	tct	aca	gcg	gtc	ggg	gtc	agt	gaa	ttc	acc	ggg	cga	aag	tgg	gcg	259
Ala	Ser	Thr	Ala	Val	Gly	Val	Ser	Glu	Phe	Thr	Gly	Arg	Lys	Trp	Ala	
		40					45				50					

aag	gcc	gcc	ggg	gtg	aaa	ctg	acc	cgc	ggc	ccg	cga	ggg	ggc	aat	gct	307
Lys	Ala	Ala	Gly	Val	Lys	Leu	Thr	Arg	Gly	Pro	Arg	Gly	Gly	Asn	Ala	
	55					60					65					

ttt	gac	acc	gcc	gag	aaa	ctt	gag	att	gca	gcc	agc	atg	cta	gag	aaa	355
Phe	Asp	Thr	Ala	Glu	Lys	Leu	Glu	Ile	Ala	Ala	Ser	Met	Leu	Glu	Lys	
	70				75				80						85	

gga tgc cta ccc cga gaa atc ggc gag tat gtc ggc atg act cgg gcc 403  
 Gly Cys Leu Pro Arg Glu Ile Gly Glu Tyr Val Gly Met Thr Arg Ala  
                     90                    95                    100

aat ata tcc cta tgg cgc aaa caa ggc cca gac aag ctt cgc caa cgc 451  
 Asn Ile Ser Leu Trp Arg Lys Gln Gly Pro Asp Lys Leu Arg Gln Arg  
                     105                    110                    115

gca gcc acc ttg cgc acc ggc aag cga gca gct gaa ttc atc cac gcc 499  
 Ala Ala Thr Leu Arg Thr Gly Lys Arg Ala Ala Glu Phe Ile His Ala  
                     120                    125                    130

ccg gtg atg ggc cct tat tat ggg cca cgc aca ctc cat caa gtg ttg 547  
 Pro Val Met Gly Pro Tyr Tyr Gly Pro Arg Thr Leu His Gln Val Leu  
                     135                    140                    145

cgt gag gac tac aca aca ctg ttt gac gag tta tct gcg ttg ggg ttg 595  
 Arg Glu Asp Tyr Thr Thr Leu Phe Asp Glu Leu Ser Ala Leu Gly Leu  
 150                    155                    160                    165

cca gca cag gtg tgt ggg gcc tta ctt cat ctt gct cca cca cca tca 643  
 Pro Ala Gln Val Cys Gly Ala Leu Leu His Leu Ala Pro Pro Pro Ser  
                     170                    175                    180

tta cgc ttt tct tat atg tcg tgt gta gtg ccg tta ttt gct gat gaa 691  
 Leu Arg Phe Ser Tyr Met Ser Cys Val Val Pro Leu Phe Ala Asp Glu  
                     185                    190                    195

atc aaa atc gta gga caa ggc aca cga tta tcg tta gaa gag aaa atg 739  
 Ile Lys Ile Val Gly Gln Gly Thr Arg Leu Ser Leu Glu Glu Lys Met  
                     200                    205                    210

atg 742  
 Met

&lt;210&gt; 260

&lt;211&gt; 214

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 260

Met His His Glu Gln Pro Glu Gly Cys Glu Val Gly Ile Arg Arg Thr  
   1                    5                    10                    15

Ile Pro Glu Glu Ser Arg Thr Ala Phe Leu Asp Met Ile Asn Gln Gly  
                     20                    25                    30

Met Ser Gly Leu Ala Ala Ser Thr Ala Val Gly Val Ser Glu Phe Thr  
                     35                    40                    45

Gly Arg Lys Trp Ala Lys Ala Ala Gly Val Lys Leu Thr Arg Gly Pro  
                     50                    55                    60

Arg Gly Gly Asn Ala Phe Asp Thr Ala Glu Lys Leu Glu Ile Ala Ala  
                     65                    70                    75                    80

Ser Met Leu Glu Lys Gly Cys Leu Pro Arg Glu Ile Gly Glu Tyr Val  
                     85                    90                    95

Gly Met Thr Arg Ala Asn Ile Ser Leu Trp Arg Lys Gln Gly Pro Asp  
 100 105 110  
 Lys Leu Arg Gln Arg Ala Ala Thr Leu Arg Thr Gly Lys Arg Ala Ala  
 115 120 125  
 Glu Phe Ile His Ala Pro Val Met Gly Pro Tyr Tyr Gly Pro Arg Thr  
 130 135 140  
 Leu His Gln Val Leu Arg Glu Asp Tyr Thr Thr Leu Phe Asp Glu Leu  
 145 150 155 160  
 Ser Ala Leu Gly Leu Pro Ala Gln Val Cys Gly Ala Leu Leu His Leu  
 165 170 175  
 Ala Pro Pro Pro Ser Leu Arg Phe Ser Tyr Met Ser Cys Val Val Pro  
 180 185 190  
 Leu Phe Ala Asp Glu Ile Lys Ile Val Gly Gln Gly Thr Arg Leu Ser  
 195 200 205  
 Leu Glu Glu Lys Met Met  
 210

<210> 261  
 <211> 484  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(484)  
 <223> RXN03161

<400> 261  
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 gttggggcag taggaagacc ggcgtggaat aatcagggtcc atg ggc atc ttc tcc 115  
 Met Gly Ile Phe Ser  
 1 5  
 ggt cgg cag ttc cct cgt gaa atc atc ctg tgg gcg gtg cgg tgg tac 163  
 Gly Arg Gln Phe Pro Arg Glu Ile Ile Leu Trp Ala Val Arg Trp Tyr  
 10 15 20  
 tgc cgc tac ggc gtg agc tat cgc gac ctc gaa gag atg atg acc gag 211  
 Cys Arg Tyr Gly Val Ser Tyr Arg Asp Leu Glu Glu Met Met Thr Glu  
 25 30 35  
 cgg gga gtg ccg gtc gat cac acc acg atc tac cgc tgg gtc cag aaa 259  
 Arg Gly Val Pro Val Asp His Thr Ile Tyr Arg Trp Val Gln Lys  
 40 45 50  
 tat gct cct gag ctg gat aag aag acc cgg tgg tat cgg caa gtt cct 307  
 Tyr Ala Pro Glu Leu Asp Lys Lys Thr Arg Trp Tyr Arg Gln Val Pro  
 55 60 65  
 gac tgg cag gcc agg tcc tgg cgg gtg gat gag acc tat atc cgg gtc 355  
 Asp Trp Gln Ala Arg Ser Trp Arg Val Asp Glu Thr Tyr Ile Arg Val  
 70 75 80 85

cgt ttc ctg gcg aag acg ctg cgg tcg aat aat 484  
Arg Phe Leu Ala Lys Thr Leu Arg Ser Asn Asn  
120 125

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<210> 262
<211> 128
<212> PRT
<213> Corynebacterium glutamicum
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<400> 262															
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Ala	Val	Arg	Trp	Tyr	Cys	Arg	Tyr	Gly	Val	Ser	Tyr	Arg	Asp	Leu	Glu
			20					25					30		
Glu	Met	Met	Thr	Glu	Arg	Gly	Val	Pro	Val	Asp	His	Thr	Thr	Ile	Tyr
		35					40					45			
Arg	Trp	Val	Gln	Lys	Tyr	Ala	Pro	Glu	Leu	Asp	Lys	Lys	Thr	Arg	Trp
	50					55					60				
Tyr	Arg	Gln	Val	Pro	Asp	Trp	Gln	Ala	Arg	Ser	Trp	Arg	Val	Asp	Glu
65					70					75					80
Thr	Tyr	Ile	Arg	Val	Gly	Gly	Lys	Trp	Cys	Tyr	Leu	Tyr	Arg	Ala	Ile
				85					90					95	
Thr	Ala	Gly	Ser	Gln	Thr	Leu	Asp	Phe	Tyr	Leu	Ser	Pro	Lys	Arg	Asn
			100					105					110		
Val	Ala	Ala	Ala	Lys	Arg	Phe	Leu	Ala	Lys	Thr	Leu	Arg	Ser	Asn	Asn
		115					120					125			

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<210> 263
<211> 393
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (50) .. (370)
<223> RXN03165
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<400> 263
gggggtaatc ataaggcgtc cactgtgacg gaatgcgttg gtgaagatc atg ggt aat 58
                                     Met Gly Asn
                                     1
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ttg ccg cag gcg ttg cgt cat agt ttt acg tgg gat cag ggt gtg cag 106

Leu Pro Gln Ala Leu Arg His Ser Phe Thr Trp Asp Gln Gly Val Gln  
           5                          10                          15  
 atg gca gag cat gcc cgg tta agc gtg gtg acc aag tgc ccg gtg ttt 154  
 Met Ala Glu His Ala Arg Leu Ser Val Val Thr Lys Cys Pro Val Phe  
   20                          25                          30                          35  
 ttc tgt gat cct cat tcg ccg tgg cag cgt ggg tcg aat gag aat acg 202  
 Phe Cys Asp Pro His Ser Pro Trp Gln Arg Gly Ser Asn Glu Asn Thr  
                           40                          45                          50  
 aat gga ttg gtc agg gat ttt ttc ccg aag ggc act aat ttt gct aaa 250  
 Asn Gly Leu Val Arg Asp Phe Phe Pro Lys Gly Thr Asn Phe Ala Lys  
                           55                          60                          65  
 gta agt gac gaa gaa gtt cag cgg gca cag gat atg ctg aat tac cga 298  
 Val Ser Asp Glu Glu Val Gln Arg Ala Gln Asp Met Leu Asn Tyr Arg  
                           70                          75                          80  
 ccg cgg aaa atg cat ggt ttt aaa agc gcg acg cag gta tat gaa ata 346  
 Pro Arg Lys Met His Gly Phe Lys Ser Ala Thr Gln Val Tyr Glu Ile  
                           85                          90                          95  
 atc gta gtt ggt gca tcc acg gat tgaattcgcc taggagattg tgc 393  
 Ile Val Val Gly Ala Ser Thr Asp  
 100                          105

&lt;210&gt; 264

&lt;211&gt; 107

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 264

Met Gly Asn Leu Pro Gln Ala Leu Arg His Ser Phe Thr Trp Asp Gln  
   1                          5                          10                          15  
 Gly Val Gln Met Ala Glu His Ala Arg Leu Ser Val Val Thr Lys Cys  
                           20                          25                          30  
 Pro Val Phe Phe Cys Asp Pro His Ser Pro Trp Gln Arg Gly Ser Asn  
                           35                          40                          45  
 Glu Asn Thr Asn Gly Leu Val Arg Asp Phe Phe Pro Lys Gly Thr Asn  
                           50                          55                          60  
 Phe Ala Lys Val Ser Asp Glu Glu Val Gln Arg Ala Gln Asp Met Leu  
                           65                          70                          75                          80  
 Asn Tyr Arg Pro Arg Lys Met His Gly Phe Lys Ser Ala Thr Gln Val  
                           85                          90                          95  
 Tyr Glu Ile Ile Val Val Gly Ala Ser Thr Asp  
                           100                          105

&lt;210&gt; 265

&lt;211&gt; 423

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(400)

&lt;223&gt; RXN00083

&lt;400&gt; 265

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gaagatacacg ggggccacgg tggggtggtg aacaagagca ggcacgaggc ctggtagata 60

cggattcgac caagaaaacg tacaccactc aggagcactc gtg ctt gcc ctt cca 115
                               Val Leu Ala Leu Pro
                               1 5

tcc tct atc atc gac ccc ctc tgg tgc cag ttc gcc gcg ctg atc cca 163
Ser Ser Ile Ile Asp Pro Leu Trp Cys Gln Phe Ala Ala Leu Ile Pro
                10                15                20

ccc gtg acc gac acc cac cca ctt cgg tgc cac cgc cca cgc atc ccg 211
Pro Val Thr Asp Thr His Pro Leu Arg Cys His Arg Pro Arg Ile Pro
                25                30                35

gac cgg atc atc ttc gac aag ctc atc cag gtc ctc gtc ctc ggc gcc 259
Asp Arg Ile Ile Phe Asp Lys Leu Ile Gln Val Leu Val Leu Gly Ala
                40                45                50

tcc tat gcc aag atc gcc gac acg aca tgc tcg gcc acc acc ttg cgc 307
Ser Tyr Ala Lys Ile Ala Asp Thr Thr Cys Ser Ala Thr Thr Leu Arg
                55                60                65

acc cgc cgg gac gag tgg atc acc gct ggc atc ttc gag cag ctg gaa 355
Thr Arg Arg Asp Glu Trp Ile Thr Ala Gly Ile Phe Glu Gln Leu Glu
                70                75                80                85

cag atc tgt ttg gaa ttc tac gac cgt atc gtc gga ctc gat ctc 400
Gln Ile Cys Leu Glu Phe Tyr Asp Arg Ile Val Gly Leu Asp Leu
                90                95                100

taagttcgga ttggctcgaa ttg 423

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&lt;210&gt; 266

&lt;211&gt; 100

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 266

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Val Leu Ala Leu Pro Ser Ser Ile Ile Asp Pro Leu Trp Cys Gln Phe
  1 5 10 15

Ala Ala Leu Ile Pro Pro Val Thr Asp Thr His Pro Leu Arg Cys His
  20 25 30

Arg Pro Arg Ile Pro Asp Arg Ile Ile Phe Asp Lys Leu Ile Gln Val
  35 40 45

Leu Val Leu Gly Ala Ser Tyr Ala Lys Ile Ala Asp Thr Thr Cys Ser
  50 55 60

Ala Thr Thr Leu Arg Thr Arg Arg Asp Glu Trp Ile Thr Ala Gly Ile
  65 70 75 80

Phe Glu Gln Leu Glu Gln Ile Cys Leu Glu Phe Tyr Asp Arg Ile Val

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85

90

95

Gly Leu Asp Leu  
100

<210> 267  
<211> 230  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (1)..(207)  
<223> RXN02004

<400> 267  
cgc gtc ggc cgt ctg atg cgt cag aac ggc att ctc atc atc cgc agc 48  
Arg Val Gly Arg Leu Met Arg Gln Asn Gly Ile Leu Ile Ile Arg Ser  
1 5 10 15  
  
cgg aag ttc aag cgc acg acc ggc agc gat cat acc ttc aac atc gca 96  
Arg Lys Phe Lys Arg Thr Thr Gly Ser Asp His Thr Phe Asn Ile Ala  
20 25 30  
  
ccg aac ttt ctg cag cag gac ttt atg gcg agc agg ccg aac cag aag 144  
Pro Asn Phe Leu Gln Gln Asp Phe Met Ala Ser Arg Pro Asn Gln Lys  
35 40 45  
  
tgg gcg ggc gac atc acc tat gtc tgg acg cgc gag ggc ctg ggt cta 192  
Trp Ala Gly Asp Ile Thr Tyr Val Trp Thr Arg Glu Gly Leu Gly Leu  
50 55 60  
  
tct ggc cga cat tct tgacctttat ccccgccggg tga 230  
Ser Gly Arg His Ser  
65

<210> 268  
<211> 69  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 268  
Arg Val Gly Arg Leu Met Arg Gln Asn Gly Ile Leu Ile Ile Arg Ser  
1 5 10 15  
  
Arg Lys Phe Lys Arg Thr Thr Gly Ser Asp His Thr Phe Asn Ile Ala  
20 25 30  
  
Pro Asn Phe Leu Gln Gln Asp Phe Met Ala Ser Arg Pro Asn Gln Lys  
35 40 45  
  
Trp Ala Gly Asp Ile Thr Tyr Val Trp Thr Arg Glu Gly Leu Gly Leu  
50 55 60  
  
Ser Gly Arg His Ser  
65

<210> 269

<211> 675  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(652)  
 <223> RXN02287

<400> 269  
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 acatctggcc ctcaaaatct tccttttact ggagaccact gtg tac tca att tca 115  
 Val Tyr Ser Ile Ser  
 1 5  
 gaa act atc gcc cga act ctt atg ccc cgc acc gat cac gtt ttc gac 163  
 Glu Thr Ile Ala Arg Thr Leu Met Pro Arg Thr Asp His Val Phe Asp  
 10 15 20  
 ctg atg ggc aac gga aac gcc tgg ttc gtc gat gcc cta gaa cgc ctc 211  
 Leu Met Gly Asn Gly Asn Ala Trp Phe Val Asp Ala Leu Glu Arg Leu  
 25 30 35  
 ggg cga ggc atc atc acc gtc cgc ccc aca gtt gaa acc gtg gcc gcc 259  
 Gly Arg Gly Ile Ile Thr Val Arg Pro Thr Val Glu Thr Val Ala Ala  
 40 45 50  
 gcg gac acc tac cac cgc gtc acc cgc cgc ccg gcg gtc gct acc acc 307  
 Ala Asp Thr Tyr His Arg Val Thr Arg Arg Pro Ala Val Ala Thr Thr  
 55 60 65  
 acc tat ggt gct ggt ttc acc aac acc atg acc acg ctt gcc gac gtc 355  
 Thr Tyr Gly Ala Gly Phe Thr Asn Thr Met Thr Thr Leu Ala Asp Val  
 70 75 80 85  
 gcc ctc tcc cgt atc cca ctt ctt tta gtt gtg ggc act gcc ccg agc 403  
 Ala Leu Ser Arg Ile Pro Leu Leu Leu Val Val Gly Thr Ala Pro Ser  
 90 95 100  
 gcc ggg cct cgc tgt ttc gac att gac cgg caa gga ctc gca cgt gcc 451  
 Ala Gly Pro Arg Cys Phe Asp Ile Asp Arg Gln Gly Leu Ala Arg Ala  
 105 110 115  
 gta ggt gtg gaa acc ttc acc gtg cat gca gat gac gtt gct gcg gta 499  
 Val Gly Val Glu Thr Phe Thr Val His Ala Asp Asp Val Ala Ala Val  
 120 125 130  
 act ctt cag gct tgg aat aat acg ccg gaa aac aca cac gtg atc ctg 547  
 Thr Leu Gln Ala Trp Asn Asn Thr Pro Glu Asn Thr His Val Ile Leu  
 135 140 145  
 gaa atc ccc tat gac cta gca gct gcc aca gcc acc gat cca aca gtg 595  
 Glu Ile Pro Tyr Asp Leu Ala Ala Ala Thr Ala Thr Asp Pro Thr Val  
 150 155 160 165  
 act aca tac ctg ctg cgc ccc gga ttt cag aaa ctc ccg atg tca ccg 643  
 Thr Thr Tyr Leu Leu Arg Pro Gly Phe Gln Lys Leu Pro Met Ser Pro  
 170 175 180  
 acc ttg tcc tagctctacg caatgcccaa aat 675

Thr Leu Ser

<210> 270  
 <211> 184  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 270  
 Val Tyr Ser Ile Ser Glu Thr Ile Ala Arg Thr Leu Met Pro Arg Thr  
   1                  5                  10                  15  
 Asp His Val Phe Asp Leu Met Gly Asn Gly Asn Ala Trp Phe Val Asp  
                   20                  25                  30  
 Ala Leu Glu Arg Leu Gly Arg Gly Ile Ile Thr Val Arg Pro Thr Val  
                   35                  40                  45  
 Glu Thr Val Ala Ala Ala Asp Thr Tyr His Arg Val Thr Arg Arg Pro  
                   50                  55                  60  
 Ala Val Ala Thr Thr Thr Tyr Gly Ala Gly Phe Thr Asn Thr Met Thr  
   65                  70                  75                  80  
 Thr Leu Ala Asp Val Ala Leu Ser Arg Ile Pro Leu Leu Leu Val Val  
                   85                  90                  95  
 Gly Thr Ala Pro Ser Ala Gly Pro Arg Cys Phe Asp Ile Asp Arg Gln  
                   100                  105                  110  
 Gly Leu Ala Arg Ala Val Gly Val Glu Thr Phe Thr Val His Ala Asp  
                   115                  120                  125  
 Asp Val Ala Ala Val Thr Leu Gln Ala Trp Asn Asn Thr Pro Glu Asn  
   130                  135                  140  
 Thr His Val Ile Leu Glu Ile Pro Tyr Asp Leu Ala Ala Ala Thr Ala  
 145                  150                  155                  160  
 Thr Asp Pro Thr Val Thr Thr Tyr Leu Leu Arg Pro Gly Phe Gln Lys  
                   165                  170                  175  
 Leu Pro Met Ser Pro Thr Leu Ser  
                   180

<210> 271  
 <211> 1431  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1408)  
 <223> RXN02963

<400> 271  
 aacctgggct agcgggtgtag acccgaaaat aaacgagcct tttgtcaggg ttaaggttta 60  
 ggtatctaag ctaaccaaac accaacaataa ggctctaccc atg aag tct acc ggc 115

											Met 1	Lys	Ser	Thr	Gly 5	
aac Asn	atc Ile	atc Ile	gct Ala	gac Asp 10	acc Thr	atc Ile	tgc Cys	cgc Arg	act Thr 15	gcg Ala	gaa Glu	cta Leu	gga Gly	ctc Leu 20	acc Thr	163
atc Ile	acc Thr	ggc Gly	gct Ala 25	tcc Ser	gat Asp	gca Ala	ggt Gly	gat Asp 30	tac Tyr	acc Thr	ctg Leu	atc Ile	gaa Glu 35	gca Ala	gac Asp	211
gca Ala	ctc Leu	gac Asp 40	tac Tyr	acc Thr	tcc Ser	acc Thr	tgc Cys 45	cca Pro	gaa Glu	tgc Cys	tcc Ser	caa Gln 50	cct Pro	ggg Gly	gtg Val	259
ttt Phe	cgt Arg 55	cat His	cac His	acc Thr	cac His	cgg Arg 60	atg Met	ctc Leu	att Ile	gat Asp	tta Leu 65	ccc Pro	atc Ile	gtc Val	ggg Gly	307
ttt Phe 70	ccc Pro	acc Thr	aaa Lys	ctg Leu	ttt Phe 75	atc Ile	cgt Arg	cta Leu	cct Pro	cgc Arg 80	tac Tyr	cgc Arg	tgc Cys	acc Thr	aac Asn 85	355
ccc Pro	aca Thr	tgt Cys	aag Lys	caa Gln 90	aag Lys	tat Tyr	ttc Phe	caa Gln 95	gca Ala	gaa Glu	cta Leu	agc Ser	tgc Cys	gct Ala 100	gac Asp	403
cac His	ggt Gly	aaa Lys	aag Lys 105	gtc Val	acc Thr	cac His	cgg Arg	gtc Val 110	acc Thr	cgc Arg	tgg Trp	att Ile	tta Leu 115	caa Gln	cgc Arg	451
ctt Leu	gct Ala	att Ile 120	gac Asp	cgg Arg	atg Met	agt Ser	gtt Val 125	cac His	gca Ala	acc Thr	gcg Ala	aaa Lys 130	gca Ala	ctt Leu	ggg Gly	499
cta Leu	ggg Gly 135	tgg Trp	gat Asp	tta Leu	acc Thr	tgc Cys 140	caa Gln	cta Leu	gcc Ala	ctc Leu	gat Asp 145	atg Met	tgc Cys	cgt Arg	gag Glu	547
ctg Leu 150	gtc Val	tat Tyr	aac Asn	gat Asp	cct Pro 155	cac His	cat His	ctt Leu	gat Asp	gga Gly 160	gtg Val	tat Tyr	gtc Val	att Ile	ggg Gly 165	595
gtg Val	gat Asp	gag Glu	cat His	aag Lys 170	tgg Trp	tca Ser	cat His	aat Asn	agg Arg 175	gct Ala	aag Lys	cat His	ggt Gly	gat Asp 180	ggg Gly	643
ttt Phe	gtc Val	acc Thr	gtg Val 185	att Ile	gtc Val	gat Asp	atg Met	acc Thr 190	ggg Gly	cat His	cgg Arg	tat Tyr	gac Asp 195	tca Ser	cgg Arg	691
tgt Cys	cct Pro	gcc Ala 200	cgg Arg	tta Leu	tta Leu	gat Asp	gtc Val 205	gtc Val	cca Pro	ggt Gly	cgt Arg	agt Ser 210	gct Ala	gat Asp	gct Ala	739
tta Leu	cgg Arg 215	tcc Ser	tgg Trp	ctt Leu	ggc Gly	tcc Ser 220	cgc Arg	ggt Gly	gaa Glu	cag Gln	ttc Phe 225	cgc Arg	aat Asn	cag Gln	ata Ile	787
cgg Arg	atc Ile	gtg Val	tcc Ser	atg Met	gat Asp	gga Gly	ttc Phe	caa Gln	ggc Gly	tac Tyr	gcc Ala	aca Thr	gca Ala	agt Ser	aaa Lys	835

230	235	240	245	
gaa ctc att cct tct gct cgt cgc gtg atg gat cca ttc cat gtt gtg				883
Glu Leu Ile Pro Ser Ala Arg Arg Val Met Asp Pro Phe His Val Val				
	250	255	260	
cgg ctt gct ggt gac aag ctc acc gcc tgc cgg caa cgc ctc cag cgg				931
Arg Leu Ala Gly Asp Lys Leu Thr Ala Cys Arg Gln Arg Leu Gln Arg				
	265	270	275	
gag aaa tac cag cgt cgt ggt tta agc cag gat ccg ttg tat aaa aac				979
Glu Lys Tyr Gln Arg Arg Gly Leu Ser Gln Asp Pro Leu Tyr Lys Asn				
	280	285	290	
cgg aag acc ttg ttg acc acg cac aag tgg ttg agt cct cgt cag caa				1027
Arg Lys Thr Leu Leu Thr Thr His Lys Trp Leu Ser Pro Arg Gln Gln				
	295	300	305	
gaa agc ttg gag cag ttg tgg gcg tat gac aaa gac tac ggg gcg tta				1075
Glu Ser Leu Glu Gln Leu Trp Ala Tyr Asp Lys Asp Tyr Gly Ala Leu				
	310	315	320	325
aag ctt gcg tgg ctt gcg tat cag gcg att att gat tgt tat cag atg				1123
Lys Leu Ala Trp Leu Ala Tyr Gln Ala Ile Ile Asp Cys Tyr Gln Met				
	330	335	340	
ggt aat aag cgt gaa gcg aag aag aaa atg cgg acc att att gat cag				1171
Gly Asn Lys Arg Glu Ala Lys Lys Lys Met Arg Thr Ile Ile Asp Gln				
	345	350	355	
ctt cgg gtg ttg aag ggg ccg aat aag gaa ctc gcg cag ttg ggt cgt				1219
Leu Arg Val Leu Lys Gly Pro Asn Lys Glu Leu Ala Gln Leu Gly Arg				
	360	365	370	
agt ttg ttt aaa cga ctt ggt gat gtg ttg gcg tat ttc gat gtt ggt				1267
Ser Leu Phe Lys Arg Leu Gly Asp Val Leu Ala Tyr Phe Asp Val Gly				
	375	380	385	
gtc tcc aac ggt ccg gtc gaa gcg atc aac gga cgg ttg gag cat ttg				1315
Val Ser Asn Gly Pro Val Glu Ala Ile Asn Gly Arg Leu Glu His Leu				
	390	395	400	405
cgt ggg att gct cta ggt ttc cgt aat ttg aac cac tac att ctg cgg				1363
Arg Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn His Tyr Ile Leu Arg				
	410	415	420	
tgc ctt atc cat tca ggg cag ttg gtc cat aag atc aat gca ctc				1408
Cys Leu Ile His Ser Gly Gln Leu Val His Lys Ile Asn Ala Leu				
	425	430	435	
taaaacagga agagccagta aac				1431

&lt;210&gt; 272

&lt;211&gt; 436

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 272

Met	Lys	Ser	Thr	Gly	Asn	Ile	Ile	Ala	Asp	Thr	Ile	Cys	Arg	Thr	Ala
1				5					10					15	

Glu Leu Gly Leu Thr Ile Thr Gly Ala Ser Asp Ala Gly Asp Tyr Thr  
                   20                                  25                                  30  
 Leu Ile Glu Ala Asp Ala Leu Asp Tyr Thr Ser Thr Cys Pro Glu Cys  
                   35                                  40                                  45  
 Ser Gln Pro Gly Val Phe Arg His His Thr His Arg Met Leu Ile Asp  
                   50                                  55                                  60  
 Leu Pro Ile Val Gly Phe Pro Thr Lys Leu Phe Ile Arg Leu Pro Arg  
                   65                                  70                                  75                                  80  
 Tyr Arg Cys Thr Asn Pro Thr Cys Lys Gln Lys Tyr Phe Gln Ala Glu  
                                   85                                  90                                  95  
 Leu Ser Cys Ala Asp His Gly Lys Lys Val Thr His Arg Val Thr Arg  
                   100                                  105                                  110  
 Trp Ile Leu Gln Arg Leu Ala Ile Asp Arg Met Ser Val His Ala Thr  
                   115                                  120                                  125  
 Ala Lys Ala Leu Gly Leu Gly Trp Asp Leu Thr Cys Gln Leu Ala Leu  
                   130                                  135                                  140  
 Asp Met Cys Arg Glu Leu Val Tyr Asn Asp Pro His His Leu Asp Gly  
                   145                                  150                                  155                                  160  
 Val Tyr Val Ile Gly Val Asp Glu His Lys Trp Ser His Asn Arg Ala  
                                   165                                  170                                  175  
 Lys His Gly Asp Gly Phe Val Thr Val Ile Val Asp Met Thr Gly His  
                   180                                  185                                  190  
 Arg Tyr Asp Ser Arg Cys Pro Ala Arg Leu Leu Asp Val Val Pro Gly  
                   195                                  200                                  205  
 Arg Ser Ala Asp Ala Leu Arg Ser Trp Leu Gly Ser Arg Gly Glu Gln  
                   210                                  215                                  220  
 Phe Arg Asn Gln Ile Arg Ile Val Ser Met Asp Gly Phe Gln Gly Tyr  
                   225                                  230                                  235                                  240  
 Ala Thr Ala Ser Lys Glu Leu Ile Pro Ser Ala Arg Arg Val Met Asp  
                                   245                                  250                                  255  
 Pro Phe His Val Val Arg Leu Ala Gly Asp Lys Leu Thr Ala Cys Arg  
                   260                                  265                                  270  
 Gln Arg Leu Gln Arg Glu Lys Tyr Gln Arg Arg Gly Leu Ser Gln Asp  
                   275                                  280                                  285  
 Pro Leu Tyr Lys Asn Arg Lys Thr Leu Leu Thr Thr His Lys Trp Leu  
                   290                                  295                                  300  
 Ser Pro Arg Gln Gln Glu Ser Leu Glu Gln Leu Trp Ala Tyr Asp Lys  
                   305                                  310                                  315                                  320  
 Asp Tyr Gly Ala Leu Lys Leu Ala Trp Leu Ala Tyr Gln Ala Ile Ile  
                                   325                                  330                                  335

Asp Cys Tyr Gln Met Gly Asn Lys Arg Glu Ala Lys Lys Lys Met Arg  
 340 345 350  
 Thr Ile Ile Asp Gln Leu Arg Val Leu Lys Gly Pro Asn Lys Glu Leu  
 355 360 365  
 Ala Gln Leu Gly Arg Ser Leu Phe Lys Arg Leu Gly Asp Val Leu Ala  
 370 375 380  
 Tyr Phe Asp Val Gly Val Ser Asn Gly Pro Val Glu Ala Ile Asn Gly  
 385 390 395 400  
 Arg Leu Glu His Leu Arg Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn  
 405 410 415  
 His Tyr Ile Leu Arg Cys Leu Ile His Ser Gly Gln Leu Val His Lys  
 420 425 430  
 Ile Asn Ala Leu  
 435

<210> 273  
 <211> 2787  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(2764)  
 <223> RXA02788

<400> 273  
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 cgctaaaaca tttcgagaag ttctaaggca ggataccgct gtg cag acc cat gag 115  
 Val Gln Thr His Glu  
 1 5  
 atc agg gag cgt ttt acc aat cac ttc gtc aat gcc ggt cac cag gcg 163  
 Ile Arg Glu Arg Phe Thr Asn His Phe Val Asn Ala Gly His Gln Ala  
 10 15 20  
 gta cct agc gcg tca ctg att ctc gac gac cct aac ctg ctg ttc gtt 211  
 Val Pro Ser Ala Ser Leu Ile Leu Asp Asp Pro Asn Leu Leu Phe Val  
 25 30 35  
 aac gca ggc atg gtt cca ttc aag ccg tac ttc ctg ggc cag cag acc 259  
 Asn Ala Gly Met Val Pro Phe Lys Pro Tyr Phe Leu Gly Gln Gln Thr  
 40 45 50  
 cca cct ttt gaa aac ggc act gcg act tcc att cag aag tgt gtt cgt 307  
 Pro Pro Phe Glu Asn Gly Thr Ala Thr Ser Ile Gln Lys Cys Val Arg  
 55 60 65  
 acc ctg gat atc gaa gaa gtg ggt atc acc act cgc cac aat acc ttc 355  
 Thr Leu Asp Ile Glu Glu Val Gly Ile Thr Thr Arg His Asn Thr Phe  
 70 75 80 85  
 ttc cag atg gca ggt aac ttc tcc ttc ggc cag tac ttc aaa gaa ggc 403  
 Phe Gln Met Ala Gly Asn Phe Ser Phe Gly Gln Tyr Phe Lys Glu Gly

				90					95					100		
gca	att	acc	cac	gca	tgg	ggc	ctt	ctg	act	ggt	tcc	gta	gca	gac	gga	451
Ala	Ile	Thr	His	Ala	Trp	Gly	Leu	Leu	Thr	Gly	Ser	Val	Ala	Asp	Gly	
			105					110					115			
ggc	ttt	ggc	ctt	gat	cca	gag	cgc	ctc	tgg	gtc	act	gtg	tac	ctc	gat	499
Gly	Phe	Gly	Leu	Asp	Pro	Glu	Arg	Leu	Trp	Val	Thr	Val	Tyr	Leu	Asp	
		120					125					130				
gat	gac	gag	gct	gca	gag	atc	tgg	gaa	aag	aag	atc	ggc	gtc	cca	tca	547
Asp	Asp	Glu	Ala	Ala	Glu	Ile	Trp	Glu	Lys	Lys	Ile	Gly	Val	Pro	Ser	
		135				140					145					
gag	cgc	atc	cag	cgc	ctg	ggt	atg	gct	gac	aac	tac	tgg	tcc	atg	ggt	595
Glu	Arg	Ile	Gln	Arg	Leu	Gly	Met	Ala	Asp	Asn	Tyr	Trp	Ser	Met	Gly	
150					155					160					165	
gta	cca	gga	cct	tgt	ggc	cct	tgc	tcc	gag	atc	tac	tac	gac	cgc	ggc	643
Val	Pro	Gly	Pro	Cys	Gly	Pro	Cys	Ser	Glu	Ile	Tyr	Tyr	Asp	Arg	Gly	
			170					175						180		
gag	aag	tac	ggc	aag	gaa	ggc	ggc	cct	gtc	gct	gac	gac	aac	cgc	tac	691
Glu	Lys	Tyr	Gly	Lys	Glu	Gly	Gly	Pro	Val	Ala	Asp	Asp	Asn	Arg	Tyr	
			185					190					195			
atg	gag	atc	tgg	aac	ctg	gtc	ttc	atg	gag	aag	gaa	cgc	gga	cag	ggt	739
Met	Glu	Ile	Trp	Asn	Leu	Val	Phe	Met	Glu	Lys	Glu	Arg	Gly	Gln	Gly	
		200					205					210				
att	ggc	aag	gac	aac	ttc	gac	atc	ctt	ggc	gat	ctt	cca	aag	aag	aac	787
Ile	Gly	Lys	Asp	Asn	Phe	Asp	Ile	Leu	Gly	Asp	Leu	Pro	Lys	Lys	Asn	
		215				220					225					
atc	gat	acc	ggc	atg	ggc	gtc	gag	cgc	gtt	gcc	tgc	atc	ctc	cag	gat	835
Ile	Asp	Thr	Gly	Met	Gly	Val	Glu	Arg	Val	Ala	Cys	Ile	Leu	Gln	Asp	
230					235					240					245	
gtt	gaa	aac	gtc	tac	gaa	acc	gac	ctg	ctg	cgc	cca	gtc	atc	gac	gtt	883
Val	Glu	Asn	Val	Tyr	Glu	Thr	Asp	Leu	Leu	Arg	Pro	Val	Ile	Asp	Val	
			250						255					260		
gca	gag	acc	ctg	acc	gga	acc	aag	tat	ggt	tct	gac	aac	acc	tct	gac	931
Ala	Glu	Thr	Leu	Thr	Gly	Thr	Lys	Tyr	Gly	Ser	Asp	Asn	Thr	Ser	Asp	
			265					270					275			
att	cgc	ttc	cgc	gtt	atc	gcc	gac	cac	tct	cgt	acc	ggc	atg	atg	ctc	979
Ile	Arg	Phe	Arg	Val	Ile	Ala	Asp	His	Ser	Arg	Thr	Gly	Met	Met	Leu	
		280					285					290				
atc	ctc	gat	ggt	gtt	acc	cca	ggc	aac	gaa	ggc	cgt	gga	tac	atc	ctg	1027
Ile	Leu	Asp	Gly	Val	Thr	Pro	Gly	Asn	Glu	Gly	Arg	Gly	Tyr	Ile	Leu	
		295				300					305					
cgc	cgc	ctg	ctt	cgc	cgc	att	atc	cgt	tcc	gca	cgt	ctg	ctc	ggt	gct	1075
Arg	Arg	Leu	Leu	Arg	Arg	Ile	Ile	Arg	Ser	Ala	Arg	Leu	Leu	Gly	Ala	
310					315					320					325	
act	ggt	gag	acc	atg	gag	cag	ttc	atg	aac	acc	atc	atg	gac	acc	atg	1123
Thr	Gly	Glu	Thr	Met	Glu	Gln	Phe	Met	Asn	Thr	Ile	Met	Asp	Thr	Met	
				330					335					340		

acc ccg tcc tac cca gaa atc gcc gac aac cgt gag cgc atc atg cgt	1171
Thr Pro Ser Tyr Pro Glu Ile Ala Asp Asn Arg Glu Arg Ile Met Arg	
345 350 355	
gtg gct gtc acc gaa gag cgc gct ttc ttg aag act ctg gtc tct gga	1219
Val Ala Val Thr Glu Glu Arg Ala Phe Leu Lys Thr Leu Val Ser Gly	
360 365 370	
acc cac ctc ttc gaa gag gct gca acc tcc atc aag gct gca gga tcc	1267
Thr His Leu Phe Glu Glu Ala Ala Thr Ser Ile Lys Ala Ala Gly Ser	
375 380 385	
acc aag gtt gcc ggt gct cag gca ttc gca ctg cac gac acc tac ggt	1315
Thr Lys Val Ala Gly Ala Gln Ala Phe Ala Leu His Asp Thr Tyr Gly	
390 395 400 405	
ttc ccc atc gac ctc acc ctc gaa atg gct gca gaa gca ggc ctt gag	1363
Phe Pro Ile Asp Leu Thr Leu Glu Met Ala Ala Glu Ala Gly Leu Glu	
410 415 420	
gtt gac gtt gaa ggc ttt gat tcc ctc atg gca gag cag cgc tcc cgt	1411
Val Asp Val Glu Gly Phe Asp Ser Leu Met Ala Glu Gln Arg Ser Arg	
425 430 435	
gca aag gct gac agc cag gca aag aag cac ggc cac acc gac ttg agc	1459
Ala Lys Ala Asp Ser Gln Ala Lys Lys His Gly His Thr Asp Leu Ser	
440 445 450	
atc tac cgc gaa tgg gtc gac aac aac cca acc gta ttc acc ggc ttt	1507
Ile Tyr Arg Glu Trp Val Asp Asn Asn Pro Thr Val Phe Thr Gly Phe	
455 460 465	
gag gaa ctg gat tcc cag tcc aag gtc ctc gga cta ctt tcc gat ggt	1555
Glu Glu Leu Asp Ser Gln Ser Lys Val Leu Gly Leu Leu Ser Asp Gly	
470 475 480 485	
gcc aag att tct gaa gcc aca gaa ggt caa gaa gtt gag gtc atc ctc	1603
Ala Lys Ile Ser Glu Ala Thr Glu Gly Gln Glu Val Glu Val Ile Leu	
490 495 500	
gac cag tca cct ctg tac gca gaa tca ggt gga cag ctc ggc gat cgt	1651
Asp Gln Ser Pro Leu Tyr Ala Glu Ser Gly Gly Gln Leu Gly Asp Arg	
505 510 515	
ggt cag atc ctg ctc gga gac acc gtg ctt gat gtc cat gac gtg cag	1699
Gly Gln Ile Leu Leu Gly Asp Thr Val Leu Asp Val His Asp Val Gln	
520 525 530	
aag atc ggt aag aaa ctg tgg gtt cac aag gca ctc gtg gca aac ggt	1747
Lys Ile Gly Lys Lys Leu Trp Val His Lys Ala Leu Val Ala Asn Gly	
535 540 545	
gga ctt gcg gta ggt gat gaa gtg gtg gca agc gtc gat aag caa tgg	1795
Gly Leu Ala Val Gly Asp Glu Val Val Ala Ser Val Asp Lys Gln Trp	
550 555 560 565	
cgc cat gct gca cgc cag gca cac acc gca acc cac ctg att cat gcc	1843
Arg His Ala Ala Arg Gln Ala His Thr Ala Thr His Leu Ile His Ala	
570 575 580	

gct ctg cgg cag gtt ctt gga cca act gcc ctc cag gca gga tcc atg	1891
Ala Leu Arg Gln Val Leu Gly Pro Thr Ala Leu Gln Ala Gly Ser Met	
585 590 595	
aac aag cca ggc tac ctg cgc ttc gac ttc aac tac acc gag cag ctc	1939
Asn Lys Pro Gly Tyr Leu Arg Phe Asp Phe Asn Tyr Thr Glu Gln Leu	
600 605 610	
acc cca gca caa gtc gag caa atc cag gcg atc acc aac gaa gcc gtg	1987
Thr Pro Ala Gln Val Glu Gln Ile Gln Ala Ile Thr Asn Glu Ala Val	
615 620 625	
gac acc gac tgg gct gtc aac acc gtg gaa acc tca ctc gag gaa gcc	2035
Asp Thr Asp Trp Ala Val Asn Thr Val Glu Thr Ser Leu Glu Glu Ala	
630 635 640 645	
aag gca atg ggt gcg atg gcg ctc ttc ggc gaa aac tac gga agc acc	2083
Lys Ala Met Gly Ala Met Ala Leu Phe Gly Glu Asn Tyr Gly Ser Thr	
650 655 660	
gtg cgc gtt gtg gaa atc ggc gga cct ttc tcc atg gaa ctc tgt ggc	2131
Val Arg Val Val Glu Ile Gly Gly Pro Phe Ser Met Glu Leu Cys Gly	
665 670 675	
ggt acg cac gtt gcg cac tcc tca cag atc ggc cca gtg gca ctg ttg	2179
Gly Thr His Val Ala His Ser Ser Gln Ile Gly Pro Val Ala Leu Leu	
680 685 690	
ggt gaa tca tcc atc ggc tcc ggc gtg cgc cgc atc gag gcc tac tcc	2227
Gly Glu Ser Ser Ile Gly Ser Gly Val Arg Arg Ile Glu Ala Tyr Ser	
695 700 705	
ggc ctg aac tcc ttc aac tac ctg tcc aag gaa cgc gca ctc gcc gag	2275
Gly Leu Asn Ser Phe Asn Tyr Leu Ser Lys Glu Arg Ala Leu Ala Glu	
710 715 720 725	
ggt ttg gca agc tcc ctg aag gct cca tcc gag gaa ctt cca gag cgc	2323
Gly Leu Ala Ser Ser Leu Lys Ala Pro Ser Glu Glu Leu Pro Glu Arg	
730 735 740	
gtc gca cag ctg gta gac aag ctg aag gca gca gag aag gaa atc gaa	2371
Val Ala Gln Leu Val Asp Lys Leu Lys Ala Ala Glu Lys Glu Ile Glu	
745 750 755	
gcc ctg cac cgt cag cag ctc atg gca caa acc gca gac ctg ttg aac	2419
Ala Leu His Arg Gln Gln Leu Met Ala Gln Thr Ala Asp Leu Leu Asn	
760 765 770	
aac gct caa gag atc ggt ggc gtc acc acc ttg ctg ctg cgc gtc aag	2467
Asn Ala Gln Glu Ile Gly Gly Val Thr Thr Leu Leu Arg Val Lys	
775 780 785	
gac aac acc aac gcc ggt gac ctg cgc acc atc gca acc acc ctg aag	2515
Asp Asn Thr Asn Ala Gly Asp Leu Arg Thr Ile Ala Thr Thr Leu Lys	
790 795 800 805	
gac aag ctc ggc gac cgc gaa ggc gtc ttg gtt att gcc tcc gac aac	2563
Asp Lys Leu Gly Asp Arg Glu Gly Val Leu Val Ile Ala Ser Asp Asn	
810 815 820	
gcc ggc aag gtt cca ttc gtg gta gct gca acc aag gcc gct gtg gct	2611

Ala Gly Lys Val Pro Phe Val Val Ala Ala Thr Lys Ala Ala Val Ala  
                   825                                  830                                  835

cgc gga gct cac tcc ggc aac ctg gtt aag ctc gtt ggt tcc tac atc 2659  
 Arg Gly Ala His Ser Gly Asn Leu Val Lys Leu Val Gly Ser Tyr Ile  
                   840                                  845                                  850

gac ggt cgc ggt ggc ggc aag gct gac ctc gca caa gga tcc ggc gcc 2707  
 Asp Gly Arg Gly Gly Gly Lys Ala Asp Leu Ala Gln Gly Ser Gly Ala  
                   855                                  860                                  865

aac att gct ggc ctg gaa tcc gca ttc ggc gca gtc cgc gct gag atc 2755  
 Asn Ile Ala Gly Leu Glu Ser Ala Phe Gly Ala Val Arg Ala Glu Ile  
                   870                                  875                                  880                                  885

gag gca ctc taagccttca gtctaggccc taa 2787  
 Glu Ala Leu

&lt;210&gt; 274

&lt;211&gt; 888

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 274

Val Gln Thr His Glu Ile Arg Glu Arg Phe Thr Asn His Phe Val Asn  
   1                                  5                                  10                                  15

Ala Gly His Gln Ala Val Pro Ser Ala Ser Leu Ile Leu Asp Asp Pro  
                   20                                  25                                  30

Asn Leu Leu Phe Val Asn Ala Gly Met Val Pro Phe Lys Pro Tyr Phe  
                   35                                  40                                  45

Leu Gly Gln Gln Thr Pro Pro Phe Glu Asn Gly Thr Ala Thr Ser Ile  
                   50                                  55                                  60

Gln Lys Cys Val Arg Thr Leu Asp Ile Glu Glu Val Gly Ile Thr Thr  
                   65                                  70                                  75                                  80

Arg His Asn Thr Phe Phe Gln Met Ala Gly Asn Phe Ser Phe Gly Gln  
                   85                                  90                                  95

Tyr Phe Lys Glu Gly Ala Ile Thr His Ala Trp Gly Leu Leu Thr Gly  
                   100                                  105                                  110

Ser Val Ala Asp Gly Gly Phe Gly Leu Asp Pro Glu Arg Leu Trp Val  
                   115                                  120                                  125

Thr Val Tyr Leu Asp Asp Asp Glu Ala Ala Glu Ile Trp Glu Lys Lys  
                   130                                  135                                  140

Ile Gly Val Pro Ser Glu Arg Ile Gln Arg Leu Gly Met Ala Asp Asn  
                   145                                  150                                  155                                  160

Tyr Trp Ser Met Gly Val Pro Gly Pro Cys Gly Pro Cys Ser Glu Ile  
                   165                                  170                                  175

Tyr Tyr Asp Arg Gly Glu Lys Tyr Gly Lys Glu Gly Gly Pro Val Ala  
                   180                                  185                                  190

Asp Asp Asn Arg Tyr Met Glu Ile Trp Asn Leu Val Phe Met Glu Lys  
 195 200 205  
 Glu Arg Gly Gln Gly Ile Gly Lys Asp Asn Phe Asp Ile Leu Gly Asp  
 210 215 220  
 Leu Pro Lys Lys Asn Ile Asp Thr Gly Met Gly Val Glu Arg Val Ala  
 225 230 235 240  
 Cys Ile Leu Gln Asp Val Glu Asn Val Tyr Glu Thr Asp Leu Leu Arg  
 245 250 255  
 Pro Val Ile Asp Val Ala Glu Thr Leu Thr Gly Thr Lys Tyr Gly Ser  
 260 265 270  
 Asp Asn Thr Ser Asp Ile Arg Phe Arg Val Ile Ala Asp His Ser Arg  
 275 280 285  
 Thr Gly Met Met Leu Ile Leu Asp Gly Val Thr Pro Gly Asn Glu Gly  
 290 295 300  
 Arg Gly Tyr Ile Leu Arg Arg Leu Leu Arg Arg Ile Ile Arg Ser Ala  
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 Arg Leu Leu Gly Ala Thr Gly Glu Thr Met Glu Gln Phe Met Asn Thr  
 325 330 335  
 Ile Met Asp Thr Met Thr Pro Ser Tyr Pro Glu Ile Ala Asp Asn Arg  
 340 345 350  
 Glu Arg Ile Met Arg Val Ala Val Thr Glu Glu Arg Ala Phe Leu Lys  
 355 360 365  
 Thr Leu Val Ser Gly Thr His Leu Phe Glu Glu Ala Ala Thr Ser Ile  
 370 375 380  
 Lys Ala Ala Gly Ser Thr Lys Val Ala Gly Ala Gln Ala Phe Ala Leu  
 385 390 395 400  
 His Asp Thr Tyr Gly Phe Pro Ile Asp Leu Thr Leu Glu Met Ala Ala  
 405 410 415  
 Glu Ala Gly Leu Glu Val Asp Val Glu Gly Phe Asp Ser Leu Met Ala  
 420 425 430  
 Glu Gln Arg Ser Arg Ala Lys Ala Asp Ser Gln Ala Lys Lys His Gly  
 435 440 445  
 His Thr Asp Leu Ser Ile Tyr Arg Glu Trp Val Asp Asn Asn Pro Thr  
 450 455 460  
 Val Phe Thr Gly Phe Glu Glu Leu Asp Ser Gln Ser Lys Val Leu Gly  
 465 470 475 480  
 Leu Leu Ser Asp Gly Ala Lys Ile Ser Glu Ala Thr Glu Gly Gln Glu  
 485 490 495  
 Val Glu Val Ile Leu Asp Gln Ser Pro Leu Tyr Ala Glu Ser Gly Gly  
 500 505 510

Gln Leu Gly Asp Arg Gly Gln Ile Leu Leu Gly Asp Thr Val Leu Asp  
 515 520 525  
 Val His Asp Val Gln Lys Ile Gly Lys Lys Leu Trp Val His Lys Ala  
 530 535 540  
 Leu Val Ala Asn Gly Gly Leu Ala Val Gly Asp Glu Val Val Ala Ser  
 545 550 555 560  
 Val Asp Lys Gln Trp Arg His Ala Ala Arg Gln Ala His Thr Ala Thr  
 565 570 575  
 His Leu Ile His Ala Ala Leu Arg Gln Val Leu Gly Pro Thr Ala Leu  
 580 585 590  
 Gln Ala Gly Ser Met Asn Lys Pro Gly Tyr Leu Arg Phe Asp Phe Asn  
 595 600 605  
 Tyr Thr Glu Gln Leu Thr Pro Ala Gln Val Glu Gln Ile Gln Ala Ile  
 610 615 620  
 Thr Asn Glu Ala Val Asp Thr Asp Trp Ala Val Asn Thr Val Glu Thr  
 625 630 635 640  
 Ser Leu Glu Glu Ala Lys Ala Met Gly Ala Met Ala Leu Phe Gly Glu  
 645 650 655  
 Asn Tyr Gly Ser Thr Val Arg Val Val Glu Ile Gly Gly Pro Phe Ser  
 660 665 670  
 Met Glu Leu Cys Gly Gly Thr His Val Ala His Ser Ser Gln Ile Gly  
 675 680 685  
 Pro Val Ala Leu Leu Gly Glu Ser Ser Ile Gly Ser Gly Val Arg Arg  
 690 695 700  
 Ile Glu Ala Tyr Ser Gly Leu Asn Ser Phe Asn Tyr Leu Ser Lys Glu  
 705 710 715 720  
 Arg Ala Leu Ala Glu Gly Leu Ala Ser Ser Leu Lys Ala Pro Ser Glu  
 725 730 735  
 Glu Leu Pro Glu Arg Val Ala Gln Leu Val Asp Lys Leu Lys Ala Ala  
 740 745 750  
 Glu Lys Glu Ile Glu Ala Leu His Arg Gln Gln Leu Met Ala Gln Thr  
 755 760 765  
 Ala Asp Leu Leu Asn Asn Ala Gln Glu Ile Gly Gly Val Thr Thr Leu  
 770 775 780  
 Leu Leu Arg Val Lys Asp Asn Thr Asn Ala Gly Asp Leu Arg Thr Ile  
 785 790 795 800  
 Ala Thr Thr Leu Lys Asp Lys Leu Gly Asp Arg Glu Gly Val Leu Val  
 805 810 815  
 Ile Ala Ser Asp Asn Ala Gly Lys Val Pro Phe Val Val Ala Ala Thr  
 820 825 830  
 Lys Ala Ala Val Ala Arg Gly Ala His Ser Gly Asn Leu Val Lys Leu

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      835              840              845
Val Gly Ser Tyr Ile Asp Gly Arg Gly Gly Gly Lys Ala Asp Leu Ala
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Gln Gly Ser Gly Ala Asn Ile Ala Gly Leu Glu Ser Ala Phe Gly Ala
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Val Arg Ala Glu Ile Glu Ala Leu
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<222> (101)..(1750)
<223> RXN00975

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attctgtgcg acgggtgtac ctcggtctaga atttctcccc atg aca cca gct gat 115
                                   Met Thr Pro Ala Asp
                                   1              5

ctc gca aca ttg att aaa gag acc gcg gta gag gtt ttg acc tcc cgc 163
Leu Ala Thr Leu Ile Lys Glu Thr Ala Val Glu Val Leu Thr Ser Arg
              10              15              20

gag ctc gat act tct gtt ctt ccg gag cag gta gtt gtg gag cgt ccg 211
Glu Leu Asp Thr Ser Val Leu Pro Glu Gln Val Val Val Glu Arg Pro
              25              30              35

cgt aac cca gag cac ggc gat tac gcc acc aac att gca ttg cag gtg 259
Arg Asn Pro Glu His Gly Asp Tyr Ala Thr Asn Ile Ala Leu Gln Val
              40              45              50

gct aaa aag gtc ggt cag aac cct cgg gat ttg gct acc tgg ctg gca 307
Ala Lys Lys Val Gly Gln Asn Pro Arg Asp Leu Ala Thr Trp Leu Ala
              55              60              65

gag gca ttg gct gca gat gac gcc att gat tct gct gaa att gct ggc 355
Glu Ala Leu Ala Ala Asp Asp Ala Ile Asp Ser Ala Glu Ile Ala Gly
              70              75              80              85

cca ggc ttt ttg aac att cgc ctt gct gca gca gca cag ggt gaa att 403
Pro Gly Phe Leu Asn Ile Arg Leu Ala Ala Ala Ala Gln Gly Glu Ile
              90              95              100

gtg gcc aag att ctg gca cag ggc gag act ttc gga aac tcc gat cac 451
Val Ala Lys Ile Leu Ala Gln Gly Glu Thr Phe Gly Asn Ser Asp His
              105              110              115

ctt tcc cac ttg gac gtg aac ctc gag ttc gtt tct gca aac cca acc 499
Leu Ser His Leu Asp Val Asn Leu Glu Phe Val Ser Ala Asn Pro Thr
              120              125              130

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gga cct att cac ctt ggc gga acc cgc tgg gct gcc gtg ggt gac tct	547
Gly Pro Ile His Leu Gly Gly Thr Arg Trp Ala Ala Val Gly Asp Ser	
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ttg ggt cgt gtg ctg gag gct tcc tcc gcg aaa gtg acc cgc gaa tac	595
Leu Gly Arg Val Leu Glu Ala Ser Ser Ala Lys Val Thr Arg Glu Tyr	
150 155 160 165	
tac ttc aac gat cac ggt cgc cag atc gat cgt ttc gct ttg tcc ctt	643
Tyr Phe Asn Asp His Gly Arg Gln Ile Asp Arg Phe Ala Leu Ser Leu	
170 175 180	
ctt gca gcg gcg aag ggc gag cca acg cca gaa gac ggt tat ggc ggc	691
Leu Ala Ala Ala Lys Gly Glu Pro Thr Pro Glu Asp Gly Tyr Gly Gly	
185 190 195	
gaa tac att aag gaa att gcg gag gca atc gtc gaa aag cat cct gaa	739
Glu Tyr Ile Lys Glu Ile Ala Glu Ala Ile Val Glu Lys His Pro Glu	
200 205 210	
gcg ttg gct ttg gag cct gcc gca acc cag gag ctt ttc cgc gct gaa	787
Ala Leu Ala Leu Glu Pro Ala Ala Thr Gln Glu Leu Phe Arg Ala Glu	
215 220 225	
ggc gtg gag atg atg ttc gag cac atc aaa tct tcc ctg cat gag ttc	835
Gly Val Glu Met Met Phe Glu His Ile Lys Ser Ser Leu His Glu Phe	
230 235 240 245	
ggc acc gat ttc gat gtc tac tac cac gag aac tcc ctg ttc gag tcc	883
Gly Thr Asp Phe Asp Val Tyr Tyr His Glu Asn Ser Leu Phe Glu Ser	
250 255 260	
ggt gcg gtg gac aag gcc gtg cag gtg ctg aag gac aac ggc aac ctg	931
Gly Ala Val Asp Lys Ala Val Gln Val Leu Lys Asp Asn Gly Asn Leu	
265 270 275	
tac gaa aac gag ggc gct tgg tgg ctg cgt tcc acc gaa ttc ggc gat	979
Tyr Glu Asn Glu Gly Ala Trp Trp Leu Arg Ser Thr Glu Phe Gly Asp	
280 285 290	
gac aaa gac cgc gtg gtg atc aag tct gac ggc gac gca gcc tac atc	1027
Asp Lys Asp Arg Val Val Ile Lys Ser Asp Gly Asp Ala Ala Tyr Ile	
295 300 305	
gct ggc gat atc gcg tac gtg gct gat aag ttc tcc cgc gga cac aac	1075
Ala Gly Asp Ile Ala Tyr Val Ala Asp Lys Phe Ser Arg Gly His Asn	
310 315 320 325	
cta aac atc tac atg ttg ggt gct gac cac cat ggt tac atc gcg cgc	1123
Leu Asn Ile Tyr Met Leu Gly Ala Asp His His Gly Tyr Ile Ala Arg	
330 335 340	
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Leu Lys Ala Ala Ala Ala Ala Leu Gly Tyr Lys Pro Glu Gly Val Glu	
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Val Leu Ile Gly Gln Met Val Asn Leu Leu Arg Asp Gly Lys Ala Val	
360 365 370	
cgt atg tcc aag cgt gca ggc acc gtg gtc acc cta gat gac ctc gtt	1267

Arg Met Ser Lys Arg Ala Gly Thr Val Val Thr Leu Asp Asp Leu Val  
 375 380 385  
 gaa gca atc ggc atc gat gcg gcg cgt tac tcc ctg atc cgt tcc tcc 1315  
 Glu Ala Ile Gly Ile Asp Ala Ala Arg Tyr Ser Leu Ile Arg Ser Ser  
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 Val Asp Ser Ser Leu Asp Ile Asp Leu Gly Leu Trp Glu Ser Gln Ser  
 410 415 420  
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 Ser Asp Asn Pro Val Tyr Tyr Val Gln Tyr Gly His Ala Arg Leu Cys  
 425 430 435  
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 Ser Ile Ala Arg Lys Ala Glu Thr Leu Gly Val Thr Glu Glu Gly Ala  
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 470 475 480 485  
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 Pro His Arg Ile Ala Arg Tyr Ala Glu Glu Leu Ala Gly Thr Phe His  
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 cgc ttc tac gat tcc tgc cac atc ctt cca aag gtt gat gag gat acg 1651  
 Arg Phe Tyr Asp Ser Cys His Ile Leu Pro Lys Val Asp Glu Asp Thr  
 505 510 515  
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 Ala Pro Ile His Thr Ala Arg Leu Ala Leu Ala Ala Ala Thr Arg Gln  
 520 525 530  
 acc ctc gct aac gcc ctg cac ctg gtt ggc gtt tcc gca ccg gag aag 1747  
 Thr Leu Ala Asn Ala Leu His Leu Val Gly Val Ser Ala Pro Glu Lys  
 535 540 545  
 atg taacaatggc tacagttgaa aat 1773  
 Met  
 550

&lt;210&gt; 276

&lt;211&gt; 550

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 276

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Val Leu Thr Ser Arg Glu Leu Asp Thr Ser Val Leu Pro Glu Gln Val  
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Val Val Glu Arg Pro Arg Asn Pro Glu His Gly Asp Tyr Ala Thr Asn

35					40					45					
Ile	Ala	Leu	Gln	Val	Ala	Lys	Lys	Val	Gly	Gln	Asn	Pro	Arg	Asp	Leu
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Ala	Thr	Trp	Leu	Ala	Glu	Ala	Leu	Ala	Ala	Asp	Asp	Ala	Ile	Asp	Ser
65					70					75					80
Ala	Glu	Ile	Ala	Gly	Pro	Gly	Phe	Leu	Asn	Ile	Arg	Leu	Ala	Ala	Ala
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Ala	Gln	Gly	Glu	Ile	Val	Ala	Lys	Ile	Leu	Ala	Gln	Gly	Glu	Thr	Phe
			100					105					110		
Gly	Asn	Ser	Asp	His	Leu	Ser	His	Leu	Asp	Val	Asn	Leu	Glu	Phe	Val
		115					120					125			
Ser	Ala	Asn	Pro	Thr	Gly	Pro	Ile	His	Leu	Gly	Gly	Thr	Arg	Trp	Ala
	130					135					140				
Ala	Val	Gly	Asp	Ser	Leu	Gly	Arg	Val	Leu	Glu	Ala	Ser	Ser	Ala	Lys
145					150					155					160
Val	Thr	Arg	Glu	Tyr	Tyr	Phe	Asn	Asp	His	Gly	Arg	Gln	Ile	Asp	Arg
				165					170					175	
Phe	Ala	Leu	Ser	Leu	Leu	Ala	Ala	Ala	Lys	Gly	Glu	Pro	Thr	Pro	Glu
			180					185					190		
Asp	Gly	Tyr	Gly	Gly	Glu	Tyr	Ile	Lys	Glu	Ile	Ala	Glu	Ala	Ile	Val
		195					200					205			
Glu	Lys	His	Pro	Glu	Ala	Leu	Ala	Leu	Glu	Pro	Ala	Ala	Thr	Gln	Glu
	210					215					220				
Leu	Phe	Arg	Ala	Glu	Gly	Val	Glu	Met	Met	Phe	Glu	His	Ile	Lys	Ser
225					230					235					240
Ser	Leu	His	Glu	Phe	Gly	Thr	Asp	Phe	Asp	Val	Tyr	Tyr	His	Glu	Asn
				245					250					255	
Ser	Leu	Phe	Glu	Ser	Gly	Ala	Val	Asp	Lys	Ala	Val	Gln	Val	Leu	Lys
			260					265					270		
Asp	Asn	Gly	Asn	Leu	Tyr	Glu	Asn	Glu	Gly	Ala	Trp	Trp	Leu	Arg	Ser
		275					280						285		
Thr	Glu	Phe	Gly	Asp	Asp	Lys	Asp	Arg	Val	Val	Ile	Lys	Ser	Asp	Gly
	290					295					300				
Asp	Ala	Ala	Tyr	Ile	Ala	Gly	Asp	Ile	Ala	Tyr	Val	Ala	Asp	Lys	Phe
305					310					315					320
Ser	Arg	Gly	His	Asn	Leu	Asn	Ile	Tyr	Met	Leu	Gly	Ala	Asp	His	His
				325					330				335		
Gly	Tyr	Ile	Ala	Arg	Leu	Lys	Ala	Ala	Ala	Ala	Ala	Leu	Gly	Tyr	Lys
			340					345					350		
Pro	Glu	Gly	Val	Glu	Val	Leu	Ile	Gly	Gln	Met	Val	Asn	Leu	Leu	Arg
		355					360					365			

Asp Gly Lys Ala Val Arg Met Ser Lys Arg Ala Gly Thr Val Val Thr  
 370 375 380  
 Leu Asp Asp Leu Val Glu Ala Ile Gly Ile Asp Ala Ala Arg Tyr Ser  
 385 390 395 400  
 Leu Ile Arg Ser Ser Val Asp Ser Ser Leu Asp Ile Asp Leu Gly Leu  
 405 410 415  
 Trp Glu Ser Gln Ser Ser Asp Asn Pro Val Tyr Tyr Val Gln Tyr Gly  
 420 425 430  
 His Ala Arg Leu Cys Ser Ile Ala Arg Lys Ala Glu Thr Leu Gly Val  
 435 440 445  
 Thr Glu Glu Gly Ala Asp Leu Ser Leu Leu Thr His Asp Arg Glu Gly  
 450 455 460  
 Asp Leu Ile Arg Thr Leu Gly Glu Phe Pro Ala Val Val Lys Ala Ala  
 465 470 475 480  
 Ala Asp Leu Arg Glu Pro His Arg Ile Ala Arg Tyr Ala Glu Glu Leu  
 485 490 495  
 Ala Gly Thr Phe His Arg Phe Tyr Asp Ser Cys His Ile Leu Pro Lys  
 500 505 510  
 Val Asp Glu Asp Thr Ala Pro Ile His Thr Ala Arg Leu Ala Leu Ala  
 515 520 525  
 Ala Ala Thr Arg Gln Thr Leu Ala Asn Ala Leu His Leu Val Gly Val  
 530 535 540  
 Ser Ala Pro Glu Lys Met  
 545 550

&lt;210&gt; 277

&lt;211&gt; 877

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(877)

&lt;223&gt; FRXA00975

&lt;400&gt; 277

tcttgacgagcgcgcgaagggcgagccaacgccagaagacggttatggcgcgcaatacattaa 60

ggaaattgagcggaggcaatcgtcgaaaagcattctgaagcg ttg gct ttg gag cct 115  
 Leu Ala Leu Glu Pro  
 1 5

gcc gca acc caa gag ctt ttc cgc gct gaa ggc gtg gag atg atg ttc 163  
 Ala Ala Thr Gln Glu Leu Phe Arg Ala Glu Gly Val Glu Met Met Phe  
 10 15 20

gag cac atc aaa tct tcc ctg cat gag ttc ggc acc gat ttc gat gtc 211  
 Glu His Ile Lys Ser Ser Leu His Glu Phe Gly Thr Asp Phe Asp Val

25										30					35					
tac	tac	cac	gag	aac	tcc	ctg	ttc	gag	tcc	ggt	gcg	gtg	gac	aag	gcc	259				
Tyr	Tyr	His	Glu	Asn	Ser	Leu	Phe	Glu	Ser	Gly	Ala	Val	Asp	Lys	Ala					
		40						45				50								
gtg	cag	gtg	ctg	aag	gac	aac	ggc	aac	ctg	tac	gaa	aac	gag	ggc	gct	307				
Val	Gln	Val	Leu	Lys	Asp	Asn	Gly	Asn	Leu	Tyr	Glu	Asn	Glu	Gly	Ala					
	55					60					65									
tgg	tgg	ctg	cgt	tcc	acc	gaa	ttc	ggc	gat	gac	aaa	gac	cgc	gtg	gtg	355				
Trp	Trp	Leu	Arg	Ser	Thr	Glu	Phe	Gly	Asp	Asp	Lys	Asp	Arg	Val	Val					
	70				75					80					85					
atc	aag	tct	gac	ggc	gac	gca	gcc	tac	atc	gct	ggc	gat	atc	gcg	tac	403				
Ile	Lys	Ser	Asp	Gly	Asp	Ala	Ala	Tyr	Ile	Ala	Gly	Asp	Ile	Ala	Tyr					
				90					95					100						
gtg	gct	gat	aag	ttc	tcc	cgc	gga	cac	aac	cta	aac	atc	tac	atg	ttg	451				
Val	Ala	Asp	Lys	Phe	Ser	Arg	Gly	His	Asn	Leu	Asn	Ile	Tyr	Met	Leu					
			105					110					115							
ggt	gct	gac	cac	cat	ggt	tac	atc	gcg	cgc	ctg	aag	gca	gcg	gcg	gcg	499				
Gly	Ala	Asp	His	His	Gly	Tyr	Ile	Ala	Arg	Leu	Lys	Ala	Ala	Ala	Ala					
		120					125					130								
gca	ctt	ggc	tac	aag	cca	gaa	ggc	gtt	gaa	gtc	ctg	att	ggc	cag	atg	547				
Ala	Leu	Gly	Tyr	Lys	Pro	Glu	Gly	Val	Glu	Val	Leu	Ile	Gly	Gln	Met					
	135					140					145									
gtg	aac	ctg	ctt	cgc	gac	ggc	aag	gca	gtg	cgt	atg	tcc	aag	cgt	gca	595				
Val	Asn	Leu	Leu	Arg	Asp	Gly	Lys	Ala	Val	Arg	Met	Ser	Lys	Arg	Ala					
	150				155					160					165					
ggc	acc	gtg	gtc	acc	cta	gat	gac	ctc	gtt	gaa	gca	atc	ggc	atc	gat	643				
Gly	Thr	Val	Val	Thr	Leu	Asp	Asp	Leu	Val	Glu	Ala	Ile	Gly	Ile	Asp					
				170					175					180						
gcg	gcg	cgt	tac	tcc	ctg	atc	cgt	tcc	tcc	gtg	gat	tct	tcc	ctg	gat	691				
Ala	Ala	Arg	Tyr	Ser	Leu	Ile	Arg	Ser	Ser	Val	Asp	Ser	Ser	Leu	Asp					
			185					190					195							
atc	gat	ctc	ggc	ctg	tgg	gaa	tcc	cag	tcc	tcc	gac	aac	cct	gtg	tac	739				
Ile	Asp	Leu	Gly	Leu	Trp	Glu	Ser	Gln	Ser	Ser	Asp	Asn	Pro	Val	Tyr					
		200					205						210							
tac	gtg	cag	tac	gga	cac	gct	cgt	ctg	tgc	tcc	atc	gcg	cgc	aag	gca	787				
Tyr	Val	Gln	Tyr	Gly	His	Ala	Arg	Leu	Cys	Ser	Ile	Ala	Arg	Lys	Ala					
	215					220					225									
gag	acc	ttg	ggt	gtc	acc	gag	gaa	ggc	gca	gac	cta	tct	cta	ctg	acc	835				
Glu	Thr	Leu	Gly	Val	Thr	Glu	Glu	Gly	Ala	Asp	Leu	Ser	Leu	Leu	Thr					
	230				235					240					245					
cac	gac	cgc	gaa	ggt	gat	ctc	atc	cgc	aca	ctc	gga	gag	ttc			877				
His	Asp	Arg	Glu	Gly	Asp	Leu	Ile	Arg	Thr	Leu	Gly	Glu	Phe							
				250					255											

&lt;210&gt; 278

&lt;211&gt; 259

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 278

Leu Ala Leu Glu Pro Ala Ala Thr Gln Glu Leu Phe Arg Ala Glu Gly  
 1 5 10 15  
 Val Glu Met Met Phe Glu His Ile Lys Ser Ser Leu His Glu Phe Gly  
 20 25 30  
 Thr Asp Phe Asp Val Tyr Tyr His Glu Asn Ser Leu Phe Glu Ser Gly  
 35 40 45  
 Ala Val Asp Lys Ala Val Gln Val Leu Lys Asp Asn Gly Asn Leu Tyr  
 50 55 60  
 Glu Asn Glu Gly Ala Trp Trp Leu Arg Ser Thr Glu Phe Gly Asp Asp  
 65 70 75 80  
 Lys Asp Arg Val Val Ile Lys Ser Asp Gly Asp Ala Ala Tyr Ile Ala  
 85 90 95  
 Gly Asp Ile Ala Tyr Val Ala Asp Lys Phe Ser Arg Gly His Asn Leu  
 100 105 110  
 Asn Ile Tyr Met Leu Gly Ala Asp His His Gly Tyr Ile Ala Arg Leu  
 115 120 125  
 Lys Ala Ala Ala Ala Ala Leu Gly Tyr Lys Pro Glu Gly Val Glu Val  
 130 135 140  
 Leu Ile Gly Gln Met Val Asn Leu Leu Arg Asp Gly Lys Ala Val Arg  
 145 150 155 160  
 Met Ser Lys Arg Ala Gly Thr Val Val Thr Leu Asp Asp Leu Val Glu  
 165 170 175  
 Ala Ile Gly Ile Asp Ala Ala Arg Tyr Ser Leu Ile Arg Ser Ser Val  
 180 185 190  
 Asp Ser Ser Leu Asp Ile Asp Leu Gly Leu Trp Glu Ser Gln Ser Ser  
 195 200 205  
 Asp Asn Pro Val Tyr Tyr Val Gln Tyr Gly His Ala Arg Leu Cys Ser  
 210 215 220  
 Ile Ala Arg Lys Ala Glu Thr Leu Gly Val Thr Glu Glu Gly Ala Asp  
 225 230 235 240  
 Leu Ser Leu Leu Thr His Asp Arg Glu Gly Asp Leu Ile Arg Thr Leu  
 245 250 255  
 Gly Glu Phe

&lt;210&gt; 279

&lt;211&gt; 723

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(700)

&lt;223&gt; FRXA00976

&lt;400&gt; 279

tatacagaga ccaatgattt ttcattaaaa aggcagggat ttgttataag tatgggtcgt 60

attctgtgcg acgggtgtac ctcggttaga atttctcccc atg aca cca gct gat 115  
 Met Thr Pro Ala Asp  
 1 5

ctc gca aca ttg att aaa gag acc gcg gta gag gtt ttg acc tcc cgc 163  
 Leu Ala Thr Leu Ile Lys Glu Thr Ala Val Glu Val Leu Thr Ser Arg  
 10 15 20

gag ctc gat act tct gtt ctt ccg gag cag gta gtt gtg gag cgt ccg 211  
 Glu Leu Asp Thr Ser Val Leu Pro Glu Gln Val Val Val Glu Arg Pro  
 25 30 35

cgt aac cca gag cac ggc gat tac gcc acc aac att gca ttg cag gtg 259  
 Arg Asn Pro Glu His Gly Asp Tyr Ala Thr Asn Ile Ala Leu Gln Val  
 40 45 50

gct aaa aag gtc ggt cag aac cct cgg gat ttg gct acc tgg ctg gca 307  
 Ala Lys Lys Val Gly Gln Asn Pro Arg Asp Leu Ala Thr Trp Leu Ala  
 55 60 65

gag gca ttg gct gca gat gac gcc att gat tct gct gaa att gct ggc 355  
 Glu Ala Leu Ala Ala Asp Asp Ala Ile Asp Ser Ala Glu Ile Ala Gly  
 70 75 80 85

cca ggc ttt ttg aac att cgc ctt gct gca gca gca cag ggt gaa att 403  
 Pro Gly Phe Leu Asn Ile Arg Leu Ala Ala Ala Gln Gly Glu Ile  
 90 95 100

gtg gcc aag att ctg gca cag ggc gag act ttc gga aac tcc gat cac 451  
 Val Ala Lys Ile Leu Ala Gln Gly Glu Thr Phe Gly Asn Ser Asp His  
 105 110 115

ctt tcc cac ttg gac gtg aac ctc gag ttc gtt tct gca aac cca acc 499  
 Leu Ser His Leu Asp Val Asn Leu Glu Phe Val Ser Ala Asn Pro Thr  
 120 125 130

gga cct att cac ctt ggc gga acc cgc tgg gct gcc gtg ggt gac tct 547  
 Gly Pro Ile His Leu Gly Gly Thr Arg Trp Ala Ala Val Gly Asp Ser  
 135 140 145

ttg ggt cgt gtg ctg gag gct tcc ggc gcg aaa gtg acc cgc gaa tac 595  
 Leu Gly Arg Val Leu Glu Ala Ser Gly Ala Lys Val Thr Arg Glu Tyr  
 150 155 160 165

tac ttc aac gat cac ggt cgc cag atc gat cgt ttc gct ttg tcg agt 643  
 Tyr Phe Asn Asp His Gly Arg Gln Ile Asp Arg Phe Ala Leu Ser Ser  
 170 175 180

tct tgc agc ggc gaa ggg cga gcc aac gcc aga aga cgg tta tgg cgg 691  
 Ser Cys Ser Gly Glu Gly Arg Ala Asn Ala Arg Arg Arg Leu Trp Arg  
 185 190 195

cga ata cat taaggaaatt gcggaggcaa tcg 723

Arg Ile His  
200

<210> 280

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 280

Met Thr Pro Ala Asp Leu Ala Thr Leu Ile Lys Glu Thr Ala Val Glu  
1 5 10 15

Val Leu Thr Ser Arg Glu Leu Asp Thr Ser Val Leu Pro Glu Gln Val  
20 25 30

Val Val Glu Arg Pro Arg Asn Pro Glu His Gly Asp Tyr Ala Thr Asn  
35 40 45

Ile Ala Leu Gln Val Ala Lys Lys Val Gly Gln Asn Pro Arg Asp Leu  
50 55 60

Ala Thr Trp Leu Ala Glu Ala Leu Ala Ala Asp Asp Ala Ile Asp Ser  
65 70 75 80

Ala Glu Ile Ala Gly Pro Gly Phe Leu Asn Ile Arg Leu Ala Ala Ala  
85 90 95

Ala Gln Gly Glu Ile Val Ala Lys Ile Leu Ala Gln Gly Glu Thr Phe  
100 105 110

Gly Asn Ser Asp His Leu Ser His Leu Asp Val Asn Leu Glu Phe Val  
115 120 125

Ser Ala Asn Pro Thr Gly Pro Ile His Leu Gly Gly Thr Arg Trp Ala  
130 135 140

Ala Val Gly Asp Ser Leu Gly Arg Val Leu Glu Ala Ser Gly Ala Lys  
145 150 155 160

Val Thr Arg Glu Tyr Tyr Phe Asn Asp His Gly Arg Gln Ile Asp Arg  
165 170 175

Phe Ala Leu Ser Ser Ser Cys Ser Gly Glu Gly Arg Ala Asn Ala Arg  
180 185 190

Arg Arg Leu Trp Arg Arg Ile His  
195 200

<210> 281

<211> 1804

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1804)

<223> RXN01730

<400> 281

tctgggctgc atgcccgccc tttttgggcg gttgagctta ttgtttaagg ctccagaaac 60

catcgactga tcaaaaccaa gcggaaggac ttccaccaac gtg ctg cgc act cat 115  
Val Leu Arg Thr His  
1 5

ctc tca ggc gag ctt cgt aaa gaa aac gca ggc cag tca gtt act ctg 163  
Leu Ser Gly Glu Leu Arg Lys Glu Asn Ala Gly Gln Ser Val Thr Leu  
10 15 20

acc ggc tgg gtc aat cgt cgc cgt gac cac ggt ggc gtg atc ttc atc 211  
Thr Gly Trp Val Asn Arg Arg Arg Asp His Gly Gly Val Ile Phe Ile  
25 30 35

gat ctt cgc gac cgt act ggc att gcc cag gtt gtt ttc cgc aat gag 259  
Asp Leu Arg Asp Arg Thr Gly Ile Ala Gln Val Val Phe Arg Asn Glu  
40 45 50

gac gtt gct gag cgt gca cac gca ctg cgc agc gaa ttc gtc cta cgc 307  
Asp Val Ala Glu Arg Ala His Ala Leu Arg Ser Glu Phe Val Leu Arg  
55 60 65

gtc acc ggc gtc gtc gaa gag cgc cca gaa ggc tct caa aac cct aac 355  
Val Thr Gly Val Val Glu Glu Arg Pro Glu Gly Ser Gln Asn Pro Asn  
70 75 80 85

ctt gca tcc ggc gac att gaa gtc agc gtc acc gaa ttt gag gta ctc 403  
Leu Ala Ser Gly Asp Ile Glu Val Ser Val Thr Glu Phe Glu Val Leu  
90 95 100

aac gag tcc gct cca ctt cct ttc cag atc gag gat tcc tcc tct gct 451  
Asn Glu Ser Ala Pro Leu Pro Phe Gln Ile Glu Asp Ser Ser Ser Ala  
105 110 115

ggt gaa gtc ggc gaa gag acc cgt ctg aag tac cgc tac ctg gac ctg 499  
Gly Glu Val Gly Glu Glu Thr Arg Leu Lys Tyr Arg Tyr Leu Asp Leu  
120 125 130

cgt cgc cca gtt cag gcg aac gcc ctg cgt ctg cgt tct gct gcc aac 547  
Arg Arg Pro Val Gln Ala Asn Ala Leu Arg Leu Arg Ser Ala Ala Asn  
135 140 145

aag gct gca cgc acc gtg ctg gac agc cac gat ttc acc gag atc gag 595  
Lys Ala Ala Arg Thr Val Leu Asp Ser His Asp Phe Thr Glu Ile Glu  
150 155 160 165

acc cca acc ttg act cgt tcc acc cca gaa ggc gca cgt gac ttc ctg 643  
Thr Pro Thr Leu Thr Arg Ser Thr Pro Glu Gly Ala Arg Asp Phe Leu  
170 175 180

gtg cca gct cgt ctg cgc cca ggc act ttc tac gca ttg cca cag tcc 691  
Val Pro Ala Arg Leu Arg Pro Gly Thr Phe Tyr Ala Leu Pro Gln Ser  
185 190 195

cca cag ctg ttc aag cag ctg ctg cag gtt gct ggc atg gag cgc tac 739  
Pro Gln Leu Phe Lys Gln Leu Leu Gln Val Ala Gly Met Glu Arg Tyr  
200 205 210

tac cag atc gct cgt tgc tac cgc gat gag gat ttc cgt gca gac cgt 787  
Tyr Gln Ile Ala Arg Cys Tyr Arg Asp Glu Asp Phe Arg Ala Asp Arg  
215 220 225

cag cca gag ttc acc cag ctg gac gtt gaa atg tcc ttc gtg gac cag	835
Gln Pro Glu Phe Thr Gln Leu Asp Val Glu Met Ser Phe Val Asp Gln	
230 235 240 245	
gat gat gtc atc gca ctg ggc gag gag atc atc tct gag gtg tgg aag	883
Asp Asp Val Ile Ala Leu Gly Glu Glu Ile Ile Ser Glu Val Trp Lys	
250 255 260	
ttg atc gga tat gag atc aag act cca atc cca cgc atg acc tac gcc	931
Leu Ile Gly Tyr Glu Ile Lys Thr Pro Ile Pro Arg Met Thr Tyr Ala	
265 270 275	
gat gca atg cgt cgc tac ggc tcc gac aag cca gac ctg cgc ttc gac	979
Asp Ala Met Arg Arg Tyr Gly Ser Asp Lys Pro Asp Leu Arg Phe Asp	
280 285 290	
atc gaa atc acc gag tgc acc gag ttc ttc cag gac acc aca ttc cgt	1027
Ile Glu Ile Thr Glu Cys Thr Glu Phe Phe Gln Asp Thr Thr Phe Arg	
295 300 305	
gtg ttc aag aac gaa tat gtc ggc gca gtt gtc atg acc ggt ggt gct	1075
Val Phe Lys Asn Glu Tyr Val Gly Ala Val Val Met Thr Gly Gly Ala	
310 315 320 325	
tcc cag cct cgc cgt cag ctc gac gca tgg cag gaa tgg gcc aag cag	1123
Ser Gln Pro Arg Arg Gln Leu Asp Ala Trp Gln Glu Trp Ala Lys Gln	
330 335 340	
cgc ggt gct aag gga ctt gct tac atc ctc gtt ggt gaa gac ggc gag	1171
Arg Gly Ala Lys Gly Leu Ala Tyr Ile Leu Val Gly Glu Asp Gly Glu	
345 350 355	
ctg tcc gga cct gtg gct aag aac atc acc gac gct gag cgc gca gga	1219
Leu Ser Gly Pro Val Ala Lys Asn Ile Thr Asp Ala Glu Arg Ala Gly	
360 365 370	
atc gca gct cac gtt ggc gca cag cca ggc gac tgc atc ttc ttc gca	1267
Ile Ala Ala His Val Gly Ala Gln Pro Gly Asp Cys Ile Phe Phe Ala	
375 380 385	
gca gga gac acc aag tct tcc ctc gca ctg ctc ggt gca gct cgt ggc	1315
Ala Gly Asp Thr Lys Ser Ser Leu Ala Leu Leu Gly Ala Ala Arg Gly	
390 395 400 405	
gag atc gct aag aag ctc gac ctg atc aag gaa ggc gac tgg gca ttc	1363
Glu Ile Ala Lys Lys Leu Asp Leu Ile Lys Glu Gly Asp Trp Ala Phe	
410 415 420	
acc tgg atc gtt gac gct cca atg ttc gag cca gca gca gac gcc acc	1411
Thr Trp Ile Val Asp Ala Pro Met Phe Glu Pro Ala Ala Asp Ala Thr	
425 430 435	
gca tcc ggt gac gtt gca ctg ggt aac tcc aag tgg acc gca gtc cac	1459
Ala Ser Gly Asp Val Ala Leu Gly Asn Ser Lys Trp Thr Ala Val His	
440 445 450	
cac gcc ttc acc tca cct aag cca gag ttc ctg gac aac ttt gac acc	1507
His Ala Phe Thr Ser Pro Lys Pro Glu Phe Leu Asp Asn Phe Asp Thr	
455 460 465	

aac cca ggt gac gca ctt gct tat gca tac gac atc gtg tgc aac ggc 1555  
 Asn Pro Gly Asp Ala Leu Ala Tyr Ala Tyr Asp Ile Val Cys Asn Gly  
 470 475 480 485  
  
 aat gaa atc ggt ggc ggt tcc atc cgt atc cac cag cgc gac gtt cag 1603  
 Asn Glu Ile Gly Gly Gly Ser Ile Arg Ile His Gln Arg Asp Val Gln  
 490 495 500  
  
 gaa cgc gtt ttc gag gtt atg ggc atc acc ggt gaa gaa gca cgc gag 1651  
 Glu Arg Val Phe Glu Val Met Gly Ile Thr Gly Glu Glu Ala Arg Glu  
 505 510 515  
  
 aag ttc ggc ttc ctg ctt gac gcc ttc gca ttc ggc gca cct cca cac 1699  
 Lys Phe Gly Phe Leu Leu Asp Ala Phe Ala Phe Gly Ala Pro Pro His  
 520 525 530  
  
 ggc gga atc gca ttc ggc tgg gac cgc atc gtg tcc ctg ctg ggc ggc 1747  
 Gly Gly Ile Ala Phe Gly Trp Asp Arg Ile Val Ser Leu Leu Gly Gly  
 535 540 545  
  
 ttt gac tcc atc cgc gac gtc atc gcg ttc cct aag tcc ggt ggc gga 1795  
 Phe Asp Ser Ile Arg Asp Val Ile Ala Phe Pro Lys Ser Gly Gly Gly  
 550 555 560 565  
  
 atc gac ccc 1804  
 Ile Asp Pro

&lt;210&gt; 282

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 282

Val Leu Arg Thr His Leu Ser Gly Glu Leu Arg Lys Glu Asn Ala Gly  
 1 5 10 15  
  
 Gln Ser Val Thr Leu Thr Gly Trp Val Asn Arg Arg Arg Asp His Gly  
 20 25 30  
  
 Gly Val Ile Phe Ile Asp Leu Arg Asp Arg Thr Gly Ile Ala Gln Val  
 35 40 45  
  
 Val Phe Arg Asn Glu Asp Val Ala Glu Arg Ala His Ala Leu Arg Ser  
 50 55 60  
  
 Glu Phe Val Leu Arg Val Thr Gly Val Val Glu Glu Arg Pro Glu Gly  
 65 70 75 80  
  
 Ser Gln Asn Pro Asn Leu Ala Ser Gly Asp Ile Glu Val Ser Val Thr  
 85 90 95  
  
 Glu Phe Glu Val Leu Asn Glu Ser Ala Pro Leu Pro Phe Gln Ile Glu  
 100 105 110  
  
 Asp Ser Ser Ser Ala Gly Glu Val Gly Glu Glu Thr Arg Leu Lys Tyr  
 115 120 125  
  
 Arg Tyr Leu Asp Leu Arg Arg Pro Val Gln Ala Asn Ala Leu Arg Leu  
 130 135 140

Arg Ser Ala Ala Asn Lys Ala Ala Arg Thr Val Leu Asp Ser His Asp  
 145 150 155 160  
 Phe Thr Glu Ile Glu Thr Pro Thr Leu Thr Arg Ser Thr Pro Glu Gly  
 165 170 175  
 Ala Arg Asp Phe Leu Val Pro Ala Arg Leu Arg Pro Gly Thr Phe Tyr  
 180 185 190  
 Ala Leu Pro Gln Ser Pro Gln Leu Phe Lys Gln Leu Leu Gln Val Ala  
 195 200 205  
 Gly Met Glu Arg Tyr Tyr Gln Ile Ala Arg Cys Tyr Arg Asp Glu Asp  
 210 215 220  
 Phe Arg Ala Asp Arg Gln Pro Glu Phe Thr Gln Leu Asp Val Glu Met  
 225 230 235 240  
 Ser Phe Val Asp Gln Asp Asp Val Ile Ala Leu Gly Glu Glu Ile Ile  
 245 250 255  
 Ser Glu Val Trp Lys Leu Ile Gly Tyr Glu Ile Lys Thr Pro Ile Pro  
 260 265 270  
 Arg Met Thr Tyr Ala Asp Ala Met Arg Arg Tyr Gly Ser Asp Lys Pro  
 275 280 285  
 Asp Leu Arg Phe Asp Ile Glu Ile Thr Glu Cys Thr Glu Phe Phe Gln  
 290 295 300  
 Asp Thr Thr Phe Arg Val Phe Lys Asn Glu Tyr Val Gly Ala Val Val  
 305 310 315 320  
 Met Thr Gly Gly Ala Ser Gln Pro Arg Arg Gln Leu Asp Ala Trp Gln  
 325 330 335  
 Glu Trp Ala Lys Gln Arg Gly Ala Lys Gly Leu Ala Tyr Ile Leu Val  
 340 345 350  
 Gly Glu Asp Gly Glu Leu Ser Gly Pro Val Ala Lys Asn Ile Thr Asp  
 355 360 365  
 Ala Glu Arg Ala Gly Ile Ala Ala His Val Gly Ala Gln Pro Gly Asp  
 370 375 380  
 Cys Ile Phe Phe Ala Ala Gly Asp Thr Lys Ser Ser Leu Ala Leu Leu  
 385 390 395 400  
 Gly Ala Ala Arg Gly Glu Ile Ala Lys Lys Leu Asp Leu Ile Lys Glu  
 405 410 415  
 Gly Asp Trp Ala Phe Thr Trp Ile Val Asp Ala Pro Met Phe Glu Pro  
 420 425 430  
 Ala Ala Asp Ala Thr Ala Ser Gly Asp Val Ala Leu Gly Asn Ser Lys  
 435 440 445  
 Trp Thr Ala Val His His Ala Phe Thr Ser Pro Lys Pro Glu Phe Leu  
 450 455 460

Asp Asn Phe Asp Thr Asn Pro Gly Asp Ala Leu Ala Tyr Ala Tyr Asp  
 465 470 475 480  
 Ile Val Cys Asn Gly Asn Glu Ile Gly Gly Gly Ser Ile Arg Ile His  
 485 490 495  
 Gln Arg Asp Val Gln Glu Arg Val Phe Glu Val Met Gly Ile Thr Gly  
 500 505 510  
 Glu Glu Ala Arg Glu Lys Phe Gly Phe Leu Leu Asp Ala Phe Ala Phe  
 515 520 525  
 Gly Ala Pro Pro His Gly Gly Ile Ala Phe Gly Trp Asp Arg Ile Val  
 530 535 540  
 Ser Leu Leu Gly Gly Phe Asp Ser Ile Arg Asp Val Ile Ala Phe Pro  
 545 550 555 560  
 Lys Ser Gly Gly Gly Ile Asp Pro  
 565

<210> 283  
 <211> 1777  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1777)  
 <223> FRXA01730

<400> 283  
 tctgggctgc atgcccgccc tttttgggcg gttgagctta ttgtttaagg ctccagaaac 60  
 catcgactga tcaaaaccaa gcggaaggac ttccaccaac gtg ctg cgc act cat 115  
 Val Leu Arg Thr His  
 1 5  
 ctc tca ggc gag ctt cgt aaa gaa aac gca ggc cag tca gtt act ctg 163  
 Leu Ser Gly Glu Leu Arg Lys Glu Asn Ala Gly Gln Ser Val Thr Leu  
 10 15 20  
 acc ggc tgg gtc aat cgt cgc cgt gac cac ggt ggc gtg atc ttc atc 211  
 Thr Gly Trp Val Asn Arg Arg Arg Asp His Gly Gly Val Ile Phe Ile  
 25 30 35  
 gat ctt cgc gac cgt act ggc att gcc cag gtt gtt ttc cgc aat gag 259  
 Asp Leu Arg Asp Arg Thr Gly Ile Ala Gln Val Val Phe Arg Asn Glu  
 40 45 50  
 gac gtt gct gag cgt gca cac gca ctg cgc agc gaa ttc gtc cta cgc 307  
 Asp Val Ala Glu Arg Ala His Ala Leu Arg Ser Glu Phe Val Leu Arg  
 55 60 65  
 gtc acc ggc gtc gtc gaa gag cgc cca gaa ggc tct caa aac cct aac 355  
 Val Thr Gly Val Val Glu Glu Arg Pro Glu Gly Ser Gln Asn Pro Asn  
 70 75 80 85  
 ctt gca tcc ggc gac att gaa gtc agc gtc acc gaa ttt gag gta ctc 403  
 Leu Ala Ser Gly Asp Ile Glu Val Ser Val Thr Glu Phe Glu Val Leu

										90											95											100	
aac	gag	tcc	gct	cca	ctt	cct	ttc	cag	atc	gag	gat	tcc	tcc	tct	gct	451																	
Asn	Glu	Ser	Ala	Pro	Leu	Pro	Phe	Gln	Ile	Glu	Asp	Ser	Ser	Ser	Ala																		
			105				110				115																						
ggt	gaa	gtc	ggc	gaa	gag	acc	cgt	ctg	aag	tac	cgc	tac	ctg	gac	ctg	499																	
Gly	Glu	Val	Gly	Glu	Glu	Thr	Arg	Leu	Lys	Tyr	Arg	Tyr	Leu	Asp	Leu																		
			120				125				130																						
cgt	cgc	cca	gtt	cag	gcg	aac	gcc	ctg	cgt	ctg	cgt	tct	gct	gcc	aac	547																	
Arg	Arg	Pro	Val	Gln	Ala	Asn	Ala	Leu	Arg	Leu	Arg	Ser	Ala	Ala	Asn																		
			135				140				145																						
aag	gct	gca	cgc	acc	gtg	ctg	gac	agc	cac	gat	ttc	acc	gag	atc	gag	595																	
Lys	Ala	Ala	Arg	Thr	Val	Leu	Asp	Ser	His	Asp	Phe	Thr	Glu	Ile	Glu																		
150				155				160				165																					
acc	cca	acc	ttg	act	cgt	tcc	acc	cca	gaa	ggc	gca	cgt	gac	ttc	ctg	643																	
Thr	Pro	Thr	Leu	Thr	Arg	Ser	Thr	Pro	Glu	Gly	Ala	Arg	Asp	Phe	Leu																		
			170				175				180																						
gtg	cca	gct	cgt	ctg	cgc	cca	ggc	act	ttc	tac	gca	ttg	cca	cag	tcc	691																	
Val	Pro	Ala	Arg	Leu	Arg	Pro	Gly	Thr	Phe	Tyr	Ala	Leu	Pro	Gln	Ser																		
			185				190				195																						
cca	cag	ctg	ttc	aag	cag	ctg	ctg	cag	gtt	gct	ggc	atg	gag	cgc	tac	739																	
Pro	Gln	Leu	Phe	Lys	Gln	Leu	Leu	Gln	Val	Ala	Gly	Met	Glu	Arg	Tyr																		
			200				205				210																						
tac	cag	atc	gct	cgt	tgc	tac	cgc	gat	gag	gat	ttc	cgt	gca	gac	cgt	787																	
Tyr	Gln	Ile	Ala	Arg	Cys	Tyr	Arg	Asp	Glu	Asp	Phe	Arg	Ala	Asp	Arg																		
			215				220				225																						
cag	cca	gag	ttc	acc	cag	ctg	gac	gtt	gaa	atg	tcc	ttc	gtg	gac	cag	835																	
Gln	Pro	Glu	Phe	Thr	Gln	Leu	Asp	Val	Glu	Met	Ser	Phe	Val	Asp	Gln																		
230				235				240				245																					
gat	gat	gtc	atc	gca	ctg	ggc	gag	gag	atc	atc	tct	gag	gtg	tgg	aag	883																	
Asp	Asp	Val	Ile	Ala	Leu	Gly	Glu	Glu	Ile	Ile	Ser	Glu	Val	Trp	Lys																		
			250				255				260																						
ttg	atc	gga	tat	gag	atc	aag	act	cca	atc	cca	cgc	atg	acc	tac	gcc	931																	
Leu	Ile	Gly	Tyr	Glu	Ile	Lys	Thr	Pro	Ile	Pro	Arg	Met	Thr	Tyr	Ala																		
			265				270				275																						
gat	gca	atg	cgt	cgc	tac	ggc	tcc	gac	aag	cca	gac	ctg	cgc	ttc	gac	979																	
Asp	Ala	Met	Arg	Arg	Tyr	Gly	Ser	Asp	Lys	Pro	Asp	Leu	Arg	Phe	Asp																		
			280				285				290																						
atc	gaa	atc	acc	gag	tgc	acc	gag	ttc	ttc	cag	gac	acc	aca	ttc	cgt	1027																	
Ile	Glu	Ile	Thr	Glu	Cys	Thr	Glu	Phe	Phe	Gln	Asp	Thr	Thr	Phe	Arg																		
			295				300				305																						
gtg	ttc	aag	aac	gaa	tat	gtc	ggc	gca	gtt	gtc	atg	acc	ggt	ggt	gct	1075																	
Val	Phe	Lys	Asn	Glu	Tyr	Val	Gly	Ala	Val	Val	Met	Thr	Gly	Gly	Ala																		
310				315				320				325																					
tcc	cag	cct	cgc	cgt	cag	ctc	gac	gca	tgg	cag	gaa	tgg	gcc	aag	cag	1123																	
Ser	Gln	Pro	Arg	Arg	Gln	Leu	Asp	Ala	Trp	Gln	Glu	Trp	Ala	Lys	Gln																		
			330				335				340																						

cgc ggt gct aag gga ctt gct tac atc ctc gtt ggt gaa gac ggc gag 1171  
 Arg Gly Ala Lys Gly Leu Ala Tyr Ile Leu Val Gly Glu Asp Gly Glu  
 345 350 355

ctg tcc gga cct gtg gct aag aac atc acc gac gct gag cgc gca gga 1219  
 Leu Ser Gly Pro Val Ala Lys Asn Ile Thr Asp Ala Glu Arg Ala Gly  
 360 365 370

atc gca gct cac gtt ggc gca cag cca ggc gac tgc atc ttc ttc gca 1267  
 Ile Ala Ala His Val Gly Ala Gln Pro Gly Asp Cys Ile Phe Phe Ala  
 375 380 385

gca gga gac acc aag tct tcc ctc gca ctg ctc ggt gca gct cgt ggc 1315  
 Ala Gly Asp Thr Lys Ser Ser Leu Ala Leu Leu Gly Ala Ala Arg Gly  
 390 395 400 405

gag atc gct aag aag ctc gac ctg atc aag gaa ggc gac tgg gca ttc 1363  
 Glu Ile Ala Lys Lys Leu Asp Leu Ile Lys Glu Gly Asp Trp Ala Phe  
 410 415 420

acc tgg atc gtt gac gct cca atg ttc gag cca gca gca gac gcc acc 1411  
 Thr Trp Ile Val Asp Ala Pro Met Phe Glu Pro Ala Ala Asp Ala Thr  
 425 430 435

gca tcc ggt gac gtt gca ctg ggt aac tcc aag tgg acc gca gtc cac 1459  
 Ala Ser Gly Asp Val Ala Leu Gly Asn Ser Lys Trp Thr Ala Val His  
 440 445 450

cac gcc ttc acc tca cct aag cca gag ttc ctg gac aac ttt gac acc 1507  
 His Ala Phe Thr Ser Pro Lys Pro Glu Phe Leu Asp Asn Phe Asp Thr  
 455 460 465

aac cca ggt gac gca ctt gct tat gca tac gac atc gtg tgc aac ggc 1555  
 Asn Pro Gly Asp Ala Leu Ala Tyr Ala Tyr Asp Ile Val Cys Asn Gly  
 470 475 480 485

aat gaa atc ggt ggc ggt tcc atc cgt atc cac cag cgc gac gtt cag 1603  
 Asn Glu Ile Gly Gly Gly Ser Ile Arg Ile His Gln Arg Asp Val Gln  
 490 495 500

gaa cgc gtt ttc gag gtt atg ggc atc acc ggt gaa gaa gca cgc gag 1651  
 Glu Arg Val Phe Glu Val Met Gly Ile Thr Gly Glu Glu Ala Arg Glu  
 505 510 515

aag ttc ggc ttc ctg ctt gac gcc ttc gca ttc ggc gca cct cca cac 1699  
 Lys Phe Gly Phe Leu Leu Asp Ala Phe Ala Phe Gly Ala Pro Pro His  
 520 525 530

ggc gga atc gca ttc ggc tgg gac cgc atc gtg tcc ctg ctg ggc ggc 1747  
 Gly Gly Ile Ala Phe Gly Trp Asp Arg Ile Val Ser Leu Leu Gly Gly  
 535 540 545

ttt gac tcc atc cgc gac gtc atc gcg ttc 1777  
 Phe Asp Ser Ile Arg Asp Val Ile Ala Phe  
 550 555

&lt;210&gt; 284

&lt;211&gt; 559

&lt;212&gt; PRT

<213> Corynebacterium glutamicum

<400> 284

Val	Leu	Arg	Thr	His	Leu	Ser	Gly	Glu	Leu	Arg	Lys	Glu	Asn	Ala	Gly
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Gln	Ser	Val	Thr	Leu	Thr	Gly	Trp	Val	Asn	Arg	Arg	Arg	Asp	His	Gly
			20					25					30		
Gly	Val	Ile	Phe	Ile	Asp	Leu	Arg	Asp	Arg	Thr	Gly	Ile	Ala	Gln	Val
		35					40					45			
Val	Phe	Arg	Asn	Glu	Asp	Val	Ala	Glu	Arg	Ala	His	Ala	Leu	Arg	Ser
	50					55					60				
Glu	Phe	Val	Leu	Arg	Val	Thr	Gly	Val	Val	Glu	Glu	Arg	Pro	Glu	Gly
65					70					75					80
Ser	Gln	Asn	Pro	Asn	Leu	Ala	Ser	Gly	Asp	Ile	Glu	Val	Ser	Val	Thr
				85					90					95	
Glu	Phe	Glu	Val	Leu	Asn	Glu	Ser	Ala	Pro	Leu	Pro	Phe	Gln	Ile	Glu
			100					105					110		
Asp	Ser	Ser	Ser	Ala	Gly	Glu	Val	Gly	Glu	Glu	Thr	Arg	Leu	Lys	Tyr
		115					120					125			
Arg	Tyr	Leu	Asp	Leu	Arg	Arg	Pro	Val	Gln	Ala	Asn	Ala	Leu	Arg	Leu
	130					135					140				
Arg	Ser	Ala	Ala	Asn	Lys	Ala	Ala	Arg	Thr	Val	Leu	Asp	Ser	His	Asp
145					150					155					160
Phe	Thr	Glu	Ile	Glu	Thr	Pro	Thr	Leu	Thr	Arg	Ser	Thr	Pro	Glu	Gly
				165					170					175	
Ala	Arg	Asp	Phe	Leu	Val	Pro	Ala	Arg	Leu	Arg	Pro	Gly	Thr	Phe	Tyr
			180					185					190		
Ala	Leu	Pro	Gln	Ser	Pro	Gln	Leu	Phe	Lys	Gln	Leu	Leu	Gln	Val	Ala
		195					200					205			
Gly	Met	Glu	Arg	Tyr	Tyr	Gln	Ile	Ala	Arg	Cys	Tyr	Arg	Asp	Glu	Asp
	210					215					220				
Phe	Arg	Ala	Asp	Arg	Gln	Pro	Glu	Phe	Thr	Gln	Leu	Asp	Val	Glu	Met
225					230					235					240
Ser	Phe	Val	Asp	Gln	Asp	Asp	Val	Ile	Ala	Leu	Gly	Glu	Glu	Ile	Ile
				245					250					255	
Ser	Glu	Val	Trp	Lys	Leu	Ile	Gly	Tyr	Glu	Ile	Lys	Thr	Pro	Ile	Pro
			260					265					270		
Arg	Met	Thr	Tyr	Ala	Asp	Ala	Met	Arg	Arg	Tyr	Gly	Ser	Asp	Lys	Pro
		275					280					285			
Asp	Leu	Arg	Phe	Asp	Ile	Glu	Ile	Thr	Glu	Cys	Thr	Glu	Phe	Phe	Gln
	290					295					300				
Asp	Thr	Thr	Phe	Arg	Val	Phe	Lys	Asn	Glu	Tyr	Val	Gly	Ala	Val	Val

305	310	315	320
Met Thr Gly Gly Ala Ser Gln Pro Arg Arg Gln Leu Asp Ala Trp Gln	325	330	335
Glu Trp Ala Lys Gln Arg Gly Ala Lys Gly Leu Ala Tyr Ile Leu Val	340	345	350
Gly Glu Asp Gly Glu Leu Ser Gly Pro Val Ala Lys Asn Ile Thr Asp	355	360	365
Ala Glu Arg Ala Gly Ile Ala Ala His Val Gly Ala Gln Pro Gly Asp	370	375	380
Cys Ile Phe Phe Ala Ala Gly Asp Thr Lys Ser Ser Leu Ala Leu Leu	385	390	400
Gly Ala Ala Arg Gly Glu Ile Ala Lys Lys Leu Asp Leu Ile Lys Glu	405	410	415
Gly Asp Trp Ala Phe Thr Trp Ile Val Asp Ala Pro Met Phe Glu Pro	420	425	430
Ala Ala Asp Ala Thr Ala Ser Gly Asp Val Ala Leu Gly Asn Ser Lys	435	440	445
Trp Thr Ala Val His His Ala Phe Thr Ser Pro Lys Pro Glu Phe Leu	450	455	460
Asp Asn Phe Asp Thr Asn Pro Gly Asp Ala Leu Ala Tyr Ala Tyr Asp	465	470	475
Ile Val Cys Asn Gly Asn Glu Ile Gly Gly Gly Ser Ile Arg Ile His	485	490	495
Gln Arg Asp Val Gln Glu Arg Val Phe Glu Val Met Gly Ile Thr Gly	500	505	510
Glu Glu Ala Arg Glu Lys Phe Gly Phe Leu Leu Asp Ala Phe Ala Phe	515	520	525
Gly Ala Pro Pro His Gly Gly Ile Ala Phe Gly Trp Asp Arg Ile Val	530	535	540
Ser Leu Leu Gly Gly Phe Asp Ser Ile Arg Asp Val Ile Ala Phe	545	550	555

&lt;210&gt; 285

&lt;211&gt; 1503

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1480)

&lt;223&gt; RXA00314

&lt;400&gt; 285

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tgaaaccttg agtgttcgca cacagggttag actaggggac	gtg act cta cgc atc	115
	Val Thr Leu Arg Ile	
	1 5	
ttt gac acc ggt acc cgt acg ctt cga gat ttt aaa cct gtt caa cca	163	
Phe Asp Thr Gly Thr Arg Thr Leu Arg Asp Phe Lys Pro Val Gln Pro		
	10 15 20	
ggt cat gcc tcg gtg tac ctg tgt ggt gcc acc ccg caa tct tca ccc	211	
Gly His Ala Ser Val Tyr Leu Cys Gly Ala Thr Pro Gln Ser Ser Pro		
	25 30 35	
cac att gga cat gtt cgt tca gca gta gcg ttt gat att ttg cgc cgc	259	
His Ile Gly His Val Arg Ser Ala Val Ala Phe Asp Ile Leu Arg Arg		
	40 45 50	
tgg ctc atg gct aag gga ctt gat gtg gca ttt gtt cgc aat gtc act	307	
Trp Leu Met Ala Lys Gly Leu Asp Val Ala Phe Val Arg Asn Val Thr		
	55 60 65	
gat atc gat gac aag att ctc acc aag gca tct gaa aat ggt cgc cct	355	
Asp Ile Asp Asp Lys Ile Leu Thr Lys Ala Ser Glu Asn Gly Arg Pro		
	70 75 80 85	
tgg tgg gaa tgg gtg tcc acc tat gaa cgt gaa ttc acc tgg acg tac	403	
Trp Trp Glu Trp Val Ser Thr Tyr Glu Arg Glu Phe Thr Trp Thr Tyr		
	90 95 100	
aac acg ttg ggt gtg ctt cct cca tca acg gag cct cgt gca aca ggc	451	
Asn Thr Leu Gly Val Leu Pro Pro Ser Thr Glu Pro Arg Ala Thr Gly		
	105 110 115	
cac gtc act cag atg att aag tac atg cag cgc ttg att gat aac ggc	499	
His Val Thr Gln Met Ile Lys Tyr Met Gln Arg Leu Ile Asp Asn Gly		
	120 125 130	
ttt gct tac gcc gtt gat ggc tct gtg tac ttt gat gtc gca gcg tgg	547	
Phe Ala Tyr Ala Val Asp Gly Ser Val Tyr Phe Asp Val Ala Ala Trp		
	135 140 145	
tcc aag gct gaa gga tct gac tat ggt tct ttg tcc gga aac cgt gtt	595	
Ser Lys Ala Glu Gly Ser Asp Tyr Gly Ser Leu Ser Gly Asn Arg Val		
	150 155 160 165	
gaa gat atg gag cag ggc gag ccc gat aac ttt ggt aag cgg ggg cca	643	
Glu Asp Met Glu Gln Gly Glu Pro Asp Asn Phe Gly Lys Arg Gly Pro		
	170 175 180	
cag gac ttt gct ctg tgg aag gct gcc aaa ccg ggt gag ccg tca tgg	691	
Gln Asp Phe Ala Leu Trp Lys Ala Ala Lys Pro Gly Glu Pro Ser Trp		
	185 190 195	
cca acc cct tgg gga gac ggc cgg ccg ggt tgg cat ttg gaa tgc tct	739	
Pro Thr Pro Trp Gly Asp Gly Arg Pro Gly Trp His Leu Glu Cys Ser		
	200 205 210	
gcc atg gcc acc tac tat ttg ggt gag caa ttt gat att cac tgt ggt	787	
Ala Met Ala Thr Tyr Tyr Leu Gly Glu Gln Phe Asp Ile His Cys Gly		
	215 220 225	
ggt ttg gat ctg caa ttt cca cac cat gaa aat gaa att gcc cag gca	835	

Gly 230	Leu	Asp	Leu	Gln	Phe 235	Pro	His	His	Glu	Asn 240	Glu	Ile	Ala	Gln	Ala 245	
cat	gcg	gct	ggc	gat	aaa	ttt	gcc	aac	tac	tgg	atg	cac	aat	cac	tgg	883
His	Ala	Ala	Gly	Asp 250	Lys	Phe	Ala	Asn	Tyr 255	Trp	Met	His	Asn	His	Trp 260	
gta	aca	atg	gcc	ggc	gag	aaa	atg	tcc	aag	tct	ttg	ggc	aat	gtt	ttg	931
Val	Thr	Met	Ala	Gly	Glu	Lys	Met	Ser 270	Lys	Ser	Leu	Gly	Asn	Val	Leu	
			265										275			
gct	gtg	ccg	gaa	atg	cta	aag	cag	gtt	cgt	cct	gtc	gag	ctt	cgt	tat	979
Ala	Val	Pro	Glu	Met	Leu	Lys	Gln	Val	Arg	Pro	Val	Glu	Leu	Arg	Tyr	
		280					285					290				
tac	ctt	ggg	tct	gcc	cat	tac	cgt	tcc	gtc	ctt	gag	tat	tcc	gag	agc	1027
Tyr	Leu	Gly	Ser	Ala	His	Tyr	Arg	Ser	Val	Leu	Glu	Tyr	Ser	Glu	Ser	
	295					300					305					
gct	ttg	agt	gaa	gct	gcg	gtg	ggc	tac	cgt	cg	att	gag	tct	ttc	ctt	1075
Ala	Leu	Ser	Glu	Ala	Ala	Val	Gly	Tyr	Arg	Arg	Ile	Glu	Ser	Phe	Leu	
310					315					320					325	
gag	cgt	gtg	ggg	gat	gtt	gag	gta	ggc	gag	tgg	acg	cca	ggc	ttt	gaa	1123
Glu	Arg	Val	Gly	Asp	Val	Glu	Val	Gly	Glu	Trp	Thr	Pro	Gly	Phe	Glu	
				330					335					340		
gtt	gcg	atg	gat	gag	gat	att	gca	gtt	cct	aag	gct	ttg	gct	gaa	atc	1171
Val	Ala	Met	Asp	Glu	Asp	Ile	Ala	Val	Pro	Lys	Ala	Leu	Ala	Glu	Ile	
			345					350					355			
cat	aac	gct	gtc	cg	gag	ggc	aat	gct	gcc	ttg	gat	aag	ggc	gat	cgt	1219
His	Asn	Ala	Val	Arg	Glu	Gly	Asn	Ala	Ala	Leu	Asp	Lys	Gly	Asp	Arg	
		360					365					370				
gag	gca	gcg	gag	aag	ctt	gct	tcc	tcg	gtt	cgt	gcg	atg	act	ggc	gtt	1267
Glu	Ala	Ala	Glu	Lys	Leu	Ala	Ser	Ser	Val	Arg	Ala	Met	Thr	Gly	Val	
	375				380						385					
ttg	ggc	ttc	gac	ccc	gtt	gaa	tgg	ggc	tca	gat	gca	ggc	gct	gat	ggc	1315
Leu	Gly	Phe	Asp	Pro	Val	Glu	Trp	Gly	Ser	Asp	Ala	Gly	Ala	Asp	Gly	
390					395					400					405	
aag	gca	gat	aag	gcg	ctt	gat	gtg	ctg	att	tct	tcg	gag	ctt	gag	cgt	1363
Lys	Ala	Asp	Lys	Ala	Leu	Asp	Val	Leu	Ile	Ser	Ser	Glu	Leu	Glu	Arg	
				410					415					420		
cgt	gca	act	gct	cgt	gct	gag	aag	aat	tgg	gcg	gtt	gct	gat	gag	gtt	1411
Arg	Ala	Thr	Ala	Arg	Ala	Glu	Lys	Asn	Trp	Ala	Val	Ala	Asp	Glu	Val	
			425					430					435			
cga	gat	cgt	ctt	gcc	gat	gct	ggc	att	gag	gtt	gtg	gat	acc	gca	gat	1459
Arg	Asp	Arg	Leu	Ala	Asp	Ala	Gly	Ile	Glu	Val	Val	Asp	Thr	Ala	Asp	
		440					445					450				
ggc	gct	aca	tgg	aaa	ttg	cag	taattacaga	cacttttaag	gag							1503
Gly	Ala	Thr	Trp	Lys	Leu	Gln										
	455					460										

<211> 460  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 286

Val	Thr	Leu	Arg	Ile	Phe	Asp	Thr	Gly	Thr	Arg	Thr	Leu	Arg	Asp	Phe
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Lys	Pro	Val	Gln	Pro	Gly	His	Ala	Ser	Val	Tyr	Leu	Cys	Gly	Ala	Thr
			20					25					30		
Pro	Gln	Ser	Ser	Pro	His	Ile	Gly	His	Val	Arg	Ser	Ala	Val	Ala	Phe
		35					40					45			
Asp	Ile	Leu	Arg	Arg	Trp	Leu	Met	Ala	Lys	Gly	Leu	Asp	Val	Ala	Phe
	50					55					60				
Val	Arg	Asn	Val	Thr	Asp	Ile	Asp	Asp	Lys	Ile	Leu	Thr	Lys	Ala	Ser
65					70					75					80
Glu	Asn	Gly	Arg	Pro	Trp	Trp	Glu	Trp	Val	Ser	Thr	Tyr	Glu	Arg	Glu
				85					90					95	
Phe	Thr	Trp	Thr	Tyr	Asn	Thr	Leu	Gly	Val	Leu	Pro	Pro	Ser	Thr	Glu
			100					105					110		
Pro	Arg	Ala	Thr	Gly	His	Val	Thr	Gln	Met	Ile	Lys	Tyr	Met	Gln	Arg
		115					120					125			
Leu	Ile	Asp	Asn	Gly	Phe	Ala	Tyr	Ala	Val	Asp	Gly	Ser	Val	Tyr	Phe
	130					135					140				
Asp	Val	Ala	Ala	Trp	Ser	Lys	Ala	Glu	Gly	Ser	Asp	Tyr	Gly	Ser	Leu
145					150					155					160
Ser	Gly	Asn	Arg	Val	Glu	Asp	Met	Glu	Gln	Gly	Glu	Pro	Asp	Asn	Phe
				165					170					175	
Gly	Lys	Arg	Gly	Pro	Gln	Asp	Phe	Ala	Leu	Trp	Lys	Ala	Ala	Lys	Pro
			180					185					190		
Gly	Glu	Pro	Ser	Trp	Pro	Thr	Pro	Trp	Gly	Asp	Gly	Arg	Pro	Gly	Trp
		195					200					205			
His	Leu	Glu	Cys	Ser	Ala	Met	Ala	Thr	Tyr	Tyr	Leu	Gly	Glu	Gln	Phe
	210					215					220				
Asp	Ile	His	Cys	Gly	Gly	Leu	Asp	Leu	Gln	Phe	Pro	His	His	Glu	Asn
225					230					235					240
Glu	Ile	Ala	Gln	Ala	His	Ala	Ala	Gly	Asp	Lys	Phe	Ala	Asn	Tyr	Trp
				245					250					255	
Met	His	Asn	His	Trp	Val	Thr	Met	Ala	Gly	Glu	Lys	Met	Ser	Lys	Ser
			260					265					270		
Leu	Gly	Asn	Val	Leu	Ala	Val	Pro	Glu	Met	Leu	Lys	Gln	Val	Arg	Pro
		275					280					285			
Val	Glu	Leu	Arg	Tyr	Tyr	Leu	Gly	Ser	Ala	His	Tyr	Arg	Ser	Val	Leu
	290					295					300				

Glu Tyr Ser Glu Ser Ala Leu Ser Glu Ala Ala Val Gly Tyr Arg Arg  
 305 310 315 320  
 Ile Glu Ser Phe Leu Glu Arg Val Gly Asp Val Glu Val Gly Glu Trp  
 325 330 335  
 Thr Pro Gly Phe Glu Val Ala Met Asp Glu Asp Ile Ala Val Pro Lys  
 340 345 350  
 Ala Leu Ala Glu Ile His Asn Ala Val Arg Glu Gly Asn Ala Ala Leu  
 355 360 365  
 Asp Lys Gly Asp Arg Glu Ala Ala Glu Lys Leu Ala Ser Ser Val Arg  
 370 375 380  
 Ala Met Thr Gly Val Leu Gly Phe Asp Pro Val Glu Trp Gly Ser Asp  
 385 390 395 400  
 Ala Gly Ala Asp Gly Lys Ala Asp Lys Ala Leu Asp Val Leu Ile Ser  
 405 410 415  
 Ser Glu Leu Glu Arg Arg Ala Thr Ala Arg Ala Glu Lys Asn Trp Ala  
 420 425 430  
 Val Ala Asp Glu Val Arg Asp Arg Leu Ala Asp Ala Gly Ile Glu Val  
 435 440 445  
 Val Asp Thr Ala Asp Gly Ala Thr Trp Lys Leu Gln  
 450 455 460

<210> 287  
 <211> 1383  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1360)  
 <223> RXA02204

<400> 287  
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 Met Gln Ser Trp Pro  
 1 5  
 aca cct gaa gta cct gct ctc gct ggc acg cct gtg cct ttg gaa ttg 163  
 Thr Pro Glu Val Pro Ala Leu Ala Gly Thr Pro Val Pro Leu Glu Leu  
 10 15 20  
 ttc gac act gca gat cag gaa gta cgc ctg gtt gaa acc cca cct gcc 211  
 Phe Asp Thr Ala Asp Gln Glu Val Arg Leu Val Glu Thr Pro Pro Ala  
 25 30 35  
 gga tcc gac aca ccg gtt ggc atg tac gtc tgt ggc atc act ccc tac 259  
 Gly Ser Asp Thr Pro Val Gly Met Tyr Val Cys Gly Ile Thr Pro Tyr  
 40 45 50

gac tcc aca cac ttg ggg cac gcg gcg aca tac ctc gct ttc gat ctg	307
Asp Ser Thr His Leu Gly His Ala Ala Thr Tyr Leu Ala Phe Asp Leu	
55 60 65	
atc tac cgc atc ctg ctg gac aat gat cac gat gtc cac tac gtc caa	355
Ile Tyr Arg Ile Leu Leu Asp Asn Asp His Asp Val His Tyr Val Gln	
70 75 80 85	
aac atc acc gat gtc gat gac cct ctg ttt gaa cgc gca gcc cgc gac	403
Asn Ile Thr Asp Val Asp Asp Pro Leu Phe Glu Arg Ala Ala Arg Asp	
90 95 100	
ggc gtc gac tgg cgc gac ctc ggc acc agc caa atc aac ctc ttc cgc	451
Gly Val Asp Trp Arg Asp Leu Gly Thr Ser Gln Ile Asn Leu Phe Arg	
105 110 115	
agc gat atg gaa gcc ctg agc atc att ccg ccg aag gac tac atc ggt	499
Ser Asp Met Glu Ala Leu Ser Ile Ile Pro Pro Lys Asp Tyr Ile Gly	
120 125 130	
gcg att gag tcc atc gac gaa gtc att gag atg gtc aag acg ctt ctc	547
Ala Ile Glu Ser Ile Asp Glu Val Ile Glu Met Val Lys Thr Leu Leu	
135 140 145	
gac gaa ggc gcc gcg tac atc gtc gag gac gcc gaa tat cca gat gtc	595
Asp Glu Gly Ala Ala Tyr Ile Val Glu Asp Ala Glu Tyr Pro Asp Val	
150 155 160 165	
tac gca tca atc aac gcc aca gac aaa ttt ggc tac gag tcc aat tac	643
Tyr Ala Ser Ile Asn Ala Thr Asp Lys Phe Gly Tyr Glu Ser Asn Tyr	
170 175 180	
gac gca gcg acc atg gct gag ttc ttc gca gaa cgc ggc ggc gac cca	691
Asp Ala Ala Thr Met Ala Glu Phe Phe Ala Glu Arg Gly Gly Asp Pro	
185 190 195	
gag cgt ccc ggc aag aaa aac ccc atg gat gcc ctc ctg tgg cgc gca	739
Glu Arg Pro Gly Lys Lys Asn Pro Met Asp Ala Leu Leu Trp Arg Ala	
200 205 210	
gcc cgc gaa ggt gaa cca agc tgg gaa tcc cca ttc ggc gca ggt cgt	787
Ala Arg Glu Gly Glu Pro Ser Trp Glu Ser Pro Phe Gly Ala Gly Arg	
215 220 225	
cct ggc tgg cac atc gag tgt tca gca atc gct acc aac cgc cta gga	835
Pro Gly Trp His Ile Glu Cys Ser Ala Ile Ala Thr Asn Arg Leu Gly	
230 235 240 245	
cac agc ttt gat atc caa ggt ggc ggc tct gac ctg atc ttc cct cac	883
His Ser Phe Asp Ile Gln Gly Gly Gly Ser Asp Leu Ile Phe Pro His	
250 255 260	
cac gag ttc tcc gca gcg cac gcc gaa gca gct cac ggt gtc gag cgc	931
His Glu Phe Ser Ala Ala His Ala Glu Ala Ala His Gly Val Glu Arg	
265 270 275	
atg gct aag cac tac gtc cac gct ggc atg ata tcc caa gat ggc gtg	979
Met Ala Lys His Tyr Val His Ala Gly Met Ile Ser Gln Asp Gly Val	
280 285 290	
aaa atg tcc aag tct ttg ggc aac ctg gaa ttt gtt tcc cgc ctc acc	1027

Lys Met Ser Lys Ser Leu Gly Asn Leu Glu Phe Val Ser Arg Leu Thr  
 295 300 305  
 gct gca ggc cac gag ccc ggc gcg atc cgc ctc ggt gtt ttt gcc aac 1075  
 Ala Ala Gly His Glu Pro Gly Ala Ile Arg Leu Gly Val Phe Ala Asn  
 310 315 320 325  
 cat tac cgt ggc aac cgt gat tgg aac gca gag agc ctc gcc acc gca 1123  
 His Tyr Arg Gly Asn Arg Asp Trp Asn Ala Glu Ser Leu Ala Thr Ala  
 330 335 340  
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 Glu Gln Arg Leu Ala Thr Trp Arg Glu Ala Ala Arg Ala Ala Thr Asn  
 345 350 355  
 agg gaa gat gcc att gca gtt gtc gag cag ctt cgt gca cac cta tct 1219  
 Arg Glu Asp Ala Ile Ala Val Val Glu Gln Leu Arg Ala His Leu Ser  
 360 365 370  
 gct gac ctt gat act ccc ggc gcg ctc gcc gcg gta gat aat tgg gca 1267  
 Ala Asp Leu Asp Thr Pro Gly Ala Leu Ala Ala Val Asp Asn Trp Ala  
 375 380 385  
 gcg ggt atc gac acc acg acc gat tca aaa gag ttc acc gag gta gga 1315  
 Ala Gly Ile Asp Thr Thr Asp Ser Lys Glu Phe Thr Glu Val Gly  
 390 395 400 405  
 aac atc gtg gtc gca gcc att gat gcc ctc ctg ggc gtg cag ctc 1360  
 Asn Ile Val Val Ala Ala Ile Asp Ala Leu Leu Gly Val Gln Leu  
 410 415 420  
 taggaaattt caggaacaat aca 1383

&lt;210&gt; 288

&lt;211&gt; 420

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 288

Met Gln Ser Trp Pro Thr Pro Glu Val Pro Ala Leu Ala Gly Thr Pro  
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 Val Pro Leu Glu Leu Phe Asp Thr Ala Asp Gln Glu Val Arg Leu Val  
 20 25 30  
 Glu Thr Pro Pro Ala Gly Ser Asp Thr Pro Val Gly Met Tyr Val Cys  
 35 40 45  
 Gly Ile Thr Pro Tyr Asp Ser Thr His Leu Gly His Ala Ala Thr Tyr  
 50 55 60  
 Leu Ala Phe Asp Leu Ile Tyr Arg Ile Leu Leu Asp Asn Asp His Asp  
 65 70 75 80  
 Val His Tyr Val Gln Asn Ile Thr Asp Val Asp Asp Pro Leu Phe Glu  
 85 90 95  
 Arg Ala Ala Arg Asp Gly Val Asp Trp Arg Asp Leu Gly Thr Ser Gln  
 100 105 110

Ile Asn Leu Phe Arg Ser Asp Met Glu Ala Leu Ser Ile Ile Pro Pro  
 115 120 125  
 Lys Asp Tyr Ile Gly Ala Ile Glu Ser Ile Asp Glu Val Ile Glu Met  
 130 135 140  
 Val Lys Thr Leu Leu Asp Glu Gly Ala Ala Tyr Ile Val Glu Asp Ala  
 145 150 155 160  
 Glu Tyr Pro Asp Val Tyr Ala Ser Ile Asn Ala Thr Asp Lys Phe Gly  
 165 170 175  
 Tyr Glu Ser Asn Tyr Asp Ala Ala Thr Met Ala Glu Phe Phe Ala Glu  
 180 185 190  
 Arg Gly Gly Asp Pro Glu Arg Pro Gly Lys Lys Asn Pro Met Asp Ala  
 195 200 205  
 Leu Leu Trp Arg Ala Ala Arg Glu Gly Glu Pro Ser Trp Glu Ser Pro  
 210 215 220  
 Phe Gly Ala Gly Arg Pro Gly Trp His Ile Glu Cys Ser Ala Ile Ala  
 225 230 235 240  
 Thr Asn Arg Leu Gly His Ser Phe Asp Ile Gln Gly Gly Gly Ser Asp  
 245 250 255  
 Leu Ile Phe Pro His His Glu Phe Ser Ala Ala His Ala Glu Ala Ala  
 260 265 270  
 His Gly Val Glu Arg Met Ala Lys His Tyr Val His Ala Gly Met Ile  
 275 280 285  
 Ser Gln Asp Gly Val Lys Met Ser Lys Ser Leu Gly Asn Leu Glu Phe  
 290 295 300  
 Val Ser Arg Leu Thr Ala Ala Gly His Glu Pro Gly Ala Ile Arg Leu  
 305 310 315 320  
 Gly Val Phe Ala Asn His Tyr Arg Gly Asn Arg Asp Trp Asn Ala Glu  
 325 330 335  
 Ser Leu Ala Thr Ala Glu Gln Arg Leu Ala Thr Trp Arg Glu Ala Ala  
 340 345 350  
 Arg Ala Ala Thr Asn Arg Glu Asp Ala Ile Ala Val Val Glu Gln Leu  
 355 360 365  
 Arg Ala His Leu Ser Ala Asp Leu Asp Thr Pro Gly Ala Leu Ala Ala  
 370 375 380  
 Val Asp Asn Trp Ala Ala Gly Ile Asp Thr Thr Thr Asp Ser Lys Glu  
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 Gly Val Gln Leu  
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 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(1509)  
 <223> RXA01124

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 cgt ttc tgc cca tcg ccc acc ggc acc cca cac gtt gga ctt gtg cgc 96  
 Arg Phe Cys Pro Ser Pro Thr Gly Thr Pro His Val Gly Leu Val Arg  
 20 25 30  
 acc gcg ctg ttc aac tgg gca tat gct cgc cac act gga ggc aag tta 144  
 Thr Ala Leu Phe Asn Trp Ala Tyr Ala Arg His Thr Gly Gly Lys Leu  
 35 40 45  
 gtt ttc cgc att gag gac act gac gct gcc cgc gat tcc gag gag tct 192  
 Val Phe Arg Ile Glu Asp Thr Asp Ala Ala Arg Asp Ser Glu Glu Ser  
 50 55 60  
 tac tcc gcc atc atc gat tcc ctg cgc tgg ttg gga atg gac tgg gat 240  
 Tyr Ser Ala Ile Ile Asp Ser Leu Arg Trp Leu Gly Met Asp Trp Asp  
 65 70 75 80  
 gag ggt gtg gaa aag ggc ggc ccg cat gag ccc tac cgc cag tcg cag 288  
 Glu Gly Val Glu Lys Gly Gly Pro His Glu Pro Tyr Arg Gln Ser Gln  
 85 90 95  
 cgc aag gac atc tat cag gat gtg ttg aag cag ctt atc gac gcc ggt 336  
 Arg Lys Asp Ile Tyr Gln Asp Val Leu Lys Gln Leu Ile Asp Ala Gly  
 100 105 110  
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 Glu Val Tyr Pro Ala Tyr Ser Thr Ala Glu Glu Val Glu Glu Arg His  
 115 120 125  
 aag gct gct ggc cgc gat cca aag ctc ggc tac gac aac ttt gac cgt 432  
 Lys Ala Ala Gly Arg Asp Pro Lys Leu Gly Tyr Asp Asn Phe Asp Arg  
 130 135 140  
 gat ctc acc gaa gag cag gtc gca gca ttt gag gct gag ggg cgt aag 480  
 Asp Leu Thr Glu Glu Gln Val Ala Ala Phe Glu Ala Glu Gly Arg Lys  
 145 150 155 160  
 cct gtg tgg cgt ctg cgc atg cca gag cag gat tgg aag tgg act gac 528  
 Pro Val Trp Arg Leu Arg Met Pro Glu Gln Asp Trp Lys Trp Thr Asp  
 165 170 175  
 ctg gtc cgc ggt gaa gtt gag ttc aag tcg ttc acc cag cct gac ttc 576  
 Leu Val Arg Gly Glu Val Glu Phe Lys Ser Phe Thr Gln Pro Asp Phe  
 180 185 190  
 gtg gtt gct cgt tcc aac ggt gag cct ttg tac acc ctg gtc aac cct 624  
 Val Val Ala Arg Ser Asn Gly Glu Pro Leu Tyr Thr Leu Val Asn Pro

195	200	205	
gtt gat gat gcg ttg atg gaa gtc acc cat gtg ctg cgt ggt gag gat Val Asp Asp Ala Leu Met Glu Val Thr His Val Leu Arg Gly Glu Asp 210 215 220			672
ctt ttg cca tcg act cct cgt cag ctt gct ctg tat gag gcg ctc aag Leu Leu Pro Ser Thr Pro Arg Gln Leu Ala Leu Tyr Glu Ala Leu Lys 225 230 235 240			720
cgc att ggc gtg gca aag gcc acc cca gcc ttt ggt cac ctg cca ttt Arg Ile Gly Val Ala Lys Ala Thr Pro Ala Phe Gly His Leu Pro Phe 245 250 255			768
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agc ctg ttc aac cac cgt gac aac ggc atc atc cca gag ggc atg ctc Ser Leu Phe Asn His Arg Asp Asn Gly Ile Ile Pro Glu Gly Met Leu 275 280 285			864
aac tac ctg gcg ctg ctg ggt tgg tca ctg tct gct gat cag gac att Asn Tyr Leu Ala Leu Leu Gly Trp Ser Leu Ser Ala Asp Gln Asp Ile 290 295 300			912
ttc ggt gtc gat gag ttg atc gct aac ttt gat gtc gct gac gtg ttg Phe Gly Val Asp Glu Leu Ile Ala Asn Phe Asp Val Ala Asp Val Leu 305 310 315 320			960
ggc aac cca gct cgc ttt gac cag aag aag ctt gag gcc atc aac gcg Gly Asn Pro Ala Arg Phe Asp Gln Lys Lys Leu Glu Ala Ile Asn Ala 325 330 335			1008
gat cac atc cga ctt ctg gag cct aag gat ttc gag gct cgc ctg cgc Asp His Ile Arg Leu Leu Glu Pro Lys Asp Phe Glu Ala Arg Leu Arg 340 345 350			1056
gcg tac atg act gag tac acc gag ttc cca gcg gat tac cca gct gag Ala Tyr Met Thr Glu Tyr Thr Glu Phe Pro Ala Asp Tyr Pro Ala Glu 355 360 365			1104
aag ttt gcc att gct gcg gag ctg gtt cag acc cgc atc aag gtg ctc Lys Phe Ala Ile Ala Ala Glu Leu Val Gln Thr Arg Ile Lys Val Leu 370 375 380			1152
agc gag gcg tgg gat ctg ctg aag ttc ctg gtc acc gct gac gaa gat Ser Glu Ala Trp Asp Leu Leu Lys Phe Leu Val Thr Ala Asp Glu Asp 385 390 395 400			1200
ctg gtg ttc aat gag aag gct gcc aag aag aac ctc aag gag acc gct Leu Val Phe Asn Glu Lys Ala Ala Lys Lys Asn Leu Lys Glu Thr Ala 405 410 415			1248
gtt gag cct ctc aac gcc ggt atc gca gcg ctg gag gca gtg gag gag Val Glu Pro Leu Asn Ala Gly Ile Ala Ala Leu Glu Ala Val Glu Glu 420 425 430			1296
tgg acc act cca aac att gaa gca gca ttg aac aag gct ctc att gag Trp Thr Thr Pro Asn Ile Glu Ala Ala Leu Asn Lys Ala Leu Ile Glu 435 440 445			1344

gat cta ggc ctg aag cct cgc gtg gcg ttc ggt gcg ttg cgc att ggt 1392  
 Asp Leu Gly Leu Lys Pro Arg Val Ala Phe Gly Ala Leu Arg Ile Gly  
 450 455 460

atc tcc ggc gag gct gta tcc cca cca ctg ttt gag tcc atg gag ctt 1440  
 Ile Ser Gly Glu Ala Val Ser Pro Pro Leu Phe Glu Ser Met Glu Leu  
 465 470 475 480

ttg ggc aag gaa tcc acg ttg gtt cgt ctg aag gtt act cgt gag cag 1488  
 Leu Gly Lys Glu Ser Thr Leu Val Arg Leu Lys Val Thr Arg Glu Gln  
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acc cca ttc gtg gtc gct gag taaaacctgt agatgaacaa aag 1532  
 Thr Pro Phe Val Val Ala Glu  
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<211> 503

<212> PRT

<213> Corynebacterium glutamicum

<400> 290

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Thr Ala Leu Phe Asn Trp Ala Tyr Ala Arg His Thr Gly Gly Lys Leu  
 35 40 45

Val Phe Arg Ile Glu Asp Thr Asp Ala Ala Arg Asp Ser Glu Glu Ser  
 50 55 60

Tyr Ser Ala Ile Ile Asp Ser Leu Arg Trp Leu Gly Met Asp Trp Asp  
 65 70 75 80

Glu Gly Val Glu Lys Gly Gly Pro His Glu Pro Tyr Arg Gln Ser Gln  
 85 90 95

Arg Lys Asp Ile Tyr Gln Asp Val Leu Lys Gln Leu Ile Asp Ala Gly  
 100 105 110

Glu Val Tyr Pro Ala Tyr Ser Thr Ala Glu Glu Val Glu Glu Arg His  
 115 120 125

Lys Ala Ala Gly Arg Asp Pro Lys Leu Gly Tyr Asp Asn Phe Asp Arg  
 130 135 140

Asp Leu Thr Glu Glu Gln Val Ala Ala Phe Glu Ala Glu Gly Arg Lys  
 145 150 155 160

Pro Val Trp Arg Leu Arg Met Pro Glu Gln Asp Trp Lys Trp Thr Asp  
 165 170 175

Leu Val Arg Gly Glu Val Glu Phe Lys Ser Phe Thr Gln Pro Asp Phe  
 180 185 190

Val Val Ala Arg Ser Asn Gly Glu Pro Leu Tyr Thr Leu Val Asn Pro

195						200						205					
Val	Asp	Asp	Ala	Leu	Met	Glu	Val	Thr	His	Val	Leu	Arg	Gly	Glu	Asp		
210						215						220					
Leu	Leu	Pro	Ser	Thr	Pro	Arg	Gln	Leu	Ala	Leu	Tyr	Glu	Ala	Leu	Lys		
225						230						235					
Arg	Ile	Gly	Val	Ala	Lys	Ala	Thr	Pro	Ala	Phe	Gly	His	Leu	Pro	Phe		
245						250						255					
Val	Met	Gly	Glu	Gly	Asn	Lys	Lys	Leu	Ser	Lys	Arg	Asp	Pro	Gln	Ser		
260						265						270					
Ser	Leu	Phe	Asn	His	Arg	Asp	Asn	Gly	Ile	Ile	Pro	Glu	Gly	Met	Leu		
275						280						285					
Asn	Tyr	Leu	Ala	Leu	Leu	Gly	Trp	Ser	Leu	Ser	Ala	Asp	Gln	Asp	Ile		
290						295						300					
Phe	Gly	Val	Asp	Glu	Leu	Ile	Ala	Asn	Phe	Asp	Val	Ala	Asp	Val	Leu		
305						310						315					
Gly	Asn	Pro	Ala	Arg	Phe	Asp	Gln	Lys	Lys	Leu	Glu	Ala	Ile	Asn	Ala		
325						330						335					
Asp	His	Ile	Arg	Leu	Leu	Glu	Pro	Lys	Asp	Phe	Glu	Ala	Arg	Leu	Arg		
340						345						350					
Ala	Tyr	Met	Thr	Glu	Tyr	Thr	Glu	Phe	Pro	Ala	Asp	Tyr	Pro	Ala	Glu		
355						360						365					
Lys	Phe	Ala	Ile	Ala	Ala	Glu	Leu	Val	Gln	Thr	Arg	Ile	Lys	Val	Leu		
370						375						380					
Ser	Glu	Ala	Trp	Asp	Leu	Leu	Lys	Phe	Leu	Val	Thr	Ala	Asp	Glu	Asp		
385						390						395					
Leu	Val	Phe	Asn	Glu	Lys	Ala	Ala	Lys	Lys	Asn	Leu	Lys	Glu	Thr	Ala		
405						410						415					
Val	Glu	Pro	Leu	Asn	Ala	Gly	Ile	Ala	Ala	Leu	Glu	Ala	Val	Glu	Glu		
420						425						430					
Trp	Thr	Thr	Pro	Asn	Ile	Glu	Ala	Ala	Leu	Asn	Lys	Ala	Leu	Ile	Glu		
435						440						445					
Asp	Leu	Gly	Leu	Lys	Pro	Arg	Val	Ala	Phe	Gly	Ala	Leu	Arg	Ile	Gly		
450						455						460					
Ile	Ser	Gly	Glu	Ala	Val	Ser	Pro	Pro	Leu	Phe	Glu	Ser	Met	Glu	Leu		
465						470						475					
Leu	Gly	Lys	Glu	Ser	Thr	Leu	Val	Arg	Leu	Lys	Val	Thr	Arg	Glu	Gln		
485						490						495					
Thr	Pro	Phe	Val	Val	Ala	Glu											
500																	

&lt;210&gt; 291

<211> 736  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220> .  
 <221> CDS  
 <222> (101)..(736)  
 <223> RXN00458

<400> 291

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                                         Met Ala Gly Arg Tyr
                                         1                               5

gca cca tca cca agc ggc gac ctt cac ttt ggc aac ctc cgc aca gca 163
Ala Pro Ser Pro Ser Gly Asp Leu His Phe Gly Asn Leu Arg Thr Ala
                               10                               15                               20

ctg ctg gcc tgg ctg ttc gcg cgc tcc gaa gga aaa aaa ttc ctc atg 211
Leu Leu Ala Trp Leu Phe Ala Arg Ser Glu Gly Lys Lys Phe Leu Met
                               25                               30                               35

cgg gtc gaa gac atc gat gaa caa cgc tca tcc aag gaa tcc gcc gaa 259
Arg Val Glu Asp Ile Asp Glu Gln Arg Ser Ser Lys Glu Ser Ala Glu
                               40                               45                               50

agc caa ctc gca gac cta tcc gcc ctg ggt ctc gat tgg gat ggc gac 307
Ser Gln Leu Ala Asp Leu Ser Ala Leu Gly Leu Asp Trp Asp Gly Asp
                               55                               60                               65

gtc ctc tac caa tcc aca cgc tac gac gcc tac cgc gca gcc ctt gaa 355
Val Leu Tyr Gln Ser Thr Arg Tyr Asp Ala Tyr Arg Ala Ala Leu Glu
                               70                               75                               80                               85

aaa cta gac acc tac gaa tgt tat tgc tcg cgc cgg gac atc caa gaa 403
Lys Leu Asp Thr Tyr Glu Cys Tyr Cys Ser Arg Arg Asp Ile Gln Glu
                               90                               95                               100

gcc tcg cgg gca ccc cat gtg gct ccg gga gtg tat ccg gga acg tgt 451
Ala Ser Arg Ala Pro His Val Ala Pro Gly Val Tyr Pro Gly Thr Cys
                               105                               110                               115

agg gga ttg aag gag gag gaa cgc gtc gaa aag cgt gca acc ttg gct 499
Arg Gly Leu Lys Glu Glu Glu Arg Val Glu Lys Arg Ala Thr Leu Ala
                               120                               125                               130

gcg caa aac cgg cac ccc gcc att cgc ctg cgc gcg cag gta acc tcg 547
Ala Gln Asn Arg His Pro Ala Ile Arg Leu Arg Ala Gln Val Thr Ser
                               135                               140                               145

ttt gat ttt cac gac cga ctt cgc ggc cca caa act ggc ccc gta gac 595
Phe Asp Phe His Asp Arg Leu Arg Gly Pro Gln Thr Gly Pro Val Asp
                               150                               155                               160                               165

gat ttc att ctg ctc cgc ggc ggg cag gaa ccc gga tgg gca tac aac 643
Asp Phe Ile Leu Leu Arg Gly Gly Gln Glu Pro Gly Trp Ala Tyr Asn
                               170                               175                               180

tta act gtc gtc gtc gac gat gcc tac caa ggc gtt gac cag gta gtc 691
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Leu Thr Val Val Val Asp Asp Ala Tyr Gln Gly Val Asp Gln Val Val  
 185 190 195

cgc ggc gac gac cta ctc gaa ttc ggc gcg cgc caa gct acc ttg 736  
 Arg Gly Asp Asp Leu Leu Glu Phe Gly Ala Arg Gln Ala Thr Leu  
 200 205 210

<210> 292  
 <211> 212  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 292  
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Lys Lys Phe Leu Met Arg Val Glu Asp Ile Asp Glu Gln Arg Ser Ser  
 35 40 45

Lys Glu Ser Ala Glu Ser Gln Leu Ala Asp Leu Ser Ala Leu Gly Leu  
 50 55 60

Asp Trp Asp Gly Asp Val Leu Tyr Gln Ser Thr Arg Tyr Asp Ala Tyr  
 65 70 75 80

Arg Ala Ala Leu Glu Lys Leu Asp Thr Tyr Glu Cys Tyr Cys Ser Arg  
 85 90 95

Arg Asp Ile Gln Glu Ala Ser Arg Ala Pro His Val Ala Pro Gly Val  
 100 105 110

Tyr Pro Gly Thr Cys Arg Gly Leu Lys Glu Glu Glu Arg Val Glu Lys  
 115 120 125

Arg Ala Thr Leu Ala Ala Gln Asn Arg His Pro Ala Ile Arg Leu Arg  
 130 135 140

Ala Gln Val Thr Ser Phe Asp Phe His Asp Arg Leu Arg Gly Pro Gln  
 145 150 155 160

Thr Gly Pro Val Asp Asp Phe Ile Leu Leu Arg Gly Gly Gln Glu Pro  
 165 170 175

Gly Trp Ala Tyr Asn Leu Thr Val Val Val Asp Asp Ala Tyr Gln Gly  
 180 185 190

Val Asp Gln Val Val Arg Gly Asp Asp Leu Leu Glu Phe Gly Ala Arg  
 195 200 205

Gln Ala Thr Leu  
 210

<210> 293  
 <211> 328  
 <212> DNA  
 <213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(328)

&lt;223&gt; FRXA00458

&lt;400&gt; 293

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                                         Met Ala Gly Arg Tyr
                                         1 5

gca cca tca cca agc ggc gac ctt cac ttt ggc aac ctc cgc aca gca 163
Ala Pro Ser Pro Ser Gly Asp Leu His Phe Gly Asn Leu Arg Thr Ala
                        10 15 20

ctg ctg gcc tgg ctg ttc gcg cgc tcc gaa gga aaa aaa ttc ctc atg 211
Leu Leu Ala Trp Leu Phe Ala Arg Ser Glu Gly Lys Lys Phe Leu Met
                        25 30 35

cgg gtc gaa gac atc gat gaa caa cgc tca ttc aag gaa tcc gcc gaa 259
Arg Val Glu Asp Ile Asp Glu Gln Arg Ser Phe Lys Glu Ser Ala Glu
                        40 45 50

agc caa ctc gca gac cta tcc gcc ctg ggt ctc gat tgg gat ggc gac 307
Ser Gln Leu Ala Asp Leu Ser Ala Leu Gly Leu Asp Trp Asp Gly Asp
                        55 60 65

gtc ctc tac caa tcc aca cgc 328
Val Leu Tyr Gln Ser Thr Arg
70 75

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&lt;210&gt; 294

&lt;211&gt; 76

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 294

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Asn Leu Arg Thr Ala Leu Leu Ala Trp Leu Phe Ala Arg Ser Glu Gly
20 25 30

Lys Lys Phe Leu Met Arg Val Glu Asp Ile Asp Glu Gln Arg Ser Phe
35 40 45

Lys Glu Ser Ala Glu Ser Gln Leu Ala Asp Leu Ser Ala Leu Gly Leu
50 55 60

Asp Trp Asp Gly Asp Val Leu Tyr Gln Ser Thr Arg
65 70 75

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&lt;210&gt; 295

&lt;211&gt; 1506

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1483)

&lt;223&gt; RXA00069

&lt;400&gt; 295

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 Val Ala Gln Gln Ser  
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atc atc gac acc gtg gtt aac ctg tgt aaa cga cgt gga ctg gtg tac 163  
 Ile Ile Asp Thr Val Val Asn Leu Cys Lys Arg Arg Gly Leu Val Tyr  
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ccc tgt ggt gag atc tac ggc ggt acc cgc tct gcg tgg gac tac ggc 211  
 Pro Cys Gly Glu Ile Tyr Gly Gly Thr Arg Ser Ala Trp Asp Tyr Gly  
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 Ile Leu Pro Arg Gln Val Trp Val Thr Ser Gly His Val Glu Val Phe  
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 Thr Asp Pro Leu Val Glu Ser Leu Asn Thr His Lys Arg Tyr Arg Ala  
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 Asn Gly Leu Ala Asp Ile Asn Asp Pro Glu Thr Gly Gln Pro Gly Asn  
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 Trp Thr Glu Pro Lys Ala Phe Ser Gly Leu Leu Lys Thr Phe Leu Gly  
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 Gln Gly Ile Phe Val Asn Phe Lys Asn Val Met Asn Thr Ser Arg Met  
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 Lys Pro Pro Phe Gly Ile Ala Asn Ile Gly Lys Ser Phe Arg Asn Glu  
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atc acc cca ggt aac ttc att ttc cgt act cgt gag ttc gag cag atg 739

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Glu	Met	Glu	Phe	Phe	Val	Lys	Pro	Gly	Glu	Asp	Glu	Glu	Trp	His	Gln		
	215					220				225							
cac	tgg	att	gat	act	cgc	ctg	cag	tgg	tac	atc	aac	ctg	ggc	att	aag	835	
His	Trp	Ile	Asp	Thr	Arg	Leu	Gln	Trp	Tyr	Ile	Asn	Leu	Gly	Ile	Lys		
230					235					240					245		
cct	gag	aac	ctg	cgt	ctg	tac	gag	cac	cct	cag	gag	aag	ctg	tct	cac	883	
Pro	Glu	Asn	Leu	Arg	Leu	Tyr	Glu	His	Pro	Gln	Glu	Lys	Leu	Ser	His		
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tac	tcc	aag	cgc	act	ggt	gat	att	gag	tac	gca	ttc	aac	ttt	gct	aac	931	
Tyr	Ser	Lys	Arg	Thr	Val	Asp	Ile	Glu	Tyr	Ala	Phe	Asn	Phe	Ala	Asn		
			265					270					275				
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Thr	Lys	Trp	Gly	Glu	Leu	Glu	Gly	Ile	Ala	Asn	Arg	Thr	Asp	Tyr	Asp		
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Leu	Arg	Val	His	Ser	Glu	Gly	Ser	Gly	Glu	Asp	Leu	Ser	Phe	Phe	Asp		
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Gln	Glu	Thr	Asn	Glu	Arg	Trp	Ile	Pro	Phe	Val	Ile	Glu	Pro	Ala	Ala		
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ggt	ctt	ggt	cgc	gca	atg	atg	atg	ttc	ctg	atg	gat	gct	tat	cac	gag	1123	
Gly	Leu	Gly	Arg	Ala	Met	Met	Met	Phe	Leu	Met	Asp	Ala	Tyr	His	Glu		
				330					335					340			
gac	gaa	gca	cca	aac	tca	aag	ggt	ggc	gtc	gat	aag	cgt	gtt	gtt	ctg	1171	
Asp	Glu	Ala	Pro	Asn	Ser	Lys	Gly	Gly	Val	Asp	Lys	Arg	Val	Val	Leu		
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aag	ctt	gac	cgt	cgc	ctt	gcg	ccg	gtt	aag	gtt	gcg	gtc	ttg	ccg	ctg	1219	
Lys	Leu	Asp	Arg	Arg	Leu	Ala	Pro	Val	Lys	Val	Ala	Val	Leu	Pro	Leu		
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tca	aag	aag	gac	act	ttg	acg	cct	ttg	gcg	gaa	aag	ctc	gca	gca	gag	1267	
Ser	Lys	Lys	Asp	Thr	Leu	Thr	Pro	Leu	Ala	Glu	Lys	Leu	Ala	Ala	Glu		
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ctg	cgt	gaa	ttc	tgg	aac	gtt	gat	tac	gac	act	tca	ggt	gcg	att	ggt	1315	
Leu	Arg	Glu	Phe	Trp	Asn	Val	Asp	Tyr	Asp	Thr	Ser	Gly	Ala	Ile	Gly		
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cgc	cgt	tac	cgt	cgt	cag	gac	gag	atc	ggt	act	cca	ttc	tgc	gtc	acc	1363	
Arg	Arg	Tyr	Arg	Arg	Gln	Asp	Glu	Ile	Gly	Thr	Pro	Phe	Cys	Val	Thr		
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gtt	gac	ttt	gat	tct	ctc	gag	gac	aac	gct	gtg	acc	gtg	cgt	gag	cgc	1411	
Val	Asp	Phe	Asp	Ser	Leu	Glu	Asp	Asn	Ala	Val	Thr	Val	Arg	Glu	Arg		
			425					430					435				
gac	acc	atg	gag	cag	gtt	cgt	gtt	cca	ctt	gat	gag	ctg	cag	ggt	tac	1459	
Asp	Thr	Met	Glu	Gln	Val	Arg	Val	Pro	Leu	Asp	Glu	Leu	Gln	Gly	Tyr		

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 <213> Corynebacterium glutamicum

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 Ala Trp Asp Tyr Gly Pro Leu Gly Val Glu Leu Lys Glu Asn Ile Lys  
 35 40 45  
 Arg Gln Trp Trp Arg Ser Met Val Thr Ser Arg Pro Asp Val Val Gly  
 50 55 60  
 Val Asp Thr Ser Val Ile Leu Pro Arg Gln Val Trp Val Thr Ser Gly  
 65 70 75 80  
 His Val Glu Val Phe Thr Asp Pro Leu Val Glu Ser Leu Asn Thr His  
 85 90 95  
 Lys Arg Tyr Arg Ala Asp His Leu Leu Glu Gln Tyr Glu Glu Lys His  
 100 105 110  
 Gly His Pro Pro Val Asn Gly Leu Ala Asp Ile Asn Asp Pro Glu Thr  
 115 120 125  
 Gly Gln Pro Gly Asn Trp Thr Glu Pro Lys Ala Phe Ser Gly Leu Leu  
 130 135 140  
 Lys Thr Phe Leu Gly Pro Val Asp Asp Glu Glu Gly Leu His Tyr Leu  
 145 150 155 160  
 Arg Pro Glu Thr Ala Gln Gly Ile Phe Val Asn Phe Lys Asn Val Met  
 165 170 175  
 Asn Thr Ser Arg Met Lys Pro Pro Phe Gly Ile Ala Asn Ile Gly Lys  
 180 185 190  
 Ser Phe Arg Asn Glu Ile Thr Pro Gly Asn Phe Ile Phe Arg Thr Arg  
 195 200 205  
 Glu Phe Glu Gln Met Glu Met Glu Phe Phe Val Lys Pro Gly Glu Asp  
 210 215 220  
 Glu Glu Trp His Gln His Trp Ile Asp Thr Arg Leu Gln Trp Tyr Ile  
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 Asn Leu Gly Ile Lys Pro Glu Asn Leu Arg Leu Tyr Glu His Pro Gln  
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<212> DNA
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Ser Lys Ser Glu Lys Leu Gln Ser Phe Ala Ala Pro Lys Gly Val Pro  
10 15 20

gat tac gcc cca cca aaa tct gca gcg ttt tta gca gtc cgt gat gcc	211
Asp Tyr Ala Pro Pro Lys Ser Ala Ala Phe Leu Ala Val Arg Asp Ala	
25 30 35	
ttt gtt aat caa gca cat aag gcc ggg ttt gag cat att gag ctg ccg	259
Phe Val Asn Gln Ala His Lys Ala Gly Phe Glu His Ile Glu Leu Pro	
40 45 50	
atc ttt gaa gac acc ggc ttg ttt gcg cgt ggt gtt ggt gag tcc act	307
Ile Phe Glu Asp Thr Gly Leu Phe Ala Arg Gly Val Gly Glu Ser Thr	
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gac gta gtg agc aag gaa atg tac acc ttc gct gat cgt ggc gag cgc	355
Asp Val Val Ser Lys Glu Met Tyr Thr Phe Ala Asp Arg Gly Glu Arg	
70 75 80 85	
tct gtc acg ctg cgc cca gaa ggc act gca ggc gtg atg cgt gca gtt	403
Ser Val Thr Leu Arg Pro Glu Gly Thr Ala Gly Val Met Arg Ala Val	
90 95 100	
att gaa cac agc ctg gac cgt gga cag ctt ccc gta aag ctg aac tac	451
Ile Glu His Ser Leu Asp Arg Gly Gln Leu Pro Val Lys Leu Asn Tyr	
105 110 115	
gcc gga cca ttc ttc cgt tat gag cgt cct cag gca ggg cgt tac cgt	499
Ala Gly Pro Phe Phe Arg Tyr Glu Arg Pro Gln Ala Gly Arg Tyr Arg	
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cag ctt cag caa gta ggc gta gag gca att ggt gtg gat gat cca gcg	547
Gln Leu Gln Gln Val Gly Val Glu Ala Ile Gly Val Asp Asp Pro Ala	
135 140 145	
ctt gat gcg gag atc att gcg ctt gct gat cgt tct tac cgc agc ttg	595
Leu Asp Ala Glu Ile Ile Ala Leu Ala Asp Arg Ser Tyr Arg Ser Leu	
150 155 160 165	
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Gly Leu Gln Asp Phe Arg Leu Glu Leu Thr Ser Leu Gly Asp Arg His	
170 175 180	
tgc cgt ccc gag tat cgt cag aag ctg cag gat ttc ttg ttt gca ctt	691
Cys Arg Pro Glu Tyr Arg Gln Lys Leu Gln Asp Phe Leu Phe Ala Leu	
185 190 195	
cct ttg gat gag gaa acc cgc aag cgc gca gag atc aac cca ctt cgg	739
Pro Leu Asp Glu Glu Thr Arg Lys Arg Ala Glu Ile Asn Pro Leu Arg	
200 205 210	
gtg ttg gat gat aag cgt cct gaa gtc caa gag atg act gcg gat gca	787
Val Leu Asp Asp Lys Arg Pro Glu Val Gln Glu Met Thr Ala Asp Ala	
215 220 225	
cca ttg atg ctg gat cac ctt gat gca gag tgc cgt gag cac ttt gaa	835
Pro Leu Met Leu Asp His Leu Asp Ala Glu Cys Arg Glu His Phe Glu	
230 235 240 245	
aca gtg act ggt ttg ctc gat gac atg ggt gtt cca tat gtg att aac	883
Thr Val Thr Gly Leu Leu Asp Asp Met Gly Val Pro Tyr Val Ile Asn	
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cca cgc atg gtt cgt ggt ttg gat tac tac acc aag act tgt ttt gag	931

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Phe	Val	His	Asp	Gly	Leu	Gly	Ala	Gln	Ser	Gly	Ile	Gly	Gly	Gly	Gly	
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cgc	tac	gac	ggc	ctg	atg	gca	cag	ctt	ggc	gga	cag	gat	ctg	tct	ggc	1027
Arg	Tyr	Asp	Gly	Leu	Met	Ala	Gln	Leu	Gly	Gly	Gln	Asp	Leu	Ser	Gly	
	295					300					305					
atc	ggc	tat	ggc	ctg	ggc	gtg	gat	cgc	acc	atg	ttg	gct	ctg	gaa	gct	1075
Ile	Gly	Tyr	Gly	Leu	Gly	Val	Asp	Arg	Thr	Met	Leu	Ala	Leu	Glu	Ala	
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gaa	ggc	gtg	act	gtt	ggc	gct	gag	cgt	cgc	gtt	gat	gtg	tac	ggc	gtt	1123
Glu	Gly	Val	Thr	Val	Gly	Ala	Glu	Arg	Arg	Val	Asp	Val	Tyr	Gly	Val	
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cca	ctg	ggc	aag	gat	gct	aag	aag	gct	ctt	gct	gga	atc	gtg	aac	acg	1171
Pro	Leu	Gly	Lys	Asp	Ala	Lys	Lys	Ala	Leu	Ala	Gly	Ile	Val	Asn	Thr	
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Leu	Arg	Ala	Ala	Gly	Ile	Ser	Thr	Asp	Met	Ser	Tyr	Gly	Asp	Arg	Gly	
		360					365					370				
ctg	aag	ggc	gcc	atg	aag	ggc	gct	gac	cgc	tcc	aac	gcg	ttg	tac	acc	1267
Leu	Lys	Gly	Ala	Met	Lys	Gly	Ala	Asp	Arg	Ser	Asn	Ala	Leu	Tyr	Thr	
	375					380					385					
ttg	gtg	ctg	ggc	gag	cag	gag	ctg	gag	aac	aac	acc	atc	gcg	gtg	aag	1315
Leu	Val	Leu	Gly	Glu	Gln	Glu	Leu	Glu	Asn	Asn	Thr	Ile	Ala	Val	Lys	
390					395					400					405	
gat	atg	cgt	gcg	cat	gag	cag	cac	gat	gtc	gca	ttg	gac	gag	gtt	gtg	1363
Asp	Met	Arg	Ala	His	Glu	Gln	His	Asp	Val	Ala	Leu	Asp	Glu	Val	Val	
				410					415					420		
gcc	ttt	ttg	cag	ggg	aaa	ctt	att	taaataattc	ataagtaaaa	aac						1410
Ala	Phe	Leu	Gln	Gly	Lys	Leu	Ile									
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&lt;210&gt; 298

&lt;211&gt; 429

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 298

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Ala	Val	Arg	Asp	Ala	Phe	Val	Asn	Gln	Ala	His	Lys	Ala	Gly	Phe	Glu	
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His	Ile	Glu	Leu	Pro	Ile	Phe	Glu	Asp	Thr	Gly	Leu	Phe	Ala	Arg	Gly	
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Asp	Arg	Gly	Glu	Arg	Ser	Val	Thr	Leu	Arg	Pro	Glu	Gly	Thr	Ala	Gly	
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Val	Met	Arg	Ala	Val	Ile	Glu	His	Ser	Leu	Asp	Arg	Gly	Gln	Leu	Pro	
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Ala	Gly	Arg	Tyr	Arg	Gln	Leu	Gln	Gln	Val	Gly	Val	Glu	Ala	Ile	Gly	
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Val	Asp	Asp	Pro	Ala	Leu	Asp	Ala	Glu	Ile	Ile	Ala	Leu	Ala	Asp	Arg	
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Ser	Tyr	Arg	Ser	Leu	Gly	Leu	Gln	Asp	Phe	Arg	Leu	Glu	Leu	Thr	Ser	
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Leu	Gly	Asp	Arg	His	Cys	Arg	Pro	Glu	Tyr	Arg	Gln	Lys	Leu	Gln	Asp	
			180					185					190			
Phe	Leu	Phe	Ala	Leu	Pro	Leu	Asp	Glu	Glu	Thr	Arg	Lys	Arg	Ala	Glu	
		195					200					205				
Ile	Asn	Pro	Leu	Arg	Val	Leu	Asp	Asp	Lys	Arg	Pro	Glu	Val	Gln	Glu	
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Met	Thr	Ala	Asp	Ala	Pro	Leu	Met	Leu	Asp	His	Leu	Asp	Ala	Glu	Cys	
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Arg	Glu	His	Phe	Glu	Thr	Val	Thr	Gly	Leu	Leu	Asp	Asp	Met	Gly	Val	
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Pro	Tyr	Val	Ile	Asn	Pro	Arg	Met	Val	Arg	Gly	Leu	Asp	Tyr	Tyr	Thr	
			260					265					270			
Lys	Thr	Cys	Phe	Glu	Phe	Val	His	Asp	Gly	Leu	Gly	Ala	Gln	Ser	Gly	
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Ile	Gly	Gly	Gly	Gly	Arg	Tyr	Asp	Gly	Leu	Met	Ala	Gln	Leu	Gly	Gly	
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Gln	Asp	Leu	Ser	Gly	Ile	Gly	Tyr	Gly	Leu	Gly	Val	Asp	Arg	Thr	Met	
305					310					315					320	
Leu	Ala	Leu	Glu	Ala	Glu	Gly	Val	Thr	Val	Gly	Ala	Glu	Arg	Arg	Val	
				325					330					335		
Asp	Val	Tyr	Gly	Val	Pro	Leu	Gly	Lys	Asp	Ala	Lys	Lys	Ala	Leu	Ala	
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Gly	Ile	Val	Asn	Thr	Leu	Arg	Ala	Ala	Gly	Ile	Ser	Thr	Asp	Met	Ser	
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Tyr	Gly	Asp	Arg	Gly	Leu	Lys	Gly	Ala	Met	Lys	Gly	Ala	Asp	Arg	Ser	
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Asn Ala Leu Tyr Thr Leu Val Leu Gly Glu Gln Glu Leu Glu Asn Asn  
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Thr Ile Ala Val Lys Asp Met Arg Ala His Glu Gln His Asp Val Ala  
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<211> 3057

<212> DNA

<213> Corynebacterium glutamicum

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Leu Phe Leu Ala Thr  
1 5

aga cca tgc cgt ggg tac cgc gtt cct cgt gtc ttc agt tgg gat acc 163  
Arg Pro Cys Arg Gly Tyr Arg Val Pro Arg Val Phe Ser Trp Asp Thr  
10 15 20

cac ggc ttg cca gct gaa ctt gag gct gaa aag cag ctc ggc atc aag 211  
His Gly Leu Pro Ala Glu Leu Glu Ala Glu Lys Gln Leu Gly Ile Lys  
25 30 35

gac aag ggc gag atc gag gcc atg ggt ctt gcc aag ttc aac gag tac 259  
Asp Lys Gly Glu Ile Glu Ala Met Gly Leu Ala Lys Phe Asn Glu Tyr  
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Cys Ala Thr Ser Val Leu Gln Tyr Thr Lys Glu Trp Glu Glu Tyr Val  
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acc cgc cag gct cgt tgg gtg gac ttt gaa aac ggc tac aag acc atg 355  
Thr Arg Gln Ala Arg Trp Val Asp Phe Glu Asn Gly Tyr Lys Thr Met  
70 75 80 85

gac ctt tct ttc atg gag tcc gtg atc tgg gcg ttc aag gaa ctc tac 403  
Asp Leu Ser Phe Met Glu Ser Val Ile Trp Ala Phe Lys Glu Leu Tyr  
90 95 100

gac aag ggc ctg atc tac cag ggt ttc cgc gtt ctt cct tac tcc tgg 451  
Asp Lys Gly Leu Ile Tyr Gln Gly Phe Arg Val Leu Pro Tyr Ser Trp  
105 110 115

gca gag cac acc cca ctg tcc aac cag gaa acc cga ctg gat gac tcc 499  
Ala Glu His Thr Pro Leu Ser Asn Gln Glu Thr Arg Leu Asp Asp Ser  
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Tyr Lys Leu Arg Gln Asp Pro Thr Leu Thr Val Thr Phe Pro Val Thr

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ttg gct gtg aac cca gcg gtg acc tac gca ttg gtt gag gtt gct gaa Leu Ala Val Asn Pro Ala Val Thr Tyr Ala Leu Val Glu Val Ala Glu 185 190 195			691
gac ggt gag gca gaa ttc gtc ggc aag cgt gtg ctt ttg gct aag gac Asp Gly Glu Ala Glu Phe Val Gly Lys Arg Val Leu Leu Ala Lys Asp 200 205 210			739
ctc gtt ggt tcc tac gcc aag gaa ctc ggt gct gag gct gtt atc gtt Leu Val Gly Ser Tyr Ala Lys Glu Leu Gly Ala Glu Ala Val Ile Val 215 220 225			787
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gag tac gtc acc acc gaa gac ggc acc ggt atc gtc cac cag gca cca Glu Tyr Val Thr Thr Glu Asp Gly Thr Gly Ile Val His Gln Ala Pro 265 270 275			931
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gaa tac caa ggt cag ctt gtt ttc gat gcc aac aag gac atc atc aag Glu Tyr Gln Gly Gln Leu Val Phe Asp Ala Asn Lys Asp Ile Ile Lys 310 315 320 325			1075
gac ttg aag gct gca ggt cgc gtg gtt cgc cac cag acc atc gaa cac Asp Leu Lys Ala Ala Gly Arg Val Val Arg His Gln Thr Ile Glu His 330 335 340			1123
tcc tac cca cac tct tgg cgt tcc ggt gag cca ctg atc tac atg gct Ser Tyr Pro His Ser Trp Arg Ser Gly Glu Pro Leu Ile Tyr Met Ala 345 350 355			1171
ctg cca tct tgg ttt gtg aat gtc acc gaa atc cgc gac cgc atg gtt Leu Pro Ser Trp Phe Val Asn Val Thr Glu Ile Arg Asp Arg Met Val 360 365 370			1219
gag gtc aac cag gac atc gag tgg atg cca gcg cac atc cgc gac ggc Glu Val Asn Gln Asp Ile Glu Trp Met Pro Ala His Ile Arg Asp Gly 375 380 385			1267

cag ttc ggc aag tgg cta gaa ggt gcc cgc gac tgg aac atc tcc cgt	1315
Gln Phe Gly Lys Trp Leu Glu Gly Ala Arg Asp Trp Asn Ile Ser Arg	
390 395 400 405	
tcc cgt tac tgg ggt tca cca att cca gca tgg gtc tcc gac aac gac	1363
Ser Arg Tyr Trp Gly Ser Pro Ile Pro Ala Trp Val Ser Asp Asn Asp	
410 415 420	
gaa tac cca cgc gtt gat gtt tat ggt tcc ctc gat gag ctt gag gct	1411
Glu Tyr Pro Arg Val Asp Val Tyr Gly Ser Leu Asp Glu Leu Glu Ala	
425 430 435	
gac ttt ggc gtg cgt cca aag tcc ctg cac cgt cca gac atc gat gaa	1459
Asp Phe Gly Val Arg Pro Lys Ser Leu His Arg Pro Asp Ile Asp Glu	
440 445 450	
cta act cgt cca aac cca gac gat cca acc ggc aag tcc acc atg cga	1507
Leu Thr Arg Pro Asn Pro Asp Asp Pro Thr Gly Lys Ser Thr Met Arg	
455 460 465	
cgc gtc acc gat gtt ttg gac gtg tgg ttc gac tcc ggt tcc atg ccg	1555
Arg Val Thr Asp Val Leu Asp Val Trp Phe Asp Ser Gly Ser Met Pro	
470 475 480 485	
ttt gcc cag gtg cac tac cca ttc gag aac aaa gaa tgg ttt gat acc	1603
Phe Ala Gln Val His Tyr Pro Phe Glu Asn Lys Glu Trp Phe Asp Thr	
490 495 500	
cac gca cca gca gac ttc atc gtg gag tac atc ggt cag acc cgc ggt	1651
His Ala Pro Ala Asp Phe Ile Val Glu Tyr Ile Gly Gln Thr Arg Gly	
505 510 515	
tgg ttc tac ctg ctg cac gtg ctg tcc acc gca ctg ttt gac cgc cca	1699
Trp Phe Tyr Leu Leu His Val Leu Ser Thr Ala Leu Phe Asp Arg Pro	
520 525 530	
gct ttc aag aag gtt gtc gca cac ggc atc gtc ttg ggt gat gac gga	1747
Ala Phe Lys Lys Val Val Ala His Gly Ile Val Leu Gly Asp Asp Gly	
535 540 545	
ctg aag atg tcc aag tcc aag ggc aac tac ccg aac gtc aac gag gtc	1795
Leu Lys Met Ser Lys Ser Lys Gly Asn Tyr Pro Asn Val Asn Glu Val	
550 555 560 565	
ttc gac cgc gac ggt tcc gac gcc atg cgt tgg ttc ctc atg agt tcc	1843
Phe Asp Arg Asp Gly Ser Asp Ala Met Arg Trp Phe Leu Met Ser Ser	
570 575 580	
cca atc ctg cgc ggc ggc aac ttg att gtc acc gaa aag ggc atc cgc	1891
Pro Ile Leu Arg Gly Gly Asn Leu Ile Val Thr Glu Lys Gly Ile Arg	
585 590 595	
gaa ggt gtg cgc caa gca cag ctt cca atg tgg aac gca tac tcc ttc	1939
Glu Gly Val Arg Gln Ala Gln Leu Pro Met Trp Asn Ala Tyr Ser Phe	
600 605 610	
ctg cag ctg tac acc tcc aag aac gca acc tgg tca gtc gac tcc act	1987
Leu Gln Leu Tyr Thr Ser Lys Asn Ala Thr Trp Ser Val Asp Ser Thr	
615 620 625	

gac	gtg	ctg	gac	cgc	tac	atc	ctg	gcg	aag	ctg	cac	gat	ttg	gtg	gca	2035
Asp	Val	Leu	Asp	Arg	Tyr	Ile	Leu	Ala	Lys	Leu	His	Asp	Leu	Val	Ala	
630					635					640					645	
gag	acc	cag	gcg	gca	ctc	gac	ggc	act	gac	att	gca	aag	gct	tgc	gac	2083
Glu	Thr	Gln	Ala	Ala	Leu	Asp	Gly	Thr	Asp	Ile	Ala	Lys	Ala	Cys	Asp	
				650					655					660		
ttg	gtt	cgt	aac	ttc	tgt	gat	gcg	ttg	acc	aac	tgg	tac	gtg	cgt	cgt	2131
Leu	Val	Arg	Asn	Phe	Cys	Asp	Ala	Leu	Thr	Asn	Trp	Tyr	Val	Arg	Arg	
			665					670					675			
tcc	cgc	gac	cgt	ttc	tgg	gct	ggt	gat	gaa	gca	cac	cca	gag	gct	ttc	2179
Ser	Arg	Asp	Arg	Phe	Trp	Ala	Gly	Asp	Glu	Ala	His	Pro	Glu	Ala	Phe	
		680					685					690				
aac	acc	ttg	tac	acc	gtg	ctg	gaa	acc	ctc	acc	cgc	gtg	gca	gct	cca	2227
Asn	Thr	Leu	Tyr	Thr	Val	Leu	Glu	Thr	Leu	Thr	Arg	Val	Ala	Ala	Pro	
	695					700					705					
ctg	ctg	cca	atg	acc	acc	gaa	gtg	atc	tgg	cgt	gga	ctg	acc	ggc	gag	2275
Leu	Leu	Pro	Met	Thr	Thr	Glu	Val	Ile	Trp	Arg	Gly	Leu	Thr	Gly	Glu	
710					715					720					725	
cgt	tct	gtg	cac	ctg	act	gat	ttc	cca	tcc	gct	gag	tct	ttc	cca	gca	2323
Arg	Ser	Val	His	Leu	Thr	Asp	Phe	Pro	Ser	Ala	Glu	Ser	Phe	Pro	Ala	
				730					735					740		
gat	gct	gat	ttg	gtt	cgc	acc	atg	gat	gag	atc	cgt	ggc	gtg	tgc	tct	2371
Asp	Ala	Asp	Leu	Val	Arg	Thr	Met	Asp	Glu	Ile	Arg	Gly	Val	Cys	Ser	
			745					750					755			
gcg	gct	tcc	tct	gtt	cgt	aag	gct	cac	aag	ctg	cgt	aac	cgt	ctg	cca	2419
Ala	Ala	Ser	Ser	Val	Arg	Lys	Ala	His	Lys	Leu	Arg	Asn	Arg	Leu	Pro	
		760					765					770				
ctt	cca	ggc	ctg	act	gtt	gct	ctt	cca	gac	tct	gct	cgc	ctg	gca	gac	2467
Leu	Pro	Gly	Leu	Thr	Val	Ala	Leu	Pro	Asp	Ser	Ala	Arg	Leu	Ala	Asp	
	775					780					785					
ttc	gct	tcg	atc	atc	cgc	gat	gag	gtc	aac	gtg	aag	aac	gtg	gat	ctg	2515
Phe	Ala	Ser	Ile	Ile	Arg	Asp	Glu	Val	Asn	Val	Lys	Asn	Val	Asp	Leu	
790					795					800					805	
acc	tct	gac	gtg	gat	tcc	gtg	gga	acc	ttc	gag	gtt	gtt	gtt	aac	gct	2563
Thr	Ser	Asp	Val	Asp	Ser	Val	Gly	Thr	Phe	Glu	Val	Val	Val	Asn	Ala	
				810					815					820		
aag	gtt	gca	ggt	cct	cgc	ttg	ggc	aag	gac	gtc	cag	cgc	gtg	atc	aag	2611
Lys	Val	Ala	Gly	Pro	Arg	Leu	Gly	Lys	Asp	Val	Gln	Arg	Val	Ile	Lys	
			825					830					835			
gct	gtg	aag	gct	ggc	aac	tac	acc	cgc	gaa	ggc	gac	gtc	gtt	gtt	gcc	2659
Ala	Val	Lys	Ala	Gly	Asn	Tyr	Thr	Arg	Glu	Gly	Asp	Val	Val	Val	Ala	
		840					845					850				
gat	ggc	atc	gag	ctc	aac	gag	ggt	gaa	ttc	acc	gag	cgt	ctc	gta	gca	2707
Asp	Gly	Ile	Glu	Leu	Asn	Glu	Gly	Glu	Phe	Thr	Glu	Arg	Leu	Val	Ala	
	855					860					865					
gca	aac	cct	gat	tcc	acc	gcg	cag	atc	gac	ggc	gtg	gat	gga	ctc	gtg	2755

Ala Asn Pro Asp Ser Thr Ala Gln Ile Asp Gly Val Asp Gly Leu Val  
 870 875 880 885

gtt ctg gac atg gaa gtc acg gaa gaa ctt gaa gca gaa ggc tgg gca 2803  
 Val Leu Asp Met Glu Val Thr Glu Glu Leu Glu Ala Glu Gly Trp Ala  
 890 895 900

gcg gac gcg atc cgt ggc ctg cag gat gct cga aag aac tcc ggc ttt 2851  
 Ala Asp Ala Ile Arg Gly Leu Gln Asp Ala Arg Lys Asn Ser Gly Phe  
 905 910 915

gag gtt tct gac cgc att tct gtt gtc gtc agc gtt cct gag gac aag 2899  
 Glu Val Ser Asp Arg Ile Ser Val Val Val Ser Val Pro Glu Asp Lys  
 920 925 930

aag gaa tgg atc acc act cac gct gat cac atc gca gcg gaa gtt ttg 2947  
 Lys Glu Trp Ile Thr Thr His Ala Asp His Ile Ala Ala Glu Val Leu  
 935 940 945

gca acc tcc ttt gag atc gtc act gat gcc ctc gac ggc gaa acc cac 2995  
 Ala Thr Ser Phe Glu Ile Val Thr Asp Ala Leu Asp Gly Glu Thr His  
 950 955 960 965

gac att gtc gct ggt gtg acc gcg aag gtt act aag aac taagagttgt 3044  
 Asp Ile Val Ala Gly Val Thr Ala Lys Val Thr Lys Asn  
 970 975

tttgttgaga aag 3057

&lt;210&gt; 300

&lt;211&gt; 978

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 300

Leu Phe Leu Ala Thr Arg Pro Cys Arg Gly Tyr Arg Val Pro Arg Val  
 1 5 10 15

Phe Ser Trp Asp Thr His Gly Leu Pro Ala Glu Leu Glu Ala Glu Lys  
 20 25 30

Gln Leu Gly Ile Lys Asp Lys Gly Glu Ile Glu Ala Met Gly Leu Ala  
 35 40 45

Lys Phe Asn Glu Tyr Cys Ala Thr Ser Val Leu Gln Tyr Thr Lys Glu  
 50 55 60

Trp Glu Glu Tyr Val Thr Arg Gln Ala Arg Trp Val Asp Phe Glu Asn  
 65 70 75 80

Gly Tyr Lys Thr Met Asp Leu Ser Phe Met Glu Ser Val Ile Trp Ala  
 85 90 95

Phe Lys Glu Leu Tyr Asp Lys Gly Leu Ile Tyr Gln Gly Phe Arg Val  
 100 105 110

Leu Pro Tyr Ser Trp Ala Glu His Thr Pro Leu Ser Asn Gln Glu Thr  
 115 120 125

Arg Leu Asp Asp Ser Tyr Lys Leu Arg Gln Asp Pro Thr Leu Thr Val

130				135				140							
Thr	Phe	Pro	Val	Thr	Gly	Val	Val	Glu	Gly	Ser	Ser	Ala	Asn	Ala	Gly
145					150					155					160
Leu	Val	Gly	Ala	Leu	Ala	Leu	Ala	Trp	Thr	Thr	Thr	Pro	Trp	Thr	Leu
				165					170					175	
Pro	Ser	Asn	Leu	Ala	Leu	Ala	Val	Asn	Pro	Ala	Val	Thr	Tyr	Ala	Leu
			180					185					190		
Val	Glu	Val	Ala	Glu	Asp	Gly	Glu	Ala	Glu	Phe	Val	Gly	Lys	Arg	Val
		195					200					205			
Leu	Leu	Ala	Lys	Asp	Leu	Val	Gly	Ser	Tyr	Ala	Lys	Glu	Leu	Gly	Ala
210						215					220				
Glu	Ala	Val	Ile	Val	Ser	Glu	His	Pro	Gly	Ser	Glu	Leu	Val	Gly	Leu
225					230					235					240
Thr	Tyr	Glu	Pro	Ile	Phe	Gly	Tyr	Phe	Arg	Asp	His	Ala	Asn	Gly	Phe
				245					250					255	
Gln	Ile	Leu	Gly	Ala	Glu	Tyr	Val	Thr	Thr	Glu	Asp	Gly	Thr	Gly	Ile
			260					265					270		
Val	His	Gln	Ala	Pro	Ala	Phe	Gly	Glu	Asp	Asp	Met	Asn	Thr	Cys	Asn
		275					280					285			
Ala	Ala	Gly	Ile	Glu	Pro	Val	Ile	Pro	Val	Asp	Ile	Asp	Gly	Lys	Phe
	290					295					300				
Thr	Gly	Leu	Val	Pro	Glu	Tyr	Gln	Gly	Gln	Leu	Val	Phe	Asp	Ala	Asn
305					310					315					320
Lys	Asp	Ile	Ile	Lys	Asp	Leu	Lys	Ala	Ala	Gly	Arg	Val	Val	Arg	His
				325					330					335	
Gln	Thr	Ile	Glu	His	Ser	Tyr	Pro	His	Ser	Trp	Arg	Ser	Gly	Glu	Pro
			340					345					350		
Leu	Ile	Tyr	Met	Ala	Leu	Pro	Ser	Trp	Phe	Val	Asn	Val	Thr	Glu	Ile
	355						360					365			
Arg	Asp	Arg	Met	Val	Glu	Val	Asn	Gln	Asp	Ile	Glu	Trp	Met	Pro	Ala
	370					375					380				
His	Ile	Arg	Asp	Gly	Gln	Phe	Gly	Lys	Trp	Leu	Glu	Gly	Ala	Arg	Asp
385					390					395					400
Trp	Asn	Ile	Ser	Arg	Ser	Arg	Tyr	Trp	Gly	Ser	Pro	Ile	Pro	Ala	Trp
				405					410					415	
Val	Ser	Asp	Asn	Asp	Glu	Tyr	Pro	Arg	Val	Asp	Val	Tyr	Gly	Ser	Leu
			420					425					430		
Asp	Glu	Leu	Glu	Ala	Asp	Phe	Gly	Val	Arg	Pro	Lys	Ser	Leu	His	Arg
		435					440					445			
Pro	Asp	Ile	Asp	Glu	Leu	Thr	Arg	Pro	Asn	Pro	Asp	Asp	Pro	Thr	Gly
	450					455					460				

Lys Ser Thr Met Arg Arg Val Thr Asp Val Leu Asp Val Trp Phe Asp  
 465 470 475 480  
 Ser Gly Ser Met Pro Phe Ala Gln Val His Tyr Pro Phe Glu Asn Lys  
 485 490 495  
 Glu Trp Phe Asp Thr His Ala Pro Ala Asp Phe Ile Val Glu Tyr Ile  
 500 505 510  
 Gly Gln Thr Arg Gly Trp Phe Tyr Leu Leu His Val Leu Ser Thr Ala  
 515 520 525  
 Leu Phe Asp Arg Pro Ala Phe Lys Lys Val Val Ala His Gly Ile Val  
 530 535 540  
 Leu Gly Asp Asp Gly Leu Lys Met Ser Lys Ser Lys Gly Asn Tyr Pro  
 545 550 555 560  
 Asn Val Asn Glu Val Phe Asp Arg Asp Gly Ser Asp Ala Met Arg Trp  
 565 570 575  
 Phe Leu Met Ser Ser Pro Ile Leu Arg Gly Gly Asn Leu Ile Val Thr  
 580 585 590  
 Glu Lys Gly Ile Arg Glu Gly Val Arg Gln Ala Gln Leu Pro Met Trp  
 595 600 605  
 Asn Ala Tyr Ser Phe Leu Gln Leu Tyr Thr Ser Lys Asn Ala Thr Trp  
 610 615 620  
 Ser Val Asp Ser Thr Asp Val Leu Asp Arg Tyr Ile Leu Ala Lys Leu  
 625 630 635 640  
 His Asp Leu Val Ala Glu Thr Gln Ala Ala Leu Asp Gly Thr Asp Ile  
 645 650 655  
 Ala Lys Ala Cys Asp Leu Val Arg Asn Phe Cys Asp Ala Leu Thr Asn  
 660 665 670  
 Trp Tyr Val Arg Arg Ser Arg Asp Arg Phe Trp Ala Gly Asp Glu Ala  
 675 680 685  
 His Pro Glu Ala Phe Asn Thr Leu Tyr Thr Val Leu Glu Thr Leu Thr  
 690 695 700  
 Arg Val Ala Ala Pro Leu Leu Pro Met Thr Thr Glu Val Ile Trp Arg  
 705 710 715 720  
 Gly Leu Thr Gly Glu Arg Ser Val His Leu Thr Asp Phe Pro Ser Ala  
 725 730 735  
 Glu Ser Phe Pro Ala Asp Ala Asp Leu Val Arg Thr Met Asp Glu Ile  
 740 745 750  
 Arg Gly Val Cys Ser Ala Ala Ser Ser Val Arg Lys Ala His Lys Leu  
 755 760 765  
 Arg Asn Arg Leu Pro Leu Pro Gly Leu Thr Val Ala Leu Pro Asp Ser  
 770 775 780

Ala Arg Leu Ala Asp Phe Ala Ser Ile Ile Arg Asp Glu Val Asn Val  
 785 790 795 800

Lys Asn Val Asp Leu Thr Ser Asp Val Asp Ser Val Gly Thr Phe Glu  
 805 810 815

Val Val Val Asn Ala Lys Val Ala Gly Pro Arg Leu Gly Lys Asp Val  
 820 825 830

Gln Arg Val Ile Lys Ala Val Lys Ala Gly Asn Tyr Thr Arg Glu Gly  
 835 840 845

Asp Val Val Val Ala Asp Gly Ile Glu Leu Asn Glu Gly Glu Phe Thr  
 850 855 860

Glu Arg Leu Val Ala Ala Asn Pro Asp Ser Thr Ala Gln Ile Asp Gly  
 865 870 875 880

Val Asp Gly Leu Val Val Leu Asp Met Glu Val Thr Glu Glu Leu Glu  
 885 890 895

Ala Glu Gly Trp Ala Ala Asp Ala Ile Arg Gly Leu Gln Asp Ala Arg  
 900 905 910

Lys Asn Ser Gly Phe Glu Val Ser Asp Arg Ile Ser Val Val Val Ser  
 915 920 925

Val Pro Glu Asp Lys Lys Glu Trp Ile Thr Thr His Ala Asp His Ile  
 930 935 940

Ala Ala Glu Val Leu Ala Thr Ser Phe Glu Ile Val Thr Asp Ala Leu  
 945 950 955 960

Asp Gly Glu Thr His Asp Ile Val Ala Gly Val Thr Ala Lys Val Thr  
 965 970 975

Lys Asn

<210> 301  
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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <223> RXN00966

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acacatgaga tgtcccgtgt acctactaca ctgtttaacc atg act aac ccg agc 115  
 Met Thr Asn Pro Ser  
 1 5

gaa ggc acc act ccc ctg gcg ttc cgt tat acc ccg gaa ctc gcc aac 163  
 Glu Gly Thr Thr Pro Leu Ala Phe Arg Tyr Thr Pro Glu Leu Ala Asn  
 10 15 20

aag atc gaa ggt gag tgg cag aat tac tgg act gac aac ggc aca ttc 211  
Lys Ile Glu Gly Glu Trp Gln Asn Tyr Trp Thr Asp Asn Gly Thr Phe  
25 30 35  
  
aac gca ccc aac cca gtg ggt gat tta gcg cct gcg gac ggt aaa gca 259  
Asn Ala Pro Asn Pro Val Gly Asp Leu Ala Pro Ala Asp Gly Lys Ala  
40 45 50  
  
ctt cct gag gac aag ctc ttt gtc cag gat atg ttc ccg tac cca tcc 307  
Leu Pro Glu Asp Lys Leu Phe Val Gln Asp Met Phe Pro Tyr Pro Ser  
55 60 65  
  
gga gct ggc ctg cac gta ggc cac cca ctc ggt tac atc gca acg gat 355  
Gly Ala Gly Leu His Val Gly His Pro Leu Gly Tyr Ile Ala Thr Asp  
70 75 80 85  
  
gtt ttc gcc cgc tac aac cgc atg ctg ggc aag aac gtt ctg cac acc 403  
Val Phe Ala Arg Tyr Asn Arg Met Leu Gly Lys Asn Val Leu His Thr  
90 95 100  
  
ttg ggc tat gac gcc ttc gga ctg cca gca gag cag tac gcg atc caa 451  
Leu Gly Tyr Asp Ala Phe Gly Leu Pro Ala Glu Gln Tyr Ala Ile Gln  
105 110 115  
  
acc ggt aca cac cca cgc acc acc acc atg gcc aac att gag aac atg 499  
Thr Gly Thr His Pro Arg Thr Thr Thr Met Ala Asn Ile Glu Asn Met  
120 125 130  
  
aag cgc cag ctc ggt gcg ctg ggt ctt ggc cat gat tcc cgt cgt gcg 547  
Lys Arg Gln Leu Gly Ala Leu Gly Leu Gly His Asp Ser Arg Arg Ala  
135 140 145  
  
gtg gcc acc acg gat cct gag ttc tac aag tgg act cag tgg atc ttc 595  
Val Ala Thr Thr Asp Pro Glu Phe Tyr Lys Trp Thr Gln Trp Ile Phe  
150 155 160 165  
  
ctg cag att ttc aat tcg tgg ttc gat gca gag cag cag aag gca 640  
Leu Gln Ile Phe Asn Ser Trp Phe Asp Ala Glu Gln Gln Lys Ala  
170 175 180

&lt;210&gt; 302

&lt;211&gt; 180

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 302

Met Thr Asn Pro Ser Glu Gly Thr Thr Pro Leu Ala Phe Arg Tyr Thr  
1 5 10 15  
  
Pro Glu Leu Ala Asn Lys Ile Glu Gly Glu Trp Gln Asn Tyr Trp Thr  
20 25 30  
  
Asp Asn Gly Thr Phe Asn Ala Pro Asn Pro Val Gly Asp Leu Ala Pro  
35 40 45  
  
Ala Asp Gly Lys Ala Leu Pro Glu Asp Lys Leu Phe Val Gln Asp Met  
50 55 60  
  
Phe Pro Tyr Pro Ser Gly Ala Gly Leu His Val Gly His Pro Leu Gly  
65 70 75 80

<400> 303																		
tggtttccac ataattcttc aagtctatct acttattgag gggaggaaga attgccctcc															60			
acacatgaga tgtcccgtgt acctactaca ctgtttaacc															atg act aac ccg agc	115		
															Met Thr Asn Pro Ser			
															1	5		
gaa ggc acc act ccc ctg gcg ttc cgt tat acc ccg gaa ctc gcc aac															163			
Glu Gly Thr Thr Pro Leu Ala Phe Arg Tyr Thr Pro Glu Leu Ala Asn																		
															10	15	20	
aag atc gaa ggt gag tgg cag aat tac tgg act gac aac ggc aca ttc															211			
Lys Ile Glu Gly Glu Trp Gln Asn Tyr Trp Thr Asp Asn Gly Thr Phe																		
															25	30	35	
aac gca ccc aac cca gtg ggt gat tta gcg cct gcg gac ggt aaa gca															259			
Asn Ala Pro Asn Pro Val Gly Asp Leu Ala Pro Ala Asp Gly Lys Ala																		
															40	45	50	
ctt cct gag gac aag ctc ttt gtc cag gat atg ttc ccg tac cca tcc															307			
Leu Pro Glu Asp Lys Leu Phe Val Gln Asp Met Phe Pro Tyr Pro Ser																		
															55	60	65	
gga gct ggc ctg cac gta ggc cac cca ctc ggt tac atc gca acg gat															355			
Gly Ala Gly Leu His Val Gly His Pro Leu Gly Tyr Ile Ala Thr Asp																		
															70	75	80	85
gtt ttc gcc cgc tac aac cgc atg ctg ggc aag aac gtt ctg cac acc															403			

Val Phe Ala Arg Tyr Asn Arg Met Leu Gly Lys Asn Val Leu His Thr  
                                     90                                    95                                    100

ttg ggc tat gac gcc ttc gga ctg cca gca gag cag tac gcg atc caa 451  
 Leu Gly Tyr Asp Ala Phe Gly Leu Pro Ala Glu Gln Tyr Ala Ile Gln  
                                     105                                    110                                    115

acc ggt aca cac cca cgc acc acc acc atg gcc aac att gag aac atg 499  
 Thr Gly Thr His Pro Arg Thr Thr Thr Met Ala Asn Ile Glu Asn Met  
                                     120                                    125                                    130

aag cgc cag ctc ggt gcg ctg ggt ctt ggc cat gat tcc cgt cgt gcg 547  
 Lys Arg Gln Leu Gly Ala Leu Gly Leu Gly His Asp Ser Arg Arg Ala  
                                     135                                    140                                    145

gtg gcc acc acg gat cct gag ttc tac aag tgg act cag tgg atc ttc 595  
 Val Ala Thr Thr Asp Pro Glu Phe Tyr Lys Trp Thr Gln Trp Ile Phe  
 150                                    155                                    160                                    165

ctg cag att ttc aat tcg tgg ttc gat gca gag 628  
 Leu Gln Ile Phe Asn Ser Trp Phe Asp Ala Glu  
                                     170                                    175

&lt;210&gt; 304

&lt;211&gt; 176

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 304

Met Thr Asn Pro Ser Glu Gly Thr Thr Pro Leu Ala Phe Arg Tyr Thr  
   1                                    5                                    10                                    15

Pro Glu Leu Ala Asn Lys Ile Glu Gly Glu Trp Gln Asn Tyr Trp Thr  
                                     20                                    25                                    30

Asp Asn Gly Thr Phe Asn Ala Pro Asn Pro Val Gly Asp Leu Ala Pro  
                                     35                                    40                                    45

Ala Asp Gly Lys Ala Leu Pro Glu Asp Lys Leu Phe Val Gln Asp Met  
                                     50                                    55                                    60

Phe Pro Tyr Pro Ser Gly Ala Gly Leu His Val Gly His Pro Leu Gly  
   65                                    70                                    75                                    80

Tyr Ile Ala Thr Asp Val Phe Ala Arg Tyr Asn Arg Met Leu Gly Lys  
                                     85                                    90                                    95

Asn Val Leu His Thr Leu Gly Tyr Asp Ala Phe Gly Leu Pro Ala Glu  
                                     100                                    105                                    110

Gln Tyr Ala Ile Gln Thr Gly Thr His Pro Arg Thr Thr Thr Met Ala  
                                     115                                    120                                    125

Asn Ile Glu Asn Met Lys Arg Gln Leu Gly Ala Leu Gly Leu Gly His  
                                     130                                    135                                    140

Asp Ser Arg Arg Ala Val Ala Thr Thr Asp Pro Glu Phe Tyr Lys Trp  
   145                                    150                                    155                                    160

Thr Gln Trp Ile Phe Leu Gln Ile Phe Asn Ser Trp Phe Asp Ala Glu

165

170

175

<210> 305  
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 <212> DNA  
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<220>  
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 <223> RXN01061

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 Ile Ser Arg Tyr Arg Glu Gln Phe Cys Asn Ile Glu Asn Glu Arg Tyr  
 1 5 10 15  
 tgg acc ggc cca cgc cca gaa acc cac gga cca aac gat cca ggc ggc 96  
 Trp Thr Gly Pro Arg Pro Glu Thr His Gly Pro Asn Asp Pro Gly Gly  
 20 25 30  
 gta gac ctc tac gtc ggt ggc gtc gag cac gca gtt ctc cac ctg ctc 144  
 Val Asp Leu Tyr Val Gly Gly Val Glu His Ala Val Leu His Leu Leu  
 35 40 45  
 tac gca cgt ttc tgg cac aag gtc ctc ttc gac ctg ggc cac gtc tcc 192  
 Tyr Ala Arg Phe Trp His Lys Val Leu Phe Asp Leu Gly His Val Ser  
 50 55 60  
 tcc aag gag cca tac cgt cgc ctg tac aac cag ggc tac atc cag gcc 240  
 Ser Lys Glu Pro Tyr Arg Arg Leu Tyr Asn Gln Gly Tyr Ile Gln Ala  
 65 70 75 80  
 ttc gcc tac acc gat tcc cgt ggc gtc tac gtg cct gcc gat gat gtc 288  
 Phe Ala Tyr Thr Asp Ser Arg Gly Val Tyr Val Pro Ala Asp Asp Val  
 85 90 95  
 gaa gag aag gac gga aag ttc ttc tac cag ggc gaa gaa gtc aac cag 336  
 Glu Glu Lys Asp Gly Lys Phe Phe Tyr Gln Gly Glu Glu Val Asn Gln  
 100 105 110  
 gaa tac gga aag atg ggc aag tcc ctg aag aac gcc gtt gcc cca gac 384  
 Glu Tyr Gly Lys Met Gly Lys Ser Leu Lys Asn Ala Val Ala Pro Asp  
 115 120 125  
 gat atc tgc aac aac ttc ggt gct gac acc ctg cgc gtt tac gag atg 432  
 Asp Ile Cys Asn Asn Phe Gly Ala Asp Thr Leu Arg Val Tyr Glu Met  
 130 135 140  
 gcc atg gga cct ttg gac acc tcc cgt cca tgg gca acc aag gac gtc 480  
 Ala Met Gly Pro Leu Asp Thr Ser Arg Pro Trp Ala Thr Lys Asp Val  
 145 150 155 160  
 gtc ggt gcg cag cgc ttc ctc cag cgt ctg tgg cgt ctc gtc gtc gat 528  
 Val Gly Ala Gln Arg Phe Leu Gln Arg Leu Trp Arg Leu Val Val Asp  
 165 170 175  
 gaa aac acc ggc gaa gtg ctc act cgc gat gaa gtc ctc acc gac gat 576  
 Glu Asn Thr Gly Glu Val Leu Thr Arg Asp Glu Val Leu Thr Asp Asp  
 180 185 190

gac aac aag caa ctg cac cgc acc atc gca ggc gtc cgc gac gac tac 624  
 Asp Asn Lys Gln Leu His Arg Thr Ile Ala Gly Val Arg Asp Asp Tyr  
 195 200 205  
  
 acc aac ttg cgc gtt aac acc gtg gtt gcc aag ctc atc gaa tac gtc 672  
 Thr Asn Leu Arg Val Asn Thr Val Val Ala Lys Leu Ile Glu Tyr Val  
 210 215 220  
  
 aac tac ctg acc aaa aca tac cca gac acc atc cca gct ggc gca gtc 720  
 Asn Tyr Leu Thr Lys Thr Tyr Pro Asp Thr Ile Pro Ala Gly Ala Val  
 225 230 235 240  
  
 ctg cca ctg atc gtc atg gtc tcc cct atc gca cca cac atc gcg gag 768  
 Leu Pro Leu Ile Val Met Val Ser Pro Ile Ala Pro His Ile Ala Glu  
 245 250 255  
  
 gaa ctc tgg aag aag ctc ggc cac gac gac acc gtc acc tac gaa cca 816  
 Glu Leu Trp Lys Lys Leu Gly His Asp Asp Thr Val Thr Tyr Glu Pro  
 260 265 270  
  
 ttc ccc acc ttt gag gaa aaa tgg ctc acc gac gat gaa atc gaa ctg 864  
 Phe Pro Thr Phe Glu Glu Lys Trp Leu Thr Asp Asp Glu Ile Glu Leu  
 275 280 285  
  
 cca gtc cag gtc aac ggc aag gtc cgc ggt cgc atc acc gtt gca gcc 912  
 Pro Val Gln Val Asn Gly Lys Val Arg Gly Arg Ile Thr Val Ala Ala  
 290 295 300  
  
 gac gcc agc cag gag cag gtc atc gag gca gcg ctt gcc gac gag aag 960  
 Asp Ala Ser Gln Glu Gln Val Ile Glu Ala Ala Leu Ala Asp Glu Lys  
 305 310 315 320  
  
 gtg cag gag caa atc tcc ggc aag aac ctg atc aag cag atc gtt gtt 1008  
 Val Gln Glu Gln Ile Ser Gly Lys Asn Leu Ile Lys Gln Ile Val Val  
 325 330 335  
  
 cca gga cgc atg gtt aac ctt gtg gtg aag taatccccct cggttttagat tcc 1061  
 Pro Gly Arg Met Val Asn Leu Val Val Lys  
 340 345

&lt;210&gt; 306

&lt;211&gt; 346

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 306

Ile Ser Arg Tyr Arg Glu Gln Phe Cys Asn Ile Glu Asn Glu Arg Tyr  
 1 5 10 15

Trp Thr Gly Pro Arg Pro Glu Thr His Gly Pro Asn Asp Pro Gly Gly  
 20 25 30

Val Asp Leu Tyr Val Gly Gly Val Glu His Ala Val Leu His Leu Leu  
 35 40 45

Tyr Ala Arg Phe Trp His Lys Val Leu Phe Asp Leu Gly His Val Ser  
 50 55 60

Ser Lys Glu Pro Tyr Arg Arg Leu Tyr Asn Gln Gly Tyr Ile Gln Ala

65	70					75					80				
Phe	Ala	Tyr	Thr	Asp	Ser	Arg	Gly	Val	Tyr	Val	Pro	Ala	Asp	Asp	Val
				85					90					95	
Glu	Glu	Lys	Asp	Gly	Lys	Phe	Phe	Tyr	Gln	Gly	Glu	Glu	Val	Asn	Gln
			100					105					110		
Glu	Tyr	Gly	Lys	Met	Gly	Lys	Ser	Leu	Lys	Asn	Ala	Val	Ala	Pro	Asp
		115					120					125			
Asp	Ile	Cys	Asn	Asn	Phe	Gly	Ala	Asp	Thr	Leu	Arg	Val	Tyr	Glu	Met
	130					135					140				
Ala	Met	Gly	Pro	Leu	Asp	Thr	Ser	Arg	Pro	Trp	Ala	Thr	Lys	Asp	Val
145					150					155					160
Val	Gly	Ala	Gln	Arg	Phe	Leu	Gln	Arg	Leu	Trp	Arg	Leu	Val	Val	Asp
				165					170					175	
Glu	Asn	Thr	Gly	Glu	Val	Leu	Thr	Arg	Asp	Glu	Val	Leu	Thr	Asp	Asp
			180					185					190		
Asp	Asn	Lys	Gln	Leu	His	Arg	Thr	Ile	Ala	Gly	Val	Arg	Asp	Asp	Tyr
		195					200					205			
Thr	Asn	Leu	Arg	Val	Asn	Thr	Val	Val	Ala	Lys	Leu	Ile	Glu	Tyr	Val
	210					215					220				
Asn	Tyr	Leu	Thr	Lys	Thr	Tyr	Pro	Asp	Thr	Ile	Pro	Ala	Gly	Ala	Val
225					230					235					240
Leu	Pro	Leu	Ile	Val	Met	Val	Ser	Pro	Ile	Ala	Pro	His	Ile	Ala	Glu
				245					250					255	
Glu	Leu	Trp	Lys	Lys	Leu	Gly	His	Asp	Asp	Thr	Val	Thr	Tyr	Glu	Pro
			260					265					270		
Phe	Pro	Thr	Phe	Glu	Glu	Lys	Trp	Leu	Thr	Asp	Asp	Glu	Ile	Glu	Leu
		275					280					285			
Pro	Val	Gln	Val	Asn	Gly	Lys	Val	Arg	Gly	Arg	Ile	Thr	Val	Ala	Ala
	290					295					300				
Asp	Ala	Ser	Gln	Glu	Gln	Val	Ile	Glu	Ala	Ala	Leu	Ala	Asp	Glu	Lys
305					310					315					320
Val	Gln	Glu	Gln	Ile	Ser	Gly	Lys	Asn	Leu	Ile	Lys	Gln	Ile	Val	Val
				325					330					335	
Pro	Gly	Arg	Met	Val	Asn	Leu	Val	Val	Lys						
			340					345							

&lt;210&gt; 307

&lt;211&gt; 471

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(471)

&lt;223&gt; FRXA01864

&lt;400&gt; 307

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aat gaa cgc tac tgg acc ggc cca cgc cca gaa acc cac gga cca aac 48
Asn Glu Arg Tyr Trp Thr Gly Pro Arg Pro Glu Thr His Gly Pro Asn
  1             5             10             15

gat cca ggc ggc gta gac ctc tac gtc ggt ggc gtc gag cac gca gtt 96
Asp Pro Gly Gly Val Asp Leu Tyr Val Gly Gly Val Glu His Ala Val
             20             25             30

ctc cac ctg ctc tac gca cgt ttc tgg cac aag gtc ctc ttc gac ctg 144
Leu His Leu Leu Tyr Ala Arg Phe Trp His Lys Val Leu Phe Asp Leu
             35             40             45

ggc cac gtc tcc tcc aag gag cca tac cgt cgc ctg tac aac cag ggc 192
Gly His Val Ser Ser Lys Glu Pro Tyr Arg Arg Leu Tyr Asn Gln Gly
             50             55             60

tac atc cag gcc ttc gcc tac acc gat tcc cgt ggc gtc tac gtg cct 240
Tyr Ile Gln Ala Phe Ala Tyr Thr Asp Ser Arg Gly Val Tyr Val Pro
             65             70             75             80

gcc gat gat gtc gaa gag aag gac gga aag ttc ttc tac cag ggc gaa 288
Ala Asp Asp Val Glu Glu Lys Asp Gly Lys Phe Phe Tyr Gln Gly Glu
             85             90             95

gaa gtc aac cag gaa tac gga aag atg ggc aag tcc ctg aag aac gcc 336
Glu Val Asn Gln Glu Tyr Gly Lys Met Gly Lys Ser Leu Lys Asn Ala
             100             105             110

gtt gcc cca gac gat atc tgc aac aac ttc ggt gct gac acc ctg cgc 384
Val Ala Pro Asp Asp Ile Cys Asn Asn Phe Gly Ala Asp Thr Leu Arg
             115             120             125

gtt tac gag atg gcc atg gga cct ttg gac acc tcc cgt cca tgg gca 432
Val Tyr Glu Met Ala Met Gly Pro Leu Asp Thr Ser Arg Pro Trp Ala
             130             135             140

acc aag gac gtc gtc ggt gcg cag cgc ttc ctc agc gtc 471
Thr Lys Asp Val Val Gly Ala Gln Arg Phe Leu Ser Val
145             150             155

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&lt;210&gt; 308

&lt;211&gt; 157

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 308

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Asn Glu Arg Tyr Trp Thr Gly Pro Arg Pro Glu Thr His Gly Pro Asn
  1             5             10             15

Asp Pro Gly Gly Val Asp Leu Tyr Val Gly Gly Val Glu His Ala Val
             20             25             30

Leu His Leu Leu Tyr Ala Arg Phe Trp His Lys Val Leu Phe Asp Leu
             35             40             45

Gly His Val Ser Ser Lys Glu Pro Tyr Arg Arg Leu Tyr Asn Gln Gly

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50					55					60					
Tyr	Ile	Gln	Ala	Phe	Ala	Tyr	Thr	Asp	Ser	Arg	Gly	Val	Tyr	Val	Pro
65					70					75					80
Ala	Asp	Asp	Val	Glu	Glu	Lys	Asp	Gly	Lys	Phe	Phe	Tyr	Gln	Gly	Glu
				85					90					95	
Glu	Val	Asn	Gln	Glu	Tyr	Gly	Lys	Met	Gly	Lys	Ser	Leu	Lys	Asn	Ala
			100					105					110		
Val	Ala	Pro	Asp	Asp	Ile	Cys	Asn	Asn	Phe	Gly	Ala	Asp	Thr	Leu	Arg
		115					120					125			
Val	Tyr	Glu	Met	Ala	Met	Gly	Pro	Leu	Asp	Thr	Ser	Arg	Pro	Trp	Ala
	130					135					140				
Thr	Lys	Asp	Val	Val	Gly	Ala	Gln	Arg	Phe	Leu	Ser	Val			
145					150					155					

&lt;210&gt; 309

&lt;211&gt; 505

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (75)..(482)

&lt;223&gt; FRXA01061

&lt;400&gt; 309

gatgaactcc tcaccgacga tgacaacaag caactgcacc gaccatcgca ggcgtccgcg 60

acgactacac	caac	ttg	cgc	gtt	aac	acc	gtg	gtt	gcc	aag	ctc	atc	gaa		110
			Leu	Arg	Val	Asn	Thr	Val	Val	Ala	Lys	Leu	Ile	Glu	
			1				5					10			

tac	gtc	aac	tac	ctg	acc	aaa	aca	tac	cca	gac	acc	atc	cca	gct	ggc	158
Tyr	Val	Asn	Tyr	Leu	Thr	Lys	Thr	Tyr	Pro	Asp	Thr	Ile	Pro	Ala	Gly	
		15				20					25					

gca	gtc	ctg	cca	ctg	atc	gtc	atg	gtc	tcc	cct	atc	gca	cca	cac	atc	206
Ala	Val	Leu	Pro	Leu	Ile	Val	Met	Val	Ser	Pro	Ile	Ala	Pro	His	Ile	
	30				35						40					

gcg	gag	gaa	ctc	tgg	aag	aag	ctc	ggc	cac	gac	gac	acc	gtc	acc	tac	254
Ala	Glu	Glu	Leu	Trp	Lys	Lys	Leu	Gly	His	Asp	Asp	Thr	Val	Thr	Tyr	
	45				50				55					60		

gaa	cca	ttc	ccc	acc	ttt	gag	gaa	aaa	tgg	ctc	acc	gac	gat	gaa	atc	302
Glu	Pro	Phe	Pro	Thr	Phe	Glu	Glu	Lys	Trp	Leu	Thr	Asp	Asp	Glu	Ile	
				65					70					75		

gaa	ctg	cca	gtc	cag	gtc	aac	ggc	aag	gtc	cgc	ggt	cgc	atc	acc	gtt	350
Glu	Leu	Pro	Val	Gln	Val	Asn	Gly	Lys	Val	Arg	Gly	Arg	Ile	Thr	Val	
		80					85						90			

gca	gcc	gac	gcc	agc	cag	gag	cag	gtc	atc	gag	gca	gcg	ctt	gcc	gac	398
Ala	Ala	Asp	Ala	Ser	Gln	Glu	Gln	Val	Ile	Glu	Ala	Ala	Leu	Ala	Asp	
		95					100					105				

gag aag gtg cag gag caa atc tcc ggc aag aac ctg atc aag cag atc 446  
 Glu Lys Val Gln Glu Gln Ile Ser Gly Lys Asn Leu Ile Lys Gln Ile  
 110 115 120

gtt gtt cca gga cgc atg gtt aac ctt gtg gtg aag taatccccct 492  
 Val Val Pro Gly Arg Met Val Asn Leu Val Val Lys  
 125 130 135

cggtttagat tcc 505

<210> 310

<211> 136

<212> PRT

<213> Corynebacterium glutamicum

<400> 310

Leu Arg Val Asn Thr Val Val Ala Lys Leu Ile Glu Tyr Val Asn Tyr  
 1 5 10 15

Leu Thr Lys Thr Tyr Pro Asp Thr Ile Pro Ala Gly Ala Val Leu Pro  
 20 25 30

Leu Ile Val Met Val Ser Pro Ile Ala Pro His Ile Ala Glu Glu Leu  
 35 40 45

Trp Lys Lys Leu Gly His Asp Asp Thr Val Thr Tyr Glu Pro Phe Pro  
 50 55 60

Thr Phe Glu Glu Lys Trp Leu Thr Asp Asp Glu Ile Glu Leu Pro Val  
 65 70 75 80

Gln Val Asn Gly Lys Val Arg Gly Arg Ile Thr Val Ala Ala Asp Ala  
 85 90 95

Ser Gln Glu Gln Val Ile Glu Ala Ala Leu Ala Asp Glu Lys Val Gln  
 100 105 110

Glu Gln Ile Ser Gly Lys Asn Leu Ile Lys Gln Ile Val Val Pro Gly  
 115 120 125

Arg Met Val Asn Leu Val Val Lys  
 130 135

<210> 311

<211> 1002

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1002)

<223> RXA00968

<400> 311

ctg atc gat gat ctg gag ctg ctc gat tgg act gag aag gtc aag tcc 48  
 Leu Ile Asp Asp Leu Glu Leu Leu Asp Trp Thr Glu Lys Val Lys Ser  
 1 5 10 15

atg cag cgt aac tgg att ggc cgt tcc cgc ggc gct gaa gtt gat ttc	96
Met Gln Arg Asn Trp Ile Gly Arg Ser Arg Gly Ala Glu Val Asp Phe	
20 25 30	
agt gca gag ggc gaa acc gtc acc gtg ttt acc acc cgc cca gat act	144
Ser Ala Glu Gly Glu Thr Val Thr Val Phe Thr Thr Arg Pro Asp Thr	
35 40 45	
ctg ttc ggc gcg acc tac atg gtt ctt gca cct gag cat gag ctg gtc	192
Leu Phe Gly Ala Thr Tyr Met Val Leu Ala Pro Glu His Glu Leu Val	
50 55 60	
gac gtg ctg ctg gag aag gct ggt tcc tac gag ggc gtt gat gcc cgt	240
Asp Val Leu Leu Glu Lys Ala Gly Ser Tyr Glu Gly Val Asp Ala Arg	
65 70 75 80	
tgg acc aat ggc cag gcg agc cct gcg gaa gct gtc gct gca tac cgc	288
Trp Thr Asn Gly Gln Ala Ser Pro Ala Glu Ala Val Ala Ala Tyr Arg	
85 90 95	
gcc tcc atc gcc gcg aag tcc gac ctg gag cgt cag gaa aac aag gaa	336
Ala Ser Ile Ala Ala Lys Ser Asp Leu Glu Arg Gln Glu Asn Lys Glu	
100 105 110	
aag acc ggc gtc ttc ctg ggc gtt tac gcg acc aac cca gtc aac ggc	384
Lys Thr Gly Val Phe Leu Gly Val Tyr Ala Thr Asn Pro Val Asn Gly	
115 120 125	
gat cag atc aca gtg ttc atc gct gac tac gtt ctg acc ggc tac ggc	432
Asp Gln Ile Thr Val Phe Ile Ala Asp Tyr Val Leu Thr Gly Tyr Gly	
130 135 140	
acc ggc gcc atc atg gcg gtt cct gct cac gac gag cgc gac tac gaa	480
Thr Gly Ala Ile Met Ala Val Pro Ala His Asp Glu Arg Asp Tyr Glu	
145 150 155 160	
ttc gcc acc gtt ttg ggt ctg cct atc aag gaa gtt gtc gca ggt ggc	528
Phe Ala Thr Val Leu Gly Leu Pro Ile Lys Glu Val Val Ala Gly Gly	
165 170 175	
aac atc gaa gag gct gct ttc acc gaa tct ggc gaa gca gtc aac tct	576
Asn Ile Glu Glu Ala Ala Phe Thr Glu Ser Gly Glu Ala Val Asn Ser	
180 185 190	
gcg aac gac aac ggc ctg gat atc aac ggc ctt gcc aag gat gag gct	624
Ala Asn Asp Asn Gly Leu Asp Ile Asn Gly Leu Ala Lys Asp Glu Ala	
195 200 205	
att gcc aag acc atc gaa tgg ttg gaa gaa aag gaa ctt ggc cgc ggc	672
Ile Ala Lys Thr Ile Glu Trp Leu Glu Glu Lys Glu Leu Gly Arg Gly	
210 215 220	
acc atc cag tac aag ctg cgc gac tgg ctg ttc gct cgc cag cgt tac	720
Thr Ile Gln Tyr Lys Leu Arg Asp Trp Leu Phe Ala Arg Gln Arg Tyr	
225 230 235 240	
tgg ggc gag cct ttc cca atc gtc tac gac gaa aac ggc caa gca cat	768
Trp Gly Glu Pro Phe Pro Ile Val Tyr Asp Glu Asn Gly Gln Ala His	
245 250 255	
gct ctg cca gac tcc atg ctt cca gtc gag ctg cca gag gta gag gac	816

Ala Leu Pro Asp Ser Met Leu Pro Val Glu Leu Pro Glu Val Glu Asp  
                   260                                  265                                  270

tac aag cct gtc tcc ttc gac cct gaa gac gca gac tcc gag cct tcc 864  
 Tyr Lys Pro Val Ser Phe Asp Pro Glu Asp Ala Asp Ser Glu Pro Ser  
                   275                                  280                                  285

cca cca ctg gct aag gcc cgc gaa tgg gtt gag gtg gaa ctc gat ctc 912  
 Pro Pro Leu Ala Lys Ala Arg Glu Trp Val Glu Val Glu Leu Asp Leu  
                   290                                  295                                  300

ggc gat ggc aag aag aag tac acc cgc gac acc aac gtc atg cca cag 960  
 Gly Asp Gly Lys Lys Lys Tyr Thr Arg Asp Thr Asn Val Met Pro Gln  
 305                                  310                                  315                                  320

tgg gca ggt tcc tcc tgg tac cag ctg cgc tac gtc gat cca 1002  
 Trp Ala Gly Ser Ser Trp Tyr Gln Leu Arg Tyr Val Asp Pro  
                                   325                                  330

&lt;210&gt; 312

&lt;211&gt; 334

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 312

Leu Ile Asp Asp Leu Glu Leu Leu Asp Trp Thr Glu Lys Val Lys Ser  
   1                                  5                                  10                                  15

Met Gln Arg Asn Trp Ile Gly Arg Ser Arg Gly Ala Glu Val Asp Phe  
                   20                                  25                                  30

Ser Ala Glu Gly Glu Thr Val Thr Val Phe Thr Thr Arg Pro Asp Thr  
                   35                                  40                                  45

Leu Phe Gly Ala Thr Tyr Met Val Leu Ala Pro Glu His Glu Leu Val  
                   50                                  55                                  60

Asp Val Leu Leu Glu Lys Ala Gly Ser Tyr Glu Gly Val Asp Ala Arg  
   65                                  70                                  75                                  80

Trp Thr Asn Gly Gln Ala Ser Pro Ala Glu Ala Val Ala Ala Tyr Arg  
                   85                                  90                                  95

Ala Ser Ile Ala Ala Lys Ser Asp Leu Glu Arg Gln Glu Asn Lys Glu  
                   100                                  105                                  110

Lys Thr Gly Val Phe Leu Gly Val Tyr Ala Thr Asn Pro Val Asn Gly  
                   115                                  120                                  125

Asp Gln Ile Thr Val Phe Ile Ala Asp Tyr Val Leu Thr Gly Tyr Gly  
   130                                  135                                  140

Thr Gly Ala Ile Met Ala Val Pro Ala His Asp Glu Arg Asp Tyr Glu  
   145                                  150                                  155                                  160

Phe Ala Thr Val Leu Gly Leu Pro Ile Lys Glu Val Val Ala Gly Gly  
                   165                                  170                                  175

Asn Ile Glu Glu Ala Ala Phe Thr Glu Ser Gly Glu Ala Val Asn Ser  
                   180                                  185                                  190

Ala Asn Asp Asn Gly Leu Asp Ile Asn Gly Leu Ala Lys Asp Glu Ala  
 195 200 205

Ile Ala Lys Thr Ile Glu Trp Leu Glu Glu Lys Glu Leu Gly Arg Gly  
 210 215 220

Thr Ile Gln Tyr Lys Leu Arg Asp Trp Leu Phe Ala Arg Gln Arg Tyr  
 225 230 235 240

Trp Gly Glu Pro Phe Pro Ile Val Tyr Asp Glu Asn Gly Gln Ala His  
 245 250 255

Ala Leu Pro Asp Ser Met Leu Pro Val Glu Leu Pro Glu Val Glu Asp  
 260 265 270

Tyr Lys Pro Val Ser Phe Asp Pro Glu Asp Ala Asp Ser Glu Pro Ser  
 275 280 285

Pro Pro Leu Ala Lys Ala Arg Glu Trp Val Glu Val Glu Leu Asp Leu  
 290 295 300

Gly Asp Gly Lys Lys Lys Tyr Thr Arg Asp Thr Asn Val Met Pro Gln  
 305 310 315 320

Trp Ala Gly Ser Ser Trp Tyr Gln Leu Arg Tyr Val Asp Pro  
 325 330

&lt;210&gt; 313

&lt;211&gt; 1701

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1678)

&lt;223&gt; RXA01522

&lt;400&gt; 313

cacgacaacg tcggcctacc ccttggaatc ggcttcaaaa acatcgaagg ctgatcccg 60

tttaccacagt tcgcatacct ttcgactacc ctaggaaatc gtg act aat tcc aat 115  
 Val Thr Asn Ser Asn  
 1 5

ccc act tcc aag aac aat tcc gcc gat ttg cct gag cag ctg cga att 163  
 Pro Thr Ser Lys Asn Asn Ser Ala Asp Leu Pro Glu Gln Leu Arg Ile  
 10 15 20

cgt cgc gaa aag cgc gag cgc att ctg gac agt gga ttg gac gcc tac 211  
 Arg Arg Glu Lys Arg Glu Arg Ile Leu Asp Ser Gly Leu Asp Ala Tyr  
 25 30 35

cca gtc gag gtt gat cgc acc atc tca atc tct gac ctg cgc tcc caa 259  
 Pro Val Glu Val Asp Arg Thr Ile Ser Ile Ser Asp Leu Arg Ser Gln  
 40 45 50

ttt gtt gtc att aca gaa gac ctc caa gag cgc gaa gaa ggc gta acc 307  
 Phe Val Val Ile Thr Glu Asp Leu Gln Glu Arg Glu Glu Gly Val Thr  
 55 60 65

tac ctc gaa gta ggc gaa gaa acc gac gtt gag gtc gca atc gct ggc	355
Tyr Leu Glu Val Gly Glu Glu Thr Asp Val Glu Val Ala Ile Ala Gly	
70 75 80 85	
cgc gtc atg ttc gtt cgc aac acc ggc aag ctc tgc ttc gca tcc atc	403
Arg Val Met Phe Val Arg Asn Thr Gly Lys Leu Cys Phe Ala Ser Ile	
90 95 100	
caa gaa gga aac ggc acc acc gtc caa gca atg ctg tcc ctg gca gca	451
Gln Glu Gly Asn Gly Thr Thr Val Gln Ala Met Leu Ser Leu Ala Ala	
105 110 115	
gtc ggt gaa gaa tcc ctc aag gcc tgg aaa gcc gat gtg gac atg ggt	499
Val Gly Glu Glu Ser Leu Lys Ala Trp Lys Ala Asp Val Asp Met Gly	
120 125 130	
gac atc gtt tcc gtc cgc ggc aaa gta atc tcc tcc aag cgt ggc gaa	547
Asp Ile Val Ser Val Arg Gly Lys Val Ile Ser Ser Lys Arg Gly Glu	
135 140 145	
ctc tcc gtg atg gct gac tcc tgg cac atg gcc tcc aag tcc ctg cgc	595
Leu Ser Val Met Ala Asp Ser Trp His Met Ala Ser Lys Ser Leu Arg	
150 155 160 165	
cca ctg cca gtc gca ttc gcg gac ctc agc gaa gac acc cgc gtc cgc	643
Pro Leu Pro Val Ala Phe Ala Asp Leu Ser Glu Asp Thr Arg Val Arg	
170 175 180	
cac cgc tac acc gac ctc atc atg cgc gaa caa gcc cgc acc aac gcg	691
His Arg Tyr Thr Asp Leu Ile Met Arg Glu Gln Ala Arg Thr Asn Ala	
185 190 195	
ctc acc cgc atc aag gtc atg cgt gca ctc cgc cac tac ctc gaa gac	739
Leu Thr Arg Ile Lys Val Met Arg Ala Leu Arg His Tyr Leu Glu Asp	
200 205 210	
caa gac ttc ctt gag gta gaa acc ccc atg ctg caa acc ctc cac ggt	787
Gln Asp Phe Leu Glu Val Glu Thr Pro Met Leu Gln Thr Leu His Gly	
215 220 225	
ggc gca gca gca cga cca ttc gaa acc cac tcc aac gcc ctc gac att	835
Gly Ala Ala Ala Arg Pro Phe Glu Thr His Ser Asn Ala Leu Asp Ile	
230 235 240 245	
gac ctc tac ctg cgc atc gca cca gag ctt tac ctc aag cgc tgc gtt	883
Asp Leu Tyr Leu Arg Ile Ala Pro Glu Leu Tyr Leu Lys Arg Cys Val	
250 255 260	
gtc ggc ggc atc gag cgc gtc ttc gaa gtc aac cgc aac ttc cgc aac	931
Val Gly Gly Ile Glu Arg Val Phe Glu Val Asn Arg Asn Phe Arg Asn	
265 270 275	
gaa ggc gtc gac tcc tcc cac tcc cca gaa ttc gcc atg ctc gaa acc	979
Glu Gly Val Asp Ser Ser His Ser Pro Glu Phe Ala Met Leu Glu Thr	
280 285 290	
tac gaa gcc tgg gga acc tac gaa acc ggc gcg aaa ctg atc aag ggt	1027
Tyr Glu Ala Trp Gly Thr Tyr Glu Thr Gly Ala Lys Leu Ile Lys Gly	
295 300 305	

ctc gtc caa tcc gtc gcc caa gaa gtc ttc gga acc acc ctg gtc acc	1075
Leu Val Gln Ser Val Ala Gln Glu Val Phe Gly Thr Thr Leu Val Thr	
310 315 320 325	
ctc gca gac ggc acc gaa tac gac ctc ggc ggc gag tgg aaa gtc atc	1123
Leu Ala Asp Gly Thr Glu Tyr Asp Leu Gly Gly Glu Trp Lys Val Ile	
330 335 340	
gag atg tac cct tcc ctc aac gaa gcc ctc gca cgc aaa ttc cca gga	1171
Glu Met Tyr Pro Ser Leu Asn Glu Ala Leu Ala Arg Lys Phe Pro Gly	
345 350 355	
caa cca gaa gta acc atc gac tcc acc gtc gaa gaa ctc cgc gaa atc	1219
Gln Pro Glu Val Thr Ile Asp Ser Thr Val Glu Glu Leu Arg Glu Ile	
360 365 370	
gcc aag gta atc ggc ctc tcc gtc ccc gaa aac ggc ggc tgg gga cac	1267
Ala Lys Val Ile Gly Leu Ser Val Pro Glu Asn Gly Gly Trp Gly His	
375 380 385	
ggc aaa ctc gtc gaa gaa atc tgg gaa ctc ctc tgc gaa gac caa ctc	1315
Gly Lys Leu Val Glu Glu Ile Trp Glu Leu Leu Cys Glu Asp Gln Leu	
390 395 400 405	
tac gga cca atc ttt gtc aaa gac ttc cca gta gaa acc ttc cca ctc	1363
Tyr Gly Pro Ile Phe Val Lys Asp Phe Pro Val Glu Thr Phe Pro Leu	
410 415 420	
aca cgc caa cac cgc acc aag cca ggc gtc acc gaa aag tgg gac ctc	1411
Thr Arg Gln His Arg Thr Lys Pro Gly Val Thr Glu Lys Trp Asp Leu	
425 430 435	
tac gtc cgc gga ttt gaa cta gca acc gga tac tcc gaa ctc atc gac	1459
Tyr Val Arg Gly Phe Glu Leu Ala Thr Gly Tyr Ser Glu Leu Ile Asp	
440 445 450	
cca gtc att caa cgc gaa cgc ttc gaa ggc caa gcc cgc ctc gcc gcc	1507
Pro Val Ile Gln Arg Glu Arg Phe Glu Gly Gln Ala Arg Leu Ala Ala	
455 460 465	
gac gga gac gac gaa gcc atg gtc ctc gac gaa gac ttc ctc acc gca	1555
Asp Gly Asp Asp Glu Ala Met Val Leu Asp Glu Asp Phe Leu Thr Ala	
470 475 480 485	
atg gaa caa ggc atg cca cca acc tcc ggc aac ggc atg gga atc gac	1603
Met Glu Gln Gly Met Pro Pro Thr Ser Gly Asn Gly Met Gly Ile Asp	
490 495 500	
cgc ctc ctc atg gcc ctc acc ggc ctc gga atc cgc gaa acc gta ctc	1651
Arg Leu Leu Met Ala Leu Thr Gly Leu Gly Ile Arg Glu Thr Val Leu	
505 510 515	
ttc cca atg gtg aaa cca gaa caa aag taggtttttg ctctttgtgc ttg	1701
Phe Pro Met Val Lys Pro Glu Gln Lys	
520 525	

&lt;210&gt; 314

&lt;211&gt; 526

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 314

Val	Thr	Asn	Ser	Asn	Pro	Thr	Ser	Lys	Asn	Asn	Ser	Ala	Asp	Leu	Pro
1				5					10					15	
Glu	Gln	Leu	Arg	Ile	Arg	Arg	Glu	Lys	Arg	Glu	Arg	Ile	Leu	Asp	Ser
			20					25					30		
Gly	Leu	Asp	Ala	Tyr	Pro	Val	Glu	Val	Asp	Arg	Thr	Ile	Ser	Ile	Ser
		35					40					45			
Asp	Leu	Arg	Ser	Gln	Phe	Val	Val	Ile	Thr	Glu	Asp	Leu	Gln	Glu	Arg
	50					55					60				
Glu	Glu	Gly	Val	Thr	Tyr	Leu	Glu	Val	Gly	Glu	Glu	Thr	Asp	Val	Glu
65					70					75					80
Val	Ala	Ile	Ala	Gly	Arg	Val	Met	Phe	Val	Arg	Asn	Thr	Gly	Lys	Leu
				85					90					95	
Cys	Phe	Ala	Ser	Ile	Gln	Glu	Gly	Asn	Gly	Thr	Thr	Val	Gln	Ala	Met
			100					105					110		
Leu	Ser	Leu	Ala	Ala	Val	Gly	Glu	Glu	Ser	Leu	Lys	Ala	Trp	Lys	Ala
		115					120					125			
Asp	Val	Asp	Met	Gly	Asp	Ile	Val	Ser	Val	Arg	Gly	Lys	Val	Ile	Ser
	130					135					140				
Ser	Lys	Arg	Gly	Glu	Leu	Ser	Val	Met	Ala	Asp	Ser	Trp	His	Met	Ala
145					150					155					160
Ser	Lys	Ser	Leu	Arg	Pro	Leu	Pro	Val	Ala	Phe	Ala	Asp	Leu	Ser	Glu
				165					170					175	
Asp	Thr	Arg	Val	Arg	His	Arg	Tyr	Thr	Asp	Leu	Ile	Met	Arg	Glu	Gln
			180					185						190	
Ala	Arg	Thr	Asn	Ala	Leu	Thr	Arg	Ile	Lys	Val	Met	Arg	Ala	Leu	Arg
		195					200					205			
His	Tyr	Leu	Glu	Asp	Gln	Asp	Phe	Leu	Glu	Val	Glu	Thr	Pro	Met	Leu
	210					215					220				
Gln	Thr	Leu	His	Gly	Gly	Ala	Ala	Ala	Arg	Pro	Phe	Glu	Thr	His	Ser
225					230					235					240
Asn	Ala	Leu	Asp	Ile	Asp	Leu	Tyr	Leu	Arg	Ile	Ala	Pro	Glu	Leu	Tyr
				245					250					255	
Leu	Lys	Arg	Cys	Val	Val	Gly	Gly	Ile	Glu	Arg	Val	Phe	Glu	Val	Asn
			260					265					270		
Arg	Asn	Phe	Arg	Asn	Glu	Gly	Val	Asp	Ser	Ser	His	Ser	Pro	Glu	Phe
		275					280					285			
Ala	Met	Leu	Glu	Thr	Tyr	Glu	Ala	Trp	Gly	Thr	Tyr	Glu	Thr	Gly	Ala
	290					295					300				
Lys	Leu	Ile	Lys	Gly	Leu	Val	Gln	Ser	Val	Ala	Gln	Glu	Val	Phe	Gly
305					310					315					320

Thr Thr Leu Val Thr Leu Ala Asp Gly Thr Glu Tyr Asp Leu Gly Gly  
 325 330 335  
 Glu Trp Lys Val Ile Glu Met Tyr Pro Ser Leu Asn Glu Ala Leu Ala  
 340 345 350  
 Arg Lys Phe Pro Gly Gln Pro Glu Val Thr Ile Asp Ser Thr Val Glu  
 355 360 365  
 Glu Leu Arg Glu Ile Ala Lys Val Ile Gly Leu Ser Val Pro Glu Asn  
 370 375 380  
 Gly Gly Trp Gly His Gly Lys Leu Val Glu Glu Ile Trp Glu Leu Leu  
 385 390 395 400  
 Cys Glu Asp Gln Leu Tyr Gly Pro Ile Phe Val Lys Asp Phe Pro Val  
 405 410 415  
 Glu Thr Phe Pro Leu Thr Arg Gln His Arg Thr Lys Pro Gly Val Thr  
 420 425 430  
 Glu Lys Trp Asp Leu Tyr Val Arg Gly Phe Glu Leu Ala Thr Gly Tyr  
 435 440 445  
 Ser Glu Leu Ile Asp Pro Val Ile Gln Arg Glu Arg Phe Glu Gly Gln  
 450 455 460  
 Ala Arg Leu Ala Ala Asp Gly Asp Asp Glu Ala Met Val Leu Asp Glu  
 465 470 475 480  
 Asp Phe Leu Thr Ala Met Glu Gln Gly Met Pro Pro Thr Ser Gly Asn  
 485 490 495  
 Gly Met Gly Ile Asp Arg Leu Leu Met Ala Leu Thr Gly Leu Gly Ile  
 500 505 510  
 Arg Glu Thr Val Leu Phe Pro Met Val Lys Pro Glu Gln Lys  
 515 520 525

&lt;210&gt; 315

&lt;211&gt; 619

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(619)

&lt;223&gt; RXA02015

&lt;400&gt; 315\*

cccagagttc gttgagaccg aacacttcct gctcgacctg ccagcactgg ctgaagcact 60

aaccgagtggtg ctgaagggac gcgaagactg gcgtccaaac gtg ttg aag ttc tcg 115  
 Val Leu Lys Phe Ser  
 1 5

ctc aac ctg ctg gac gat atc cgc cca cgc gca atg tcg cgc gat atc 163  
 Leu Asn Leu Leu Asp Asp Ile Arg Pro Arg Ala Met Ser Arg Asp Ile  
 10 15 20

gac tgg ggc atc cca atc cca gtt gaa gga tgg caa gac aac aac gcc 211  
 Asp Trp Gly Ile Pro Ile Pro Val Glu Gly Trp Gln Asp Asn Asn Ala  
                   25                                  30                                  35

aag aag ctc tac gtc tgg ttc gac gct gtc gtg ggc tac ttg tcc gca 259  
 Lys Lys Leu Tyr Val Trp Phe Asp Ala Val Val Gly Tyr Leu Ser Ala  
                   40                                  45                                  50

tcc atc gaa tgg gcc tac cgc tcc ggc gac cca gaa gca tgg cgc acc 307  
 Ser Ile Glu Trp Ala Tyr Arg Ser Gly Asp Pro Glu Ala Trp Arg Thr  
                   55                                  60                                  65

ttc tgg aat gat cca gaa acc aag tcc tac tac ttc atg ggc aaa gac 355  
 Phe Trp Asn Asp Pro Glu Thr Lys Ser Tyr Tyr Phe Met Gly Lys Asp  
                   70                                  75                                  80                                  85

aac atc acc ttc cac tcc cag atc tgg cca gcg gag ctt ctc ggc tac 403  
 Asn Ile Thr Phe His Ser Gln Ile Trp Pro Ala Glu Leu Leu Gly Tyr  
                                   90                                  95                                  100

gca ggc aag ggc tcc cgc ggt gga gaa atc ggt gac ctg ggt gtt ctg 451  
 Ala Gly Lys Gly Ser Arg Gly Gly Glu Ile Gly Asp Leu Gly Val Leu  
                   105                                  110                                  115

aac ctg cct act gag gtt gtt tcc tct gag ttc ctg act atg tct gga 499  
 Asn Leu Pro Thr Glu Val Val Ser Ser Glu Phe Leu Thr Met Ser Gly  
                   120                                  125                                  130

tcc aag ttc tcc tca tcc aag ggc gtt gtc atc tac gtg aag gac ttc 547  
 Ser Lys Phe Ser Ser Ser Lys Gly Val Val Ile Tyr Val Lys Asp Phe  
                   135                                  140                                  145

ctc aag gag ttc ggc cca gat gcg ctg cga tac ttc atc gct gcg agg 595  
 Leu Lys Glu Phe Gly Pro Asp Ala Leu Arg Tyr Phe Ile Ala Ala Arg  
                   150                                  155                                  160                                  165

ccc aga aac aac gac acc gac ttc 619  
 Pro Arg Asn Asn Asp Thr Asp Phe  
                                   170

&lt;210&gt; 316

&lt;211&gt; 173

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 316

Val Leu Lys Phe Ser Leu Asn Leu Leu Asp Asp Ile Arg Pro Arg Ala  
                   1                                  5                                  10                                  15

Met Ser Arg Asp Ile Asp Trp Gly Ile Pro Ile Pro Val Glu Gly Trp  
                   20                                  25                                  30

Gln Asp Asn Asn Ala Lys Lys Leu Tyr Val Trp Phe Asp Ala Val Val  
                   35                                  40                                  45

Gly Tyr Leu Ser Ala Ser Ile Glu Trp Ala Tyr Arg Ser Gly Asp Pro  
                   50                                  55                                  60

Glu Ala Trp Arg Thr Phe Trp Asn Asp Pro Glu Thr Lys Ser Tyr Tyr

65	70	75	80
Phe Met Gly Lys Asp Asn Ile Thr Phe His Ser Gln Ile Trp Pro Ala	85	90	95
Glu Leu Leu Gly Tyr Ala Gly Lys Gly Ser Arg Gly Gly Glu Ile Gly	100	105	110
Asp Leu Gly Val Leu Asn Leu Pro Thr Glu Val Val Ser Ser Glu Phe	115	120	125
Leu Thr Met Ser Gly Ser Lys Phe Ser Ser Ser Lys Gly Val Val Ile	130	135	140
Tyr Val Lys Asp Phe Leu Lys Glu Phe Gly Pro Asp Ala Leu Arg Tyr	145	150	155
Phe Ile Ala Ala Arg Pro Arg Asn Asn Asp Thr Asp Phe	165	170	
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<211> 1212			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
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<222> (101)..(1189)			
<223> RXA01582			
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tcgccggtga gtaaacccca attcatgccc agcgggtatg atg gcg ggg tta gtt 115			
Met Ala Gly Leu Val 5			
gac tta aca ata aac atg agg gaa ggg ctg gac tac acg gtg tcc gaa 163			
Asp Leu Thr Ile Asn Met Arg Glu Gly Leu Asp Tyr Thr Val Ser Glu 20			
att cag ttg acc gaa gcc agt ttg aac gag gcg gcc gac gcc gcg atc 211			
Ile Gln Leu Thr Glu Ala Ser Leu Asn Glu Ala Ala Asp Ala Ala Ile 35			
aag gct ttc gac ggt gca caa aac cta gat gaa ctc gca gca cta cgc 259			
Lys Ala Phe Asp Gly Ala Gln Asn Leu Asp Glu Leu Ala Ala Leu Arg 50			
cgc gat cac ttg ggt gat gcc gca cct att ccg cag gca cga cgc tca 307			
Arg Asp His Leu Gly Asp Ala Ala Pro Ile Pro Gln Ala Arg Arg Ser 65			
ttg gga act att cct aaa gat cag cgc aag gat gcg ggc cgc ttt gtc 355			
Leu Gly Thr Ile Pro Lys Asp Gln Arg Lys Asp Ala Gly Arg Phe Val 85			
aac atg gca ctt ggt cgc gca gaa aag cac ttt gct cag gtc aag gtt 403			
Asn Met Ala Leu Gly Arg Ala Glu Lys His Phe Ala Gln Val Lys Val 100			

gtt ttg gaa gaa aag cgc aac gca gaa gtc cta gag ctt gag cgc gtt	451
Val Leu Glu Glu Lys Arg Asn Ala Glu Val Leu Glu Leu Glu Arg Val	
105 110 115	
gac gtc acc gtt cca acc acc cgc gag cag gtt ggt gcg ctg cac ccc	499
Asp Val Thr Val Pro Thr Thr Arg Glu Gln Val Gly Ala Leu His Pro	
120 125 130	
atc acg atc ctc aac gag cag atc gca gac atc ttc gtg ggc atg ggc	547
Ile Thr Ile Leu Asn Glu Gln Ile Ala Asp Ile Phe Val Gly Met Gly	
135 140 145	
tgg gaa atc gcc gag ggc cca gag gtg gaa gca gaa tac ttc aac ttc	595
Trp Glu Ile Ala Glu Gly Pro Glu Val Glu Ala Glu Tyr Phe Asn Phe	
150 155 160 165	
gac gca ctg aac ttc ctg cct gat cac cca gct cgt aca ctg cag gac	643
Asp Ala Leu Asn Phe Leu Pro Asp His Pro Ala Arg Thr Leu Gln Asp	
170 175 180	
acc ttc cac att gcg ccg gaa ggc tcc cgc cag gtg ctg cgt acc cac	691
Thr Phe His Ile Ala Pro Glu Gly Ser Arg Gln Val Leu Arg Thr His	
185 190 195	
acc tca cca gtt cag gtg cgc acc atg ctc aac cgt gaa gtt ccg atc	739
Thr Ser Pro Val Gln Val Arg Thr Met Leu Asn Arg Glu Val Pro Ile	
200 205 210	
tac atc gca tgc cct ggc cgt gtg ttc cgt acc gac gaa ctc gat gca	787
Tyr Ile Ala Cys Pro Gly Arg Val Phe Arg Thr Asp Glu Leu Asp Ala	
215 220 225	
aca cac acc cct gtg ttc cac cag atc gaa ggc ctt gca gtt gat aag	835
Thr His Thr Pro Val Phe His Gln Ile Glu Gly Leu Ala Val Asp Lys	
230 235 240 245	
ggt ctg act atg gct cac ctg cgc ggc acc ttg gat cac ctg gcc aag	883
Gly Leu Thr Met Ala His Leu Arg Gly Thr Leu Asp His Leu Ala Lys	
250 255 260	
gaa ctc ttc ggc cca gag acc aag act cgt atg cgc tcc aac tac ttc	931
Glu Leu Phe Gly Pro Glu Thr Lys Thr Arg Met Arg Ser Asn Tyr Phe	
265 270 275	
cca ttc acc gag cct tcc gct gag gtt gat gtg tgg ttc cct aac aag	979
Pro Phe Thr Glu Pro Ser Ala Glu Val Asp Val Trp Phe Pro Asn Lys	
280 285 290	
aag ggt ggt gca ggc tgg atc gag tgg ggt ggc tgt ggc atg gtc aac	1027
Lys Gly Gly Ala Gly Trp Ile Glu Trp Gly Gly Cys Gly Met Val Asn	
295 300 305	
cca aac gtg ctt cgt gcc gtg ggt gtt gac cca gag gag tac acc gga	1075
Pro Asn Val Leu Arg Ala Val Gly Val Asp Pro Glu Glu Tyr Thr Gly	
310 315 320 325	
ttc gcg ttc ggc atg ggc att gaa cgt acc ctg cag ttc cgc aac ggc	1123
Phe Ala Phe Gly Met Gly Ile Glu Arg Thr Leu Gln Phe Arg Asn Gly	
330 335 340	

ctg agc gat atg cgc gac atg gtt gag ggc gat att cgc ttc acc ctc 1171  
 Leu Ser Asp Met Arg Asp Met Val Glu Gly Asp Ile Arg Phe Thr Leu  
                   345                                  350                                  355

cca ttc ggc att cag gca taactcatcc cgcacacgac tta 1212  
 Pro Phe Gly Ile Gln Ala  
                   360

<210> 318

<211> 363

<212> PRT

<213> Corynebacterium glutamicum

<400> 318

Met Ala Gly Leu Val Asp Leu Thr Ile Asn Met Arg Glu Gly Leu Asp  
   1                                  5                                  10                                  15

Tyr Thr Val Ser Glu Ile Gln Leu Thr Glu Ala Ser Leu Asn Glu Ala  
                   20                                  25                                  30

Ala Asp Ala Ala Ile Lys Ala Phe Asp Gly Ala Gln Asn Leu Asp Glu  
                   35                                  40                                  45

Leu Ala Ala Leu Arg Arg Asp His Leu Gly Asp Ala Ala Pro Ile Pro  
                   50                                  55                                  60

Gln Ala Arg Arg Ser Leu Gly Thr Ile Pro Lys Asp Gln Arg Lys Asp  
                   65                                  70                                  75                                  80

Ala Gly Arg Phe Val Asn Met Ala Leu Gly Arg Ala Glu Lys His Phe  
                   85                                  90                                  95

Ala Gln Val Lys Val Val Leu Glu Glu Lys Arg Asn Ala Glu Val Leu  
                   100                                  105                                  110

Glu Leu Glu Arg Val Asp Val Thr Val Pro Thr Thr Arg Glu Gln Val  
                   115                                  120                                  125

Gly Ala Leu His Pro Ile Thr Ile Leu Asn Glu Gln Ile Ala Asp Ile  
                   130                                  135                                  140

Phe Val Gly Met Gly Trp Glu Ile Ala Glu Gly Pro Glu Val Glu Ala  
                   145                                  150                                  155                                  160

Glu Tyr Phe Asn Phe Asp Ala Leu Asn Phe Leu Pro Asp His Pro Ala  
                   165                                  170                                  175

Arg Thr Leu Gln Asp Thr Phe His Ile Ala Pro Glu Gly Ser Arg Gln  
                   180                                  185                                  190

Val Leu Arg Thr His Thr Ser Pro Val Gln Val Arg Thr Met Leu Asn  
                   195                                  200                                  205

Arg Glu Val Pro Ile Tyr Ile Ala Cys Pro Gly Arg Val Phe Arg Thr  
                   210                                  215                                  220

Asp Glu Leu Asp Ala Thr His Thr Pro Val Phe His Gln Ile Glu Gly  
                   225                                  230                                  235                                  240

Leu Ala Val Asp Lys Gly Leu Thr Met Ala His Leu Arg Gly Thr Leu

245										250					255				
Asp	His	Leu	Ala	Lys	Glu	Leu	Phe	Gly	Pro	Glu	Thr	Lys	Thr	Arg	Met				
		260						265					270						
Arg	Ser	Asn	Tyr	Phe	Pro	Phe	Thr	Glu	Pro	Ser	Ala	Glu	Val	Asp	Val				
		275					280					285							
Trp	Phe	Pro	Asn	Lys	Lys	Gly	Gly	Ala	Gly	Trp	Ile	Glu	Trp	Gly	Gly				
	290					295					300								
Cys	Gly	Met	Val	Asn	Pro	Asn	Val	Leu	Arg	Ala	Val	Gly	Val	Asp	Pro				
305					310					315					320				
Glu	Glu	Tyr	Thr	Gly	Phe	Ala	Phe	Gly	Met	Gly	Ile	Glu	Arg	Thr	Leu				
				325					330					335					
Gln	Phe	Arg	Asn	Gly	Leu	Ser	Asp	Met	Arg	Asp	Met	Val	Glu	Gly	Asp				
			340					345					350						
Ile	Arg	Phe	Thr	Leu	Pro	Phe	Gly	Ile	Gln	Ala									
		355					360												

<210> 319  
 <211> 2466  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(2443)  
 <223> RXN01583

<400> 319  
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 ggccaatccc tgaaaccacc ggaccactcg ttttcggcgc gtg gaa acc atc gaa 115  
 Val Glu Thr Ile Glu  
 1 5  
 gag ctc acc gag ttc aag aag ccc atc cgc cac tgc cac gtc aat gtt 163  
 Glu Leu Thr Glu Phe Lys Lys Pro Ile Arg His Cys His Val Asn Val  
 10 15 20  
 ggc gac gcc aac gga acc ggc gaa ctg cag tcc atc gtt tgt ggc gcc 211  
 Gly Asp Ala Asn Gly Thr Gly Glu Leu Gln Ser Ile Val Cys Gly Ala  
 25 30 35  
 cgc aac ttc aag gaa ggc gac acc gtt gtc gtg tcc ctt cct ggc gct 259  
 Arg Asn Phe Lys Glu Gly Asp Thr Val Val Val Ser Leu Pro Gly Ala  
 40 45 50  
 gtg ctg cct ggc gat ttc gcg atc tct gct cgt gaa act tac gga cgc 307  
 Val Leu Pro Gly Asp Phe Ala Ile Ser Ala Arg Glu Thr Tyr Gly Arg  
 55 60 65  
 atg tct gca ggc atg atc tgt tct gcc tct gag ctg ggt ctt gct gat 355  
 Met Ser Ala Gly Met Ile Cys Ser Ala Ser Glu Leu Gly Leu Ala Asp  
 70 75 80 85

aag cag aac tcc ggc atc atc acc ctg gat cct tct tac ggc gag cct	403
Lys Gln Asn Ser Gly Ile Ile Thr Leu Asp Pro Ser Tyr Gly Glu Pro	
90 95 100	
ggc gaa gac gca cgt caa gca ctg gga ctt gaa gat acc gtt ttc gat	451
Gly Glu Asp Ala Arg Gln Ala Leu Gly Leu Glu Asp Thr Val Phe Asp	
105 110 115	
gtc aac gtc acc cca gac cgc ggt tac gca ctg tct gct cgt ggc ctg	499
Val Asn Val Thr Pro Asp Arg Gly Tyr Ala Leu Ser Ala Arg Gly Leu	
120 125 130	
acc cgc gaa ctg gca tcg gct ttc agc ctg acc ttc acc gac cct gcg	547
Thr Arg Glu Leu Ala Ser Ala Phe Ser Leu Thr Phe Thr Asp Pro Ala	
135 140 145	
atc gag cca gct gta gca ggc att gag gtc aag gtc cca gca gtt gaa	595
Ile Glu Pro Ala Val Ala Gly Ile Glu Val Lys Val Pro Ala Val Glu	
150 155 160 165	
ggt tcc ttg att aac gtg gag ctg cgt gaa gag acc aag gca atc cgt	643
Gly Ser Leu Ile Asn Val Glu Leu Arg Glu Glu Thr Lys Ala Ile Arg	
170 175 180	
ttc ggt ctg cgt aaa gtc tct ggc att gat cca gca gca gaa tcc cca	691
Phe Gly Leu Arg Lys Val Ser Gly Ile Asp Pro Ala Ala Glu Ser Pro	
185 190 195	
ttc tgg atg cag cgt gaa ctc atg ctc tct ggt cag cga cca gtc aac	739
Phe Trp Met Gln Arg Glu Leu Met Leu Ser Gly Gln Arg Pro Val Asn	
200 205 210	
gcc gcc acc gac gtc acc aac tac gtc atg ttg ctg ctc ggc cag ccg	787
Ala Ala Thr Asp Val Thr Asn Tyr Val Met Leu Leu Leu Gly Gln Pro	
215 220 225	
atg cat gct ttc gac gca gcc aag gtt act ggc gat ctt gtt gtc cgc	835
Met His Ala Phe Asp Ala Ala Lys Val Thr Gly Asp Leu Val Val Arg	
230 235 240 245	
aac gca act gca ggc gag aag ttc gaa acc ctc gat cac gtc aag cgc	883
Asn Ala Thr Ala Gly Glu Lys Phe Glu Thr Leu Asp His Val Lys Arg	
250 255 260	
acc ctc aat gag gaa gac gtt gtg atc acc gat gac aac ggc att cag	931
Thr Leu Asn Glu Glu Asp Val Val Ile Thr Asp Asp Asn Gly Ile Gln	
265 270 275	
tct ttg gct ggc gtt atg ggt ggt ctc acc tcc gag atc tct gac acc	979
Ser Leu Ala Gly Val Met Gly Gly Leu Thr Ser Glu Ile Ser Asp Thr	
280 285 290	
acc acc gat gtc tac ttc gag gcc gca acc tgg gac acc atc acc gtt	1027
Thr Thr Asp Val Tyr Phe Glu Ala Ala Thr Trp Asp Thr Ile Thr Val	
295 300 305	
gcg cgc acc tca cgt cgc cac aag ttg agc tcc gaa gct tct cga cgt	1075
Ala Arg Thr Ser Arg Arg His Lys Leu Ser Ser Glu Ala Ser Arg Arg	
310 315 320 325	
ttc gag cgt ggc gtt gac cct gcg atc gtg gaa atc gcc ctc gat atc	1123

Phe	Glu	Arg	Gly	Val	Asp	Pro	Ala	Ile	Val	Glu	Ile	Ala	Leu	Asp	Ile	
				330					335					340		
gca	gca	acc	ctt	ctc	gtg	gag	atc	gca	ggc	ggc	acc	gtc	gat	gcg	ggt	1171
Ala	Ala	Thr	Leu	Leu	Val	Glu	Ile	Ala	Gly	Gly	Thr	Val	Asp	Ala	Gly	
			345					350					355			
cgc	acc	ctc	gtt	ggt	gat	gtc	cct	gcc	atg	caa	ccc	atc	acc	atg	aag	1219
Arg	Thr	Leu	Val	Gly	Asp	Val	Pro	Ala	Met	Gln	Pro	Ile	Thr	Met	Lys	
		360					365					370				
gtc	act	cga	cct	tcc	gag	ctc	gca	ggc	gtg	gat	tat	tcc	gca	gaa	act	1267
Val	Thr	Arg	Pro	Ser	Glu	Leu	Ala	Gly	Val	Asp	Tyr	Ser	Ala	Glu	Thr	
	375					380				385						
gtg	atc	gct	cgt	ctg	gaa	gag	gtc	gga	tgc	acc	gtc	gct	gtt	tcc	ggc	1315
Val	Ile	Ala	Arg	Leu	Glu	Glu	Val	Gly	Cys	Thr	Val	Ala	Val	Ser	Gly	
390					395				400						405	
gac	acc	ttg	gaa	gta	acc	cct	cca	acc	tgg	cgc	ggt	gac	ctc	acc	atg	1363
Asp	Thr	Leu	Glu	Val	Thr	Pro	Pro	Thr	Trp	Arg	Gly	Asp	Leu	Thr	Met	
			410					415					420			
tcc	gct	gac	ctc	gtg	gaa	gaa	gta	ctc	cgc	ctc	gaa	ggt	ttg	gaa	gca	1411
Ser	Ala	Asp	Leu	Val	Glu	Glu	Val	Leu	Arg	Leu	Glu	Gly	Leu	Glu	Ala	
			425				430						435			
att	cca	acc	atc	atc	cca	acc	gca	cca	gca	ggc	cgt	gga	cta	acc	gat	1459
Ile	Pro	Thr	Ile	Ile	Pro	Thr	Ala	Pro	Ala	Gly	Arg	Gly	Leu	Thr	Asp	
		440					445					450				
gca	cag	aag	cgc	cgc	cgc	gcc	gtt	ggc	cac	gct	ttg	gct	tac	gct	ggc	1507
Ala	Gln	Lys	Arg	Arg	Arg	Ala	Val	Gly	His	Ala	Leu	Ala	Tyr	Ala	Gly	
	455					460					465					
tac	gcc	gaa	atc	atc	cca	agc	cca	ttc	atg	gac	cca	gag	gtc	ttc	gat	1555
Tyr	Ala	Glu	Ile	Ile	Pro	Ser	Pro	Phe	Met	Asp	Pro	Glu	Val	Phe	Asp	
470					475				480						485	
gta	tgg	gga	ctc	gca	gca	gac	gac	gag	cgc	cgc	aag	acc	gtt	tcc	gtt	1603
Val	Trp	Gly	Leu	Ala	Ala	Asp	Asp	Glu	Arg	Arg	Lys	Thr	Val	Ser	Val	
			490					495						500		
ctc	aac	cca	ctt	gag	gca	gaa	cgc	aac	gtc	ctg	agc	acc	tcc	ttg	ctg	1651
Leu	Asn	Pro	Leu	Glu	Ala	Glu	Arg	Asn	Val	Leu	Ser	Thr	Ser	Leu	Leu	
		505						510					515			
ccc	tcc	atg	ctc	gat	gct	gtc	aag	cgc	aac	gtt	gca	cgt	gga	cac	aac	1699
Pro	Ser	Met	Leu	Asp	Ala	Val	Lys	Arg	Asn	Val	Ala	Arg	Gly	His	Asn	
		520					525					530				
gat	ttc	tcc	ctg	ttc	ggc	ctg	cag	cag	gtc	gcc	ttc	gag	cac	gga	tcc	1747
Asp	Phe	Ser	Leu	Phe	Gly	Leu	Gln	Gln	Val	Ala	Phe	Glu	His	Gly	Ser	
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ggc	gtt	tcc	cca	atg	cca	tct	gtt	gct	tca	cgc	cct	gaa	gag	tct	gtc	1795
Gly	Val	Ser	Pro	Met	Pro	Ser	Val	Ala	Ser	Arg	Pro	Glu	Glu	Ser	Val	
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gtg	gca	gaa	ctg	gtg	gat	tca	ctg	cca	aac	cag	cca	ctg	cat	gtc	gca	1843
Val	Ala	Glu	Leu	Val	Asp	Ser	Leu	Pro	Asn	Gln	Pro	Leu	His	Val	Ala	

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acc	gtg	ggc	acc	ggc	aac	atc	gag	ttc	gaa	ggc	cca	tgg	ggc	aag	ggc	1891				
Thr	Val	Gly	Thr	Gly	Asn	Ile	Glu	Phe	Glu	Gly	Pro	Trp	Gly	Lys	Gly					
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cgc	gcc	tac	acc	ttc	ggc	gac	gcg	att	gaa	tcc	gcg	cgc	gca	gtc	gcc	1939				
Arg	Ala	Tyr	Thr	Phe	Ala	Asp	Ala	Ile	Glu	Ser	Ala	Arg	Ala	Val	Ala					
		600					605					610								
cgc	gct	gct	ggc	gtc	acc	ttg	gag	ctg	gcc	aac	gcc	gac	gcg	ctt	cct	1987				
Arg	Ala	Ala	Gly	Val	Thr	Leu	Glu	Leu	Ala	Asn	Ala	Asp	Ala	Leu	Pro					
	615					620					625									
tgg	cac	cca	ggt	cgt	tgc	gcc	gca	ttg	ctt	atc	gac	ggt	acc	ccc	gtc	2035				
Trp	His	Pro	Gly	Arg	Cys	Ala	Ala	Leu	Leu	Ile	Asp	Gly	Thr	Pro	Val					
630					635					640					645					
ggt	tac	gct	ggc	gaa	ctt	cac	cca	cag	atc	ctg	gaa	aag	gcc	ggt	cta	2083				
Gly	Tyr	Ala	Gly	Glu	Leu	His	Pro	Gln	Ile	Leu	Glu	Lys	Ala	Gly	Leu					
			650						655					660						
cca	gca	cgc	acc	tgt	gca	atg	gaa	ctg	gat	ctc	agc	gca	ctg	cca	ctg	2131				
Pro	Ala	Arg	Thr	Cys	Ala	Met	Glu	Leu	Asp	Leu	Ser	Ala	Leu	Pro	Leu					
			665					670					675							
gta	gaa	aac	ctc	cca	gcg	cca	gtc	ctg	tcc	tcc	ttc	cca	gca	ctg	cac	2179				
Val	Glu	Asn	Leu	Pro	Ala	Pro	Val	Leu	Ser	Ser	Phe	Pro	Ala	Leu	His					
		680					685					690								
caa	gac	atc	gcc	cta	gtt	gtg	gat	gag	acc	atc	ccg	gcc	gaa	gat	gtc	2227				
Gln	Asp	Ile	Ala	Leu	Val	Val	Asp	Glu	Thr	Ile	Pro	Ala	Glu	Asp	Val					
	695					700					705									
cgc	gca	gtt	gtc	gaa	ggc	ggc	ggc	gaa	ctg	atc	gaa	acg	gtc	gag		2275				
Arg	Ala	Val	Val	Glu	Ala	Gly	Ala	Gly	Glu	Leu	Ile	Glu	Thr	Val	Glu					
710					715				720					725						
ctt	ttc	cac	gtc	ttc	cgc	tcc	gaa	cag	cgc	ggc	gag	aac	aag	aaa	tcc	2323				
Leu	Phe	His	Val	Phe	Arg	Ser	Glu	Gln	Arg	Gly	Glu	Asn	Lys	Lys	Ser					
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ctc	gcg	ttc	tcc	ctg	cgt	ttc	cgc	gca	gcc	ggc	cgc	acc	ctc	acc	gat	2371				
Leu	Ala	Phe	Ser	Leu	Arg	Phe	Arg	Ala	Ala	Gly	Arg	Thr	Leu	Thr	Asp					
			745					750					755							
gag	gaa	gcc	aac	gaa	gca	cga	ctt	cag	gca	gca	gag	cta	gca	aag	gag	2419				
Glu	Glu	Ala	Asn	Glu	Ala	Arg	Leu	Gln	Ala	Ala	Glu	Leu	Ala	Lys	Glu					
		760					765					770								
aaa	ttc	aac	gct	gaa	atg	cgt	ggc	tagttttcaca	taggtttctat	agg						2466				
Lys	Phe	Asn	Ala	Glu	Met	Arg	Gly													
	775					780														

&lt;210&gt; 320

&lt;211&gt; 781

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 320

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Cys	His	Val	Asn	Val	Gly	Asp	Ala	Asn	Gly	Thr	Gly	Glu	Leu	Gln	Ser	
			20					25					30			
Ile	Val	Cys	Gly	Ala	Arg	Asn	Phe	Lys	Glu	Gly	Asp	Thr	Val	Val	Val	
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Ser	Leu	Pro	Gly	Ala	Val	Leu	Pro	Gly	Asp	Phe	Ala	Ile	Ser	Ala	Arg	
	50					55					60					
Glu	Thr	Tyr	Gly	Arg	Met	Ser	Ala	Gly	Met	Ile	Cys	Ser	Ala	Ser	Glu	
65					70					75					80	
Leu	Gly	Leu	Ala	Asp	Lys	Gln	Asn	Ser	Gly	Ile	Ile	Thr	Leu	Asp	Pro	
				85					90					95		
Ser	Tyr	Gly	Glu	Pro	Gly	Glu	Asp	Ala	Arg	Gln	Ala	Leu	Gly	Leu	Glu	
			100					105					110			
Asp	Thr	Val	Phe	Asp	Val	Asn	Val	Thr	Pro	Asp	Arg	Gly	Tyr	Ala	Leu	
		115					120					125				
Ser	Ala	Arg	Gly	Leu	Thr	Arg	Glu	Leu	Ala	Ser	Ala	Phe	Ser	Leu	Thr	
	130					135					140					
Phe	Thr	Asp	Pro	Ala	Ile	Glu	Pro	Ala	Val	Ala	Gly	Ile	Glu	Val	Lys	
145					150					155					160	
Val	Pro	Ala	Val	Glu	Gly	Ser	Leu	Ile	Asn	Val	Glu	Leu	Arg	Glu	Glu	
				165					170					175		
Thr	Lys	Ala	Ile	Arg	Phe	Gly	Leu	Arg	Lys	Val	Ser	Gly	Ile	Asp	Pro	
			180					185					190			
Ala	Ala	Glu	Ser	Pro	Phe	Trp	Met	Gln	Arg	Glu	Leu	Met	Leu	Ser	Gly	
		195					200					205				
Gln	Arg	Pro	Val	Asn	Ala	Ala	Thr	Asp	Val	Thr	Asn	Tyr	Val	Met	Leu	
	210				215						220					
Leu	Leu	Gly	Gln	Pro	Met	His	Ala	Phe	Asp	Ala	Ala	Lys	Val	Thr	Gly	
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Asp	Leu	Val	Val	Arg	Asn	Ala	Thr	Ala	Gly	Glu	Lys	Phe	Glu	Thr	Leu	
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Asp	His	Val	Lys	Arg	Thr	Leu	Asn	Glu	Glu	Asp	Val	Val	Ile	Thr	Asp	
			260					265					270			
Asp	Asn	Gly	Ile	Gln	Ser	Leu	Ala	Gly	Val	Met	Gly	Gly	Leu	Thr	Ser	
		275					280					285				
Glu	Ile	Ser	Asp	Thr	Thr	Thr	Asp	Val	Tyr	Phe	Glu	Ala	Ala	Thr	Trp	
	290					295					300					
Asp	Thr	Ile	Thr	Val	Ala	Arg	Thr	Ser	Arg	Arg	His	Lys	Leu	Ser	Ser	
305					310					315				320		
Glu	Ala	Ser	Arg	Arg	Phe	Glu	Arg	Gly	Val	Asp	Pro	Ala	Ile	Val	Glu	

325										330					335				
Ile	Ala	Leu	Asp	Ile	Ala	Ala	Thr	Leu	Leu	Val	Glu	Ile	Ala	Gly	Gly				
			340					345					350						
Thr	Val	Asp	Ala	Gly	Arg	Thr	Leu	Val	Gly	Asp	Val	Pro	Ala	Met	Gln				
		355					360					365							
Pro	Ile	Thr	Met	Lys	Val	Thr	Arg	Pro	Ser	Glu	Leu	Ala	Gly	Val	Asp				
	370					375					380								
Tyr	Ser	Ala	Glu	Thr	Val	Ile	Ala	Arg	Leu	Glu	Glu	Val	Gly	Cys	Thr				
385					390					395					400				
Val	Ala	Val	Ser	Gly	Asp	Thr	Leu	Glu	Val	Thr	Pro	Pro	Thr	Trp	Arg				
				405					410					415					
Gly	Asp	Leu	Thr	Met	Ser	Ala	Asp	Leu	Val	Glu	Glu	Val	Leu	Arg	Leu				
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Glu	Gly	Leu	Glu	Ala	Ile	Pro	Thr	Ile	Ile	Pro	Thr	Ala	Pro	Ala	Gly				
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Arg	Gly	Leu	Thr	Asp	Ala	Gln	Lys	Arg	Arg	Arg	Ala	Val	Gly	His	Ala				
	450					455					460								
Leu	Ala	Tyr	Ala	Gly	Tyr	Ala	Glu	Ile	Ile	Pro	Ser	Pro	Phe	Met	Asp				
465					470					475					480				
Pro	Glu	Val	Phe	Asp	Val	Trp	Gly	Leu	Ala	Ala	Asp	Asp	Glu	Arg	Arg				
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Lys	Thr	Val	Ser	Val	Leu	Asn	Pro	Leu	Glu	Ala	Glu	Arg	Asn	Val	Leu				
			500					505					510						
Ser	Thr	Ser	Leu	Leu	Pro	Ser	Met	Leu	Asp	Ala	Val	Lys	Arg	Asn	Val				
		515					520					525							
Ala	Arg	Gly	His	Asn	Asp	Phe	Ser	Leu	Phe	Gly	Leu	Gln	Gln	Val	Ala				
	530					535					540								
Phe	Glu	His	Gly	Ser	Gly	Val	Ser	Pro	Met	Pro	Ser	Val	Ala	Ser	Arg				
545					550					555					560				
Pro	Glu	Glu	Ser	Val	Val	Ala	Glu	Leu	Val	Asp	Ser	Leu	Pro	Asn	Gln				
				565					570					575					
Pro	Leu	His	Val	Ala	Thr	Val	Gly	Thr	Gly	Asn	Ile	Glu	Phe	Glu	Gly				
			580					585					590						
Pro	Trp	Gly	Lys	Gly	Arg	Ala	Tyr	Thr	Phe	Ala	Asp	Ala	Ile	Glu	Ser				
		595					600					605							
Ala	Arg	Ala	Val	Ala	Arg	Ala	Ala	Gly	Val	Thr	Leu	Glu	Leu	Ala	Asn				
	610					615					620								
Ala	Asp	Ala	Leu	Pro	Trp	His	Pro	Gly	Arg	Cys	Ala	Ala	Leu	Leu	Ile				
625					630					635					640				
Asp	Gly	Thr	Pro	Val	Gly	Tyr	Ala	Gly	Glu	Leu	His	Pro	Gln	Ile	Leu				
				645					650					655					

Glu Lys Ala Gly Leu Pro Ala Arg Thr Cys Ala Met Glu Leu Asp Leu  
 660 665 670  
 Ser Ala Leu Pro Leu Val Glu Asn Leu Pro Ala Pro Val Leu Ser Ser  
 675 680 685  
 Phe Pro Ala Leu His Gln Asp Ile Ala Leu Val Val Asp Glu Thr Ile  
 690 695 700  
 Pro Ala Glu Asp Val Arg Ala Val Val Glu Ala Gly Ala Gly Glu Leu  
 705 710 715 720  
 Ile Glu Thr Val Glu Leu Phe His Val Phe Arg Ser Glu Gln Arg Gly  
 725 730 735  
 Glu Asn Lys Lys Ser Leu Ala Phe Ser Leu Arg Phe Arg Ala Ala Gly  
 740 745 750  
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 Val Glu Thr Ile Glu 5  
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 gag ctc acc gag ttc aag aag ccc atc cgc cac tgc cac gtc aat gtt 163  
 Glu Leu Thr Glu Phe Lys Lys Pro Ile Arg His Cys His Val Asn Val 20  
 10 15  
 ggc gac gcc aac gga acc ggc gaa ctg cag tcc atc gtt tgt ggc gcc 211  
 Gly Asp Ala Asn Gly Thr Gly Glu Leu Gln Ser Ile Val Cys Gly Ala 35  
 25 30  
 cgc aac ttc aag gaa ggc gac acc gtt gtc gtg tcc ctt cct ggc gct 259  
 Arg Asn Phe Lys Glu Gly Asp Thr Val Val Val Ser Leu Pro Gly Ala 50  
 40 45  
 gtg ctg cct ggc gat ttc gcg atc tct gct cgt gaa act tac gga cgc 307  
 Val Leu Pro Gly Asp Phe Ala Ile Ser Ala Arg Glu Thr Tyr Gly Arg 65  
 55 60  
 atg tct gca ggc atg atc tgt tct gcc tct gag ctg ggt ctt gct gat 355  
 Met Ser Ala Gly Met Ile Cys Ser Ala Ser Glu Leu Gly Leu Ala Asp

70	75	80	85	
aag cag aac tcc ggc atc atc acc ctg gat cct tct tac ggc gag cct				403
Lys Gln Asn Ser Gly Ile Ile Thr Leu Asp Pro Ser Tyr Gly Glu Pro	90	95	100	
ggc gaa gac gca cgt caa gca ctg gga ctt gaa gat acc gtt ttc gat				451
Gly Glu Asp Ala Arg Gln Ala Leu Gly Leu Glu Asp Thr Val Phe Asp	105	110	115	
gtc aac gtc acc cca gac cgc ggt tac gca ctg tct gct cgt ggc ctg				499
Val Asn Val Thr Pro Asp Arg Gly Tyr Ala Leu Ser Ala Arg Gly Leu	120	125	130	
acc cgc gaa ctg gca tcg gct ttc agc ctg acc ttc acc gac cct gcg				547
Thr Arg Glu Leu Ala Ser Ala Phe Ser Leu Thr Phe Thr Asp Pro Ala	135	140	145	
atc gag cca gct gta gca ggc att gag gtc aag gtc cca gca gtt gaa				595
Ile Glu Pro Ala Val Ala Gly Ile Glu Val Lys Val Pro Ala Val Glu	155	160	165	
ggt tcc ttg att aac gtg gag ctg cgt gaa gag acc aag gca atc cgt				643
Gly Ser Leu Ile Asn Val Glu Leu Arg Glu Glu Thr Lys Ala Ile Arg	170	175	180	
ttc ggt ctg cgt aaa gtc tct ggc att gat cca gca gca gaa tcc cca				691
Phe Gly Leu Arg Lys Val Ser Gly Ile Asp Pro Ala Ala Glu Ser Pro	185	190	195	
ttc tgg atg cag cgt gaa ctc atg ctc tct ggt cag cga cca gtc aac				739
Phe Trp Met Gln Arg Glu Leu Met Leu Ser Gly Gln Arg Pro Val Asn	200	205	210	
gcc gcc acc gac gtc acc aac tac gtc atg ttg ctg ctc ggc cag ccg				787
Ala Ala Thr Asp Val Thr Asn Tyr Val Met Leu Leu Leu Gly Gln Pro	215	220	225	
atg cat gct ttc gac gca gcc aag gtt act ggc gat ctt gtt gtc cgc				835
Met His Ala Phe Asp Ala Ala Lys Val Thr Gly Asp Leu Val Val Arg	235	240	245	
aac gca act gca ggc gag aag ttc gaa acc ctc gat cac gtc aag cgc				883
Asn Ala Thr Ala Gly Glu Lys Phe Glu Thr Leu Asp His Val Lys Arg	250	255	260	
acc ctc aat gag gaa gac gtt gtg atc acc gat gac aac ggc att cag				931
Thr Leu Asn Glu Glu Asp Val Val Ile Thr Asp Asp Asn Gly Ile Gln	265	270	275	
tct ttg gct ggc gtt atg ggt ggt ctc acc tcc gag atc tct gac acc				979
Ser Leu Ala Gly Val Met Gly Gly Leu Thr Ser Glu Ile Ser Asp Thr	280	285	290	
acc acc gat gtc tac ttc gag gcc gca acc tgg gac acc atc acc gtt				1027
Thr Thr Asp Val Tyr Phe Glu Ala Ala Thr Trp Asp Thr Ile Thr Val	295	300	305	
gcg cgc acc tca cgt cgc cac aag ttg agc tcc gaa gct tct cga cgt				1075
Ala Arg Thr Ser Arg Arg His Lys Leu Ser Ser Glu Ala Ser Arg Arg	315	320	325	
310				

ttc gag cgt ggc gtt gac cct gcg atc gtg gaa atc gcc ctc gat atc	1123
Phe Glu Arg Gly Val Asp Pro Ala Ile Val Glu Ile Ala Leu Asp Ile	
330 335 340	
gca gca acc ctt ctc gtg gag atc gca ggc ggc acc gtc gat gcg ggt	1171
Ala Ala Thr Leu Leu Val Glu Ile Ala Gly Gly Thr Val Asp Ala Gly	
345 350 355	
cgc acc ctc gtt ggt gat gtc cct gcc atg caa ccc atc acc atg aag	1219
Arg Thr Leu Val Gly Asp Val Pro Ala Met Gln Pro Ile Thr Met Lys	
360 365 370	
gtc act cga cct tcc gag ctc gca ggc gtg gat tat tcc gca gaa act	1267
Val Thr Arg Pro Ser Glu Leu Ala Gly Val Asp Tyr Ser Ala Glu Thr	
375 380 385	
gtg atc gct cgt ctg gaa gag gtc gga tgc acc gtc gct gtt tcc ggc	1315
Val Ile Ala Arg Leu Glu Glu Val Gly Cys Thr Val Ala Val Ser Gly	
390 395 400 405	
gac acc ttg gaa gta acc cct cca acc tgg cgc ggt gac ctc acc atg	1363
Asp Thr Leu Glu Val Thr Pro Pro Thr Trp Arg Gly Asp Leu Thr Met	
410 415 420	
tcc gct gac ctc gtg gaa gaa gta ctc cgc ctc gaa ggt ttg gaa gca	1411
Ser Ala Asp Leu Val Glu Glu Val Leu Arg Leu Glu Gly Leu Glu Ala	
425 430 435	
att cca acc atc atc cca acc gca cca gca ggc cgt gga cta acc gat	1459
Ile Pro Thr Ile Ile Pro Thr Ala Pro Ala Gly Arg Gly Leu Thr Asp	
440 445 450	
gca cag aag cgc cgc cgc gcc gtt ggc cac gct ttg gct tac gct ggc	1507
Ala Gln Lys Arg Arg Arg Ala Val Gly His Ala Leu Ala Tyr Ala Gly	
455 460 465	
tac gcc gaa atc atc cca agc cca ttc atg gac cca gag gtc ttc gat	1555
Tyr Ala Glu Ile Ile Pro Ser Pro Phe Met Asp Pro Glu Val Phe Asp	
470 475 480 485	
gta tgg gga ctc gca gca gac gac gag cgc cgc aag acc gtt tcc gtt	1603
Val Trp Gly Leu Ala Ala Asp Asp Glu Arg Arg Lys Thr Val Ser Val	
490 495 500	
ctc aac cca ctt gag gca gaa cgc aac gtc ctg agc acc tcc ttg ctg	1651
Leu Asn Pro Leu Glu Ala Glu Arg Asn Val Leu Ser Thr Ser Leu Leu	
505 510 515	
ccc tcc atg ctc gat gct gtc aag cgc aac gtt gca cgt gga cac aac	1699
Pro Ser Met Leu Asp Ala Val Lys Arg Asn Val Ala Arg Gly His Asn	
520 525 530	
gat ttc tcc ctg ttc ggc ctg cag cag gtc gcc ttc gag cac gga tcc	1747
Asp Phe Ser Leu Phe Gly Leu Gln Gln Val Ala Phe Glu His Gly Ser	
535 540 545	
ggc gtt tcc cca atg cca tct gtt gct tca cgc cct gaa gag tct gtc	1795
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1816

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 20 25 30  
 Ile Val Cys Gly Ala Arg Asn Phe Lys Glu Gly Asp Thr Val Val Val  
 35 40 45  
 Ser Leu Pro Gly Ala Val Leu Pro Gly Asp Phe Ala Ile Ser Ala Arg  
 50 55 60  
 Glu Thr Tyr Gly Arg Met Ser Ala Gly Met Ile Cys Ser Ala Ser Glu  
 65 70 75 80  
 Leu Gly Leu Ala Asp Lys Gln Asn Ser Gly Ile Ile Thr Leu Asp Pro  
 85 90 95  
 Ser Tyr Gly Glu Pro Gly Glu Asp Ala Arg Gln Ala Leu Gly Leu Glu  
 100 105 110  
 Asp Thr Val Phe Asp Val Asn Val Thr Pro Asp Arg Gly Tyr Ala Leu  
 115 120 125  
 Ser Ala Arg Gly Leu Thr Arg Glu Leu Ala Ser Ala Phe Ser Leu Thr  
 130 135 140  
 Phe Thr Asp Pro Ala Ile Glu Pro Ala Val Ala Gly Ile Glu Val Lys  
 145 150 155 160  
 Val Pro Ala Val Glu Gly Ser Leu Ile Asn Val Glu Leu Arg Glu Glu  
 165 170 175  
 Thr Lys Ala Ile Arg Phe Gly Leu Arg Lys Val Ser Gly Ile Asp Pro  
 180 185 190  
 Ala Ala Glu Ser Pro Phe Trp Met Gln Arg Glu Leu Met Leu Ser Gly  
 195 200 205  
 Gln Arg Pro Val Asn Ala Ala Thr Asp Val Thr Asn Tyr Val Met Leu  
 210 215 220  
 Leu Leu Gly Gln Pro Met His Ala Phe Asp Ala Ala Lys Val Thr Gly  
 225 230 235 240  
 Asp Leu Val Val Arg Asn Ala Thr Ala Gly Glu Lys Phe Glu Thr Leu  
 245 250 255  
 Asp His Val Lys Arg Thr Leu Asn Glu Glu Asp Val Val Ile Thr Asp  
 260 265 270

Asp Asn Gly Ile Gln Ser Leu Ala Gly Val Met Gly Gly Leu Thr Ser  
 275 280 285  
 Glu Ile Ser Asp Thr Thr Thr Asp Val Tyr Phe Glu Ala Ala Thr Trp  
 290 295 300  
 Asp Thr Ile Thr Val Ala Arg Thr Ser Arg Arg His Lys Leu Ser Ser  
 305 310 315 320  
 Glu Ala Ser Arg Arg Phe Glu Arg Gly Val Asp Pro Ala Ile Val Glu  
 325 330 335  
 Ile Ala Leu Asp Ile Ala Ala Thr Leu Leu Val Glu Ile Ala Gly Gly  
 340 345 350  
 Thr Val Asp Ala Gly Arg Thr Leu Val Gly Asp Val Pro Ala Met Gln  
 355 360 365  
 Pro Ile Thr Met Lys Val Thr Arg Pro Ser Glu Leu Ala Gly Val Asp  
 370 375 380  
 Tyr Ser Ala Glu Thr Val Ile Ala Arg Leu Glu Glu Val Gly Cys Thr  
 385 390 395 400  
 Val Ala Val Ser Gly Asp Thr Leu Glu Val Thr Pro Pro Thr Trp Arg  
 405 410 415  
 Gly Asp Leu Thr Met Ser Ala Asp Leu Val Glu Glu Val Leu Arg Leu  
 420 425 430  
 Glu Gly Leu Glu Ala Ile Pro Thr Ile Ile Pro Thr Ala Pro Ala Gly  
 435 440 445  
 Arg Gly Leu Thr Asp Ala Gln Lys Arg Arg Arg Ala Val Gly His Ala  
 450 455 460  
 Leu Ala Tyr Ala Gly Tyr Ala Glu Ile Ile Pro Ser Pro Phe Met Asp  
 465 470 475 480  
 Pro Glu Val Phe Asp Val Trp Gly Leu Ala Ala Asp Asp Glu Arg Arg  
 485 490 495  
 Lys Thr Val Ser Val Leu Asn Pro Leu Glu Ala Glu Arg Asn Val Leu  
 500 505 510  
 Ser Thr Ser Leu Leu Pro Ser Met Leu Asp Ala Val Lys Arg Asn Val  
 515 520 525  
 Ala Arg Gly His Asn Asp Phe Ser Leu Phe Gly Leu Gln Gln Val Ala  
 530 535 540  
 Phe Glu His Gly Ser Gly Val Ser Pro Met Pro Ser Val Ala Ser Arg  
 545 550 555 560  
 Pro Glu Glu Ser Val Val Ala Glu Leu Val Asp Ser  
 565 570

&lt;210&gt; 323

&lt;211&gt; 305

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(282)

&lt;223&gt; FRXA01717

&lt;400&gt; 323

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cct tcc cag caa atg cac caa gac atc gcc cta gtt gtg gat gag acc 48
Pro Ser Gln Gln Met His Gln Asp Ile Ala Leu Val Val Asp Glu Thr
  1             5             10             15

atc ccg gcg gaa gat gtc cgc gca gtt gtc aaa gcc ggc gcc ggc gaa 96
Ile Pro Ala Glu Asp Val Arg Ala Val Val Lys Ala Gly Ala Gly Glu
             20             25             30

ctg atc gaa acg gtc gag ctt ttc cac gtc ttc cgc tcc gaa cag cgc 144
Leu Ile Glu Thr Val Glu Leu Phe His Val Phe Arg Ser Glu Gln Arg
             35             40             45

ggc gag aac aag aaa tcc ctc gcg ttc tcc ctg cgt ttc cgc gca gcc 192
Gly Glu Asn Lys Lys Ser Leu Ala Phe Ser Leu Arg Phe Arg Ala Ala
             50             55             60

ggc cgc acc ctc acc gat gag gaa gcc aac gaa gca cga ctt cag gca 240
Gly Arg Thr Leu Thr Asp Glu Glu Ala Asn Glu Ala Arg Leu Gln Ala
             65             70             75             80

gca gag cta gca aag gag aaa ttc aac gct gaa atg cgt ggc 282
Ala Glu Leu Ala Lys Glu Lys Phe Asn Ala Glu Met Arg Gly
             85             90

tagtttcaca taggttctat agg 305

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&lt;210&gt; 324

&lt;211&gt; 94

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 324

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Pro Ser Gln Gln Met His Gln Asp Ile Ala Leu Val Val Asp Glu Thr
  1             5             10             15

Ile Pro Ala Glu Asp Val Arg Ala Val Val Lys Ala Gly Ala Gly Glu
             20             25             30

Leu Ile Glu Thr Val Glu Leu Phe His Val Phe Arg Ser Glu Gln Arg
             35             40             45

Gly Glu Asn Lys Lys Ser Leu Ala Phe Ser Leu Arg Phe Arg Ala Ala
             50             55             60

Gly Arg Thr Leu Thr Asp Glu Glu Ala Asn Glu Ala Arg Leu Gln Ala
             65             70             75             80

Ala Glu Leu Ala Lys Glu Lys Phe Asn Ala Glu Met Arg Gly
             85             90

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<400> 325																
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gggcagtcga agccaagttg agagggtata tttgtcacct atg atc aca cgt ctt 115																
Met Ile Thr Arg Leu 1 5																
tcc acg ctg ttt ttg cgc acc ctg cgc gaa gac cct gca gat gca gaa 163																
Ser Thr Leu Phe Leu Arg Thr Leu Arg Glu Asp Pro Ala Asp Ala Glu 10 15 20																
gtt cca agc cac aag ctg ctt gtc cgt gca gga tat atc cgc cga gtt 211																
Val Pro Ser His Lys Leu Leu Val Arg Ala Gly Tyr Ile Arg Arg Val 25 30 35																
gcc cca ggt atc tac tcc tgg ttg cca ctg ggt ttg cgc gca gtg cgc 259																
Ala Pro Gly Ile Tyr Ser Trp Leu Pro Leu Gly Leu Arg Ala Val Arg 40 45 50																
aac att gaa gct gtc gta cgc gag gaa atg gat gcg atc gga gga cag 307																
Asn Ile Glu Ala Val Val Arg Glu Glu Met Asp Ala Ile Gly Gly Gln 55 60 65																
gag ctg ctc ttc cca aca ctc ctg cca cgt gag cct tat gaa acc aca 355																
Glu Leu Leu Phe Pro Thr Leu Leu Pro Arg Glu Pro Tyr Glu Thr Thr 70 75 80 85																
cag cgt tgg aca gaa tac ggc gat tcg ctg ttc cgt ctg aag gac cgc 403																
Gln Arg Trp Thr Glu Tyr Gly Asp Ser Leu Phe Arg Leu Lys Asp Arg 90 95 100																
aag ggt gcc gac tac ctg ctc gga cca acc cac gag gaa atg ttc gcc 451																
Lys Gly Ala Asp Tyr Leu Leu Gly Pro Thr His Glu Glu Met Phe Ala 105 110 115																
gcc acg gtg aag gat ctg tac aac tcc tac aag gac ttc cca gtc acc 499																
Ala Thr Val Lys Asp Leu Tyr Asn Ser Tyr Lys Asp Phe Pro Val Thr 120 125 130																
ttg tac cag atc cag acc aag tac cgc gat gag gaa cgc cca cgc gca 547																
Leu Tyr Gln Ile Gln Thr Lys Tyr Arg Asp Glu Glu Arg Pro Arg Ala 135 140 145																
ggc gtg ctc cgc gga cgc gaa ttt gtg atg aag gat tct tac tcc ttc 595																
Gly Val Leu Arg Gly Arg Glu Phe Val Met Lys Asp Ser Tyr Ser Phe 150 155 160 165																
gac atc tcg gat gct ggt ttg gac gag tcc tac gca aag cac cgc gca 643																
Asp Ile Ser Asp Ala Gly Leu Asp Glu Ser Tyr Ala Lys His Arg Ala 170 175 180																

gcg tat cag cgc atc ttt gac cgc ctt ggc ttg gaa tac gcc atc tgc	691
Ala Tyr Gln Arg Ile Phe Asp Arg Leu Gly Leu Glu Tyr Ala Ile Cys	
185 190 195	
cag gca acc tct ggt gcc atg ggc gga tcc gct tcc gag gaa ttc ctt	739
Gln Ala Thr Ser Gly Ala Met Gly Gly Ser Ala Ser Glu Glu Phe Leu	
200 205 210	
gca gta tct gaa aac ggc gaa gat acc ttc gtg cgc tct acc tcc ggc	787
Ala Val Ser Glu Asn Gly Glu Asp Thr Phe Val Arg Ser Thr Ser Gly	
215 220 225	
aat tac gcc gca aac gtg gaa gct gtt gtt acc cag cca ggc gtt gag	835
Asn Tyr Ala Ala Asn Val Glu Ala Val Val Thr Gln Pro Gly Val Glu	
230 235 240 245	
cgt gac atc gaa ggc ctg cca gaa cca gtc acc tac gaa act cct gtt	883
Arg Asp Ile Glu Gly Leu Pro Glu Pro Val Thr Tyr Glu Thr Pro Val	
250 255 260	
tct gaa acc atc gat gct ttg gtt gat tgg gct aac tcc atc gac gtg	931
Ser Glu Thr Ile Asp Ala Leu Val Asp Trp Ala Asn Ser Ile Asp Val	
265 270 275	
cag atc gag ggc cgc gag gtc acc gca gat gac acc ctc aag tgc att	979
Gln Ile Glu Gly Arg Glu Val Thr Ala Asp Asp Thr Leu Lys Cys Ile	
280 285 290	
gtg gtg aag gtc cgc gag cca ggt gcc gaa gaa gca gaa ctc act gga	1027
Val Val Lys Val Arg Glu Pro Gly Ala Glu Glu Ala Glu Leu Thr Gly	
295 300 305	
atc ttg ctt cca ggt gac cgc gaa gta gac atg aag cgc ctc gag gca	1075
Ile Leu Leu Pro Gly Asp Arg Glu Val Asp Met Lys Arg Leu Glu Ala	
310 315 320 325	
tca ctt gag cca gca gaa gtt gaa ctc gca gtg gaa tcc gac ttt gcc	1123
Ser Leu Glu Pro Ala Glu Val Glu Leu Ala Val Glu Ser Asp Phe Ala	
330 335 340	
gac aac cca ttc ctg gtc aag ggc tac gtc gga cca gtt ggc ctg gcc	1171
Asp Asn Pro Phe Leu Val Lys Gly Tyr Val Gly Pro Val Gly Leu Ala	
345 350 355	
aag aac ggc gtg aag gtc ctt gcc gat cct cgc gtt gtc acc ggt acc	1219
Lys Asn Gly Val Lys Val Leu Ala Asp Pro Arg Val Val Thr Gly Thr	
360 365 370	
tcc tgg atc acc ggc gcc gat gaa aag gaa cgc cac gtc gta ggc ctc	1267
Ser Trp Ile Thr Gly Ala Asp Glu Lys Glu Arg His Val Val Gly Leu	
375 380 385	
gtc gcc gga cgc gat ttc acc cca gac ggc ttc atc gaa gct gca gaa	1315
Val Ala Gly Arg Asp Phe Thr Pro Asp Gly Phe Ile Glu Ala Ala Glu	
390 395 400 405	
atc aag gaa ggc gac cca gcg cca gca ggc gag ggc acc ctc acc ctt	1363
Ile Lys Glu Gly Asp Pro Ala Pro Ala Gly Glu Gly Thr Leu Thr Leu	
410 415 420	
gct cgc ggc atc gaa att ggc ata tct tcc agc tcg gcc gca agt aca	1411

Ala Arg Gly Ile Glu Ile Gly Ile Ser Ser Ser Ser Ala Ala Ser Thr  
                   425                  430                  435

ccg aag cct tcg acg tcc aaa tcc tgg acg aaa acg gca agc gcg cca 1459  
 Pro Lys Pro Ser Thr Ser Lys Ser Trp Thr Lys Thr Ala Ser Ala Pro  
                   440                  445                  450

tcc caa cca tgg gct cta cgg gct cgg tgt cac ccg cct gct cgc cgt 1507  
 Ser Gln Pro Trp Ala Leu Arg Ala Arg Cys His Pro Pro Ala Arg Arg  
                   455                  460                  465

cct ggc aga aca gcg cca cga tgacgctggc ctcaactggt ccg 1551  
 Pro Gly Arg Thr Ala Pro Arg  
 470                  475

&lt;210&gt; 326

&lt;211&gt; 476

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 326

Met Ile Thr Arg Leu Ser Thr Leu Phe Leu Arg Thr Leu Arg Glu Asp  
   1                  5                  10                  15

Pro Ala Asp Ala Glu Val Pro Ser His Lys Leu Leu Val Arg Ala Gly  
                   20                  25                  30

Tyr Ile Arg Arg Val Ala Pro Gly Ile Tyr Ser Trp Leu Pro Leu Gly  
                   35                  40                  45

Leu Arg Ala Val Arg Asn Ile Glu Ala Val Val Arg Glu Glu Met Asp  
   50                  55                  60

Ala Ile Gly Gly Gln Glu Leu Leu Phe Pro Thr Leu Leu Pro Arg Glu  
 . 65                  70                  75                  80

Pro Tyr Glu Thr Thr Gln Arg Trp Thr Glu Tyr Gly Asp Ser Leu Phe  
                   85                  90                  95

Arg Leu Lys Asp Arg Lys Gly Ala Asp Tyr Leu Leu Gly Pro Thr His  
                   100                  105                  110

Glu Glu Met Phe Ala Ala Thr Val Lys Asp Leu Tyr Asn Ser Tyr Lys  
   115                  120                  125

Asp Phe Pro Val Thr Leu Tyr Gln Ile Gln Thr Lys Tyr Arg Asp Glu  
   130                  135                  140

Glu Arg Pro Arg Ala Gly Val Leu Arg Gly Arg Glu Phe Val Met Lys  
 145                  150                  155                  160

Asp Ser Tyr Ser Phe Asp Ile Ser Asp Ala Gly Leu Asp Glu Ser Tyr  
                   165                  170                  175

Ala Lys His Arg Ala Ala Tyr Gln Arg Ile Phe Asp Arg Leu Gly Leu  
                   180                  185                  190

Glu Tyr Ala Ile Cys Gln Ala Thr Ser Gly Ala Met Gly Gly Ser Ala  
                   195                  200                  205

Ser Glu Glu Phe Leu Ala Val Ser Glu Asn Gly Glu Asp Thr Phe Val  
 210 215 220  
 Arg Ser Thr Ser Gly Asn Tyr Ala Ala Asn Val Glu Ala Val Val Thr  
 225 230 235 240  
 Gln Pro Gly Val Glu Arg Asp Ile Glu Gly Leu Pro Glu Pro Val Thr  
 245 250 255  
 Tyr Glu Thr Pro Val Ser Glu Thr Ile Asp Ala Leu Val Asp Trp Ala  
 260 265 270  
 Asn Ser Ile Asp Val Gln Ile Glu Gly Arg Glu Val Thr Ala Asp Asp  
 275 280 285  
 Thr Leu Lys Cys Ile Val Val Lys Val Arg Glu Pro Gly Ala Glu Glu  
 290 295 300  
 Ala Glu Leu Thr Gly Ile Leu Leu Pro Gly Asp Arg Glu Val Asp Met  
 305 310 315 320  
 Lys Arg Leu Glu Ala Ser Leu Glu Pro Ala Glu Val Glu Leu Ala Val  
 325 330 335  
 Glu Ser Asp Phe Ala Asp Asn Pro Phe Leu Val Lys Gly Tyr Val Gly  
 340 345 350  
 Pro Val Gly Leu Ala Lys Asn Gly Val Lys Val Leu Ala Asp Pro Arg  
 355 360 365  
 Val Val Thr Gly Thr Ser Trp Ile Thr Gly Ala Asp Glu Lys Glu Arg  
 370 375 380  
 His Val Val Gly Leu Val Ala Gly Arg Asp Phe Thr Pro Asp Gly Phe  
 385 390 395 400  
 Ile Glu Ala Ala Glu Ile Lys Glu Gly Asp Pro Ala Pro Ala Gly Glu  
 405 410 415  
 Gly Thr Leu Thr Leu Ala Arg Gly Ile Glu Ile Gly Ile Ser Ser Ser  
 420 425 430  
 Ser Ala Ala Ser Thr Pro Lys Pro Ser Thr Ser Lys Ser Trp Thr Lys  
 435 440 445  
 Thr Ala Ser Ala Pro Ser Gln Pro Trp Ala Leu Arg Ala Arg Cys His  
 450 455 460  
 Pro Pro Ala Arg Arg Pro Gly Arg Thr Ala Pro Arg  
 465 470 475

<210> 327

<211> 1031

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (94)..(1008)

<223> FRXA01938

&lt;400&gt; 327

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attcttactc cttcgacatc tcgggatgct ggt ttg gac gag tcc tac gca aag 114  
 Leu Asp Glu Ser Tyr Ala Lys  
 1 5

cac cgc gca gcg tat cag cgc atc ttt gac cgc ctt ggc ttg gaa tac 162  
 His Arg Ala Ala Tyr Gln Arg Ile Phe Asp Arg Leu Gly Leu Glu Tyr  
 10 15 20

gcc atc tgc cag gca acc tct ggt gcc atg ggc gga tcc gct tcc gag 210  
 Ala Ile Cys Gln Ala Thr Ser Gly Ala Met Gly Gly Ser Ala Ser Glu  
 25 30 35

gaa ttc ctt gca gta tct gaa aac ggc gaa gat acc ttc gtg cgc tct 258  
 Glu Phe Leu Ala Val Ser Glu Asn Gly Glu Asp Thr Phe Val Arg Ser  
 40 45 50 55

acc tcc ggc aat tac gcc gca aac gtg gaa gct gtt gtt acc cag cca 306  
 Thr Ser Gly Asn Tyr Ala Ala Asn Val Glu Ala Val Val Thr Gln Pro  
 60 65 70

ggc gtt gag cgt gac atc gaa ggc ctg cca gaa cca gtc acc tac gaa 354  
 Gly Val Glu Arg Asp Ile Glu Gly Leu Pro Glu Pro Val Thr Tyr Glu  
 75 80 85

act cct gtt tct gaa acc atc gat gct ttg gtt gat tgg gct aac tcc 402  
 Thr Pro Val Ser Glu Thr Ile Asp Ala Leu Val Asp Trp Ala Asn Ser  
 90 95 100

atc gac gtg cag atc gag ggc cgc gag gtc acc gca gat gac acc ctc 450  
 Ile Asp Val Gln Ile Glu Gly Arg Glu Val Thr Ala Asp Asp Thr Leu  
 105 110 115

aag tgc att gtg gtg aag gtc cgc gag cca ggt gcc gaa gaa gca gaa 498  
 Lys Cys Ile Val Val Lys Val Arg Glu Pro Gly Ala Glu Glu Ala Glu  
 120 125 130 135

ctc act gga atc ttg ctt cca ggt gac cgc gaa gta gac atg aag cgc 546  
 Leu Thr Gly Ile Leu Leu Pro Gly Asp Arg Glu Val Asp Met Lys Arg  
 140 145 150

ctc gag gca tca ctt gag cca gca gaa gtt gaa ctc gca gtg gaa tcc 594  
 Leu Glu Ala Ser Leu Glu Pro Ala Glu Val Glu Leu Ala Val Glu Ser  
 155 160 165

gac ttt gcc gac aac cca ttc ctg gtc aag ggc tac gtc gga cca gtt 642  
 Asp Phe Ala Asp Asn Pro Phe Leu Val Lys Gly Tyr Val Gly Pro Val  
 170 175 180

ggc ctg gcc aag aac ggc gtg aag gtc ctt gcc gat cct cgc gtt gtc 690  
 Gly Leu Ala Lys Asn Gly Val Lys Val Leu Ala Asp Pro Arg Val Val  
 185 190 195

acc ggt acc tcc tgg atc acc ggc gcc gat gaa aag gaa cgc cac gtc 738  
 Thr Gly Thr Ser Trp Ile Thr Gly Ala Asp Glu Lys Glu Arg His Val  
 200 205 210 215

gta ggc ctc gtc gcc gga cgc gat ttc acc cca gac ggc ttc atc gaa 786

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<210> 328
<211> 305
<212> PRT
<213> Corynebacterium glutamicum
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Asp	Arg	Leu	Gly 20	Leu	Glu	Tyr	Ala	Ile 25	Cys	Gln	Ala	Thr	Ser 30	Gly	Ala
Met	Gly	Gly 35	Ser	Ala	Ser	Glu	Glu 40	Phe	Leu	Ala	Val	Ser 45	Glu	Asn	Gly
Glu	Asp 50	Thr	Phe	Val	Arg	Ser 55	Thr	Ser	Gly	Asn	Tyr 60	Ala	Ala	Asn	Val
Glu 65	Ala	Val	Val	Thr	Gln 70	Pro	Gly	Val	Glu	Arg 75	Asp	Ile	Glu	Gly	Leu 80
Pro	Glu	Pro	Val	Thr 85	Tyr	Glu	Thr	Pro	Val 90	Ser	Glu	Thr	Ile	Asp 95	Ala
Leu	Val	Asp	Trp 100	Ala	Asn	Ser	Ile	Asp 105	Val	Gln	Ile	Glu	Gly 110	Arg	Glu
Val	Thr 115	Ala	Asp	Asp	Thr	Leu	Lys 120	Cys	Ile	Val	Val 125	Lys	Val	Arg	Glu
Pro	Gly 130	Ala	Glu	Glu	Ala	Glu 135	Leu	Thr	Gly	Ile	Leu 140	Leu	Pro	Gly	Asp
Arg 145	Glu	Val	Asp	Met	Lys 150	Arg	Leu	Glu	Ala	Ser 155	Leu	Glu	Pro	Ala	Glu 160
Val	Glu	Leu	Ala	Val	Glu	Ser	Asp	Phe	Ala	Asp	Asn	Pro	Phe	Leu	Val

gct ttt gga aag aag atc gga cag gcc tct ccg gag gac cgc cct gca 307  
Ala Phe Gly Lys Lys Ile Gly Gln Ala Ser Pro Glu Asp Arg Pro Ala

55					60					65						
ctt	ctg	gag	ggt	tcc	aac	gaa	ctc	aaa	gcc	aag	gtg	aag	gat	gct	gag	355
Leu	Leu	Glu	Gly	Ser	Asn	Glu	Leu	Lys	Ala	Lys	Val	Lys	Asp	Ala	Glu	
70					75					80					85	
gct	gca	cag	gaa	gct	gct	gag	gcg	aaa	gtc	aat	gag	ctg	cag	atg	aag	403
Ala	Ala	Gln	Glu	Ala	Ala	Glu	Ala	Lys	Val	Asn	Glu	Leu	Gln	Met	Lys	
				90					95					100		
ctc	tcc	aac	gtg	gtt	tcc	ggc	gcg	cct	gct	ggg	ggc	gaa	gat	gat	ttc	451
Leu	Ser	Asn	Val	Val	Ser	Gly	Ala	Pro	Ala	Gly	Gly	Glu	Asp	Asp	Phe	
			105					110					115			
gtc	gtc	ctg	gag	acc	atc	ggc	gag	cct	cgc	act	ttt	gat	ttc	gag	cca	499
Val	Val	Leu	Glu	Thr	Ile	Gly	Glu	Pro	Arg	Thr	Phe	Asp	Phe	Glu	Pro	
		120					125					130				
aag	gat	cac	ctg	gag	ctc	ggt	gaa	tcc	ctc	gga	ctt	atc	gat	atg	aag	547
Lys	Asp	His	Leu	Glu	Leu	Gly	Glu	Ser	Leu	Gly	Leu	Ile	Asp	Met	Lys	
	135					140					145					
cgc	ggc	acc	aag	gtt	tcc	ggt	gca	cgt	ttc	tac	tac	ctc	acc	ggt	gac	595
Arg	Gly	Thr	Lys	Val	Ser	Gly	Ala	Arg	Phe	Tyr	Tyr	Leu	Thr	Gly	Asp	
150					155				160						165	
ggc	gca	atg	ctg	cag	ttg	ggc	atg	ctc	atg	ttg	gct	gct	cag	aag	gcg	643
Gly	Ala	Met	Leu	Gln	Leu	Gly	Met	Leu	Met	Leu	Ala	Ala	Gln	Lys	Ala	
				170					175					180		
cgc	gaa	gct	gga	ttt	agc	atg	atg	atc	cct	cca	gtt	ttg	gtg	cgc	cct	691
Arg	Glu	Ala	Gly	Phe	Ser	Met	Met	Ile	Pro	Pro	Val	Leu	Val	Arg	Pro	
			185					190					195			
gaa	atc	atg	gcg	ggc	act	gga	ttc	ttg	ggt	gat	cac	tcc	gag	gag	atc	739
Glu	Ile	Met	Ala	Gly	Thr	Gly	Phe	Leu	Gly	Asp	His	Ser	Glu	Glu	Ile	
		200					205					210				
tac	tac	ctc	gaa	cgc	gat	gac	atg	tac	ttg	gtg	ggg	acc	tct	gag	gtg	787
Tyr	Tyr	Leu	Glu	Arg	Asp	Asp	Met	Tyr	Leu	Val	Gly	Thr	Ser	Glu	Val	
		215				220					225					
gct	ctt	gcg	ggt	tac	cac	aag	gac	gaa	atc	att	gat	ctc	aac	gaa	ggc	835
Ala	Leu	Ala	Gly	Tyr	His	Lys	Asp	Glu	Ile	Ile	Asp	Leu	Asn	Glu	Gly	
230					235					240					245	
cca	gtg	aag	tac	gcc	ggt	tgg	agc	tcc	tgc	ttc	cgc	cgt	gag	gct	ggt	883
Pro	Val	Lys	Tyr	Ala	Gly	Trp	Ser	Ser	Cys	Phe	Arg	Arg	Glu	Ala	Gly	
				250					255					260		
tcc	tac	ggc	aag	gac	acc	cga	ggc	att	ttg	cgt	gtg	cac	cag	ttc	gac	931
Ser	Tyr	Gly	Lys	Asp	Thr	Arg	Gly	Ile	Leu	Arg	Val	His	Gln	Phe	Asp	
			265					270					275			
aag	gtt	gag	atg	ttt	gtc	tac	tgc	aag	cct	gaa	gat	gct	gaa	gat	gta	979
Lys	Val	Glu	Met	Phe	Val	Tyr	Cys	Lys	Pro	Glu	Asp	Ala	Glu	Asp	Val	
		280					285					290				
cac	cag	cag	ctg	ctc	ggc	atg	gaa	aag	gaa	atg	ctc	gca	gcc	atc	gag	1027
His	Gln	Gln	Leu	Leu	Gly	Met	Glu	Lys	Glu	Met	Leu	Ala	Ala	Ile	Glu	
		295				300					305					

gtt cct tac cgc gtc atc gac gtt gcc ggt gga gac ttg ggt gca tct 1075  
 Val Pro Tyr Arg Val Ile Asp Val Ala Gly Gly Asp Leu Gly Ala Ser  
 310 315 320 325  
  
 gct gcc cgc aag ttc gac acc gag gca tgg gtg cca acc cag gac acc 1123  
 Ala Ala Arg Lys Phe Asp Thr Glu Ala Trp Val Pro Thr Gln Asp Thr  
 330 335 340  
  
 tac cgt gaa ctc acc tcg acc tct aac tgc acc act ttc cag gct cgt 1171  
 Tyr Arg Glu Leu Thr Ser Thr Ser Asn Cys Thr Thr Phe Gln Ala Arg  
 345 350 355  
  
 cgc ctg cag act cgt tac cgc gat gaa aac ggc aag cca cag atc gcc 1219  
 Arg Leu Gln Thr Arg Tyr Arg Asp Glu Asn Gly Lys Pro Gln Ile Ala  
 360 365 370  
  
 gca acc ctg aac ggt acg ttg gct acc act cgt tgg ctt gtc gcg atc 1267  
 Ala Thr Leu Asn Gly Thr Leu Ala Thr Thr Arg Trp Leu Val Ala Ile  
 375 380 385  
  
 ctg gag aac aac cag cag gcc gat ggc tct gtt gtt gtt cct gag gcg 1315  
 Leu Glu Asn Asn Gln Gln Ala Asp Gly Ser Val Val Val Pro Glu Ala  
 390 395 400 405  
  
 ctt cgt cca ttc gtg ggc aaa gac gtg ctc aag cca gtg aaa caa gcc 1363  
 Leu Arg Pro Phe Val Gly Lys Asp Val Leu Lys Pro Val Lys Gln Ala  
 410 415 420  
  
 ggt taattaagcg gaaagctcgt ggt 1389  
 Gly

&lt;210&gt; 330

&lt;211&gt; 422

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 330

Met Ile Asp Leu Lys Phe Leu Arg Asp Asn Pro Asp Val Val Arg Ala  
 1 5 10 15  
  
 Ser Gln Ile Thr Arg Gly Glu Asp Pro Ala Leu Val Asp Glu Leu Ile  
 20 25 30  
  
 Ser Ala Asp Glu Ser Arg Arg Glu Ala Ile Lys Ala Ala Asp Asp Leu  
 35 40 45  
  
 Arg Ala Glu Gln Lys Ala Phe Gly Lys Lys Ile Gly Gln Ala Ser Pro  
 50 55 60  
  
 Glu Asp Arg Pro Ala Leu Leu Glu Gly Ser Asn Glu Leu Lys Ala Lys  
 65 70 75 80  
  
 Val Lys Asp Ala Glu Ala Ala Gln Glu Ala Ala Glu Ala Lys Val Asn  
 85 90 95  
  
 Glu Leu Gln Met Lys Leu Ser Asn Val Val Ser Gly Ala Pro Ala Gly  
 100 105 110

Gly Glu Asp Asp Phe Val Val Leu Glu Thr Ile Gly Glu Pro Arg Thr  
 115 120 125  
 Phe Asp Phe Glu Pro Lys Asp His Leu Glu Leu Gly Glu Ser Leu Gly  
 130 135 140  
 Leu Ile Asp Met Lys Arg Gly Thr Lys Val Ser Gly Ala Arg Phe Tyr  
 145 150 155 160  
 Tyr Leu Thr Gly Asp Gly Ala Met Leu Gln Leu Gly Met Leu Met Leu  
 165 170 175  
 Ala Ala Gln Lys Ala Arg Glu Ala Gly Phe Ser Met Met Ile Pro Pro  
 180 185 190  
 Val Leu Val Arg Pro Glu Ile Met Ala Gly Thr Gly Phe Leu Gly Asp  
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 His Ser Glu Glu Ile Tyr Tyr Leu Glu Arg Asp Asp Met Tyr Leu Val  
 210 215 220  
 Gly Thr Ser Glu Val Ala Leu Ala Gly Tyr His Lys Asp Glu Ile Ile  
 225 230 235 240  
 Asp Leu Asn Glu Gly Pro Val Lys Tyr Ala Gly Trp Ser Ser Cys Phe  
 245 250 255  
 Arg Arg Glu Ala Gly Ser Tyr Gly Lys Asp Thr Arg Gly Ile Leu Arg  
 260 265 270  
 Val His Gln Phe Asp Lys Val Glu Met Phe Val Tyr Cys Lys Pro Glu  
 275 280 285  
 Asp Ala Glu Asp Val His Gln Gln Leu Leu Gly Met Glu Lys Glu Met  
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 Asp Leu Gly Ala Ser Ala Ala Arg Lys Phe Asp Thr Glu Ala Trp Val  
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 Pro Thr Gln Asp Thr Tyr Arg Glu Leu Thr Ser Thr Ser Asn Cys Thr  
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 Thr Phe Gln Ala Arg Arg Leu Gln Thr Arg Tyr Arg Asp Glu Asn Gly  
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 Lys Pro Gln Ile Ala Ala Thr Leu Asn Gly Thr Leu Ala Thr Thr Arg  
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 Trp Leu Val Ala Ile Leu Glu Asn Asn Gln Gln Ala Asp Gly Ser Val  
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cca acc ggt cca tcc ctc cac gca gga cac ctc gtt cca ctg ctc atg 259																
Pro Thr Gly Pro Ser Leu His Ala Gly His Leu Val Pro Leu Leu Met 50																
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Leu Arg Arg Phe Gln Gln Ala Gly His Asn Pro Ile Val Leu Ala Gly 65																
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Gly Ala Thr Gly Met Ile Gly Asp Pro Arg Asp Val Gly Glu Arg Thr 85																
atg aac tcc gca gac acc gtc tct gat tgg gca gaa cgc atc tcc ggt 403																
Met Asn Ser Ala Asp Thr Val Ser Asp Trp Ala Glu Arg Ile Ser Gly 100																
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Gln Leu Ser Arg Phe Val Asp Phe Asp Gly Glu His Ala Ala Arg Leu 115																
gtc aac aac gcc gag tgg acc aac gaa atg tcc gta gtg acc ttc ctc 499																
Val Asn Asn Ala Glu Trp Thr Asn Glu Met Ser Val Val Thr Phe Leu 130																
cgt gat gta gga aag cac ttc tcc ctc aac acc atg ctc gcc cgc gac 547																
Arg Asp Val Gly Lys His Phe Ser Leu Asn Thr Met Leu Ala Arg Asp 145																
acc gtc aag cgt cgc ctc gag tcc gac ggc att tcc tac acc gag ttc 595																
Thr Val Lys Arg Arg Leu Glu Ser Asp Gly Ile Ser Tyr Thr Glu Phe 165																
tcc tac atg ctg cta cag gcc aac gac tac gtt gaa ctg aac aag cgc 643																
Ser Tyr Met Leu Leu Gln Ala Asn Asp Tyr Val Glu Leu Asn Lys Arg 180																

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Phe Gly Cys Thr Leu Gln Val Gly Gly Gly Asp Gln Trp Gly Asn Ile	
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ggt tct ggc gtt gac ctc aac cgt cgc gtc aac ggc acc tct gtc cac	739
Val Ser Gly Val Asp Leu Asn Arg Arg Val Asn Gly Thr Ser Val His	
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gca gtg acc gta cct ttg gtt acc gat tcc gac ggc aag aag ttc ggc	787
Ala Val Thr Val Pro Leu Val Thr Asp Ser Asp Gly Lys Lys Phe Gly	
215 220 225	
aag tcc acc ggc ggc gga agc ctc tgg ttg gat ccg gaa atg acc agc	835
Lys Ser Thr Gly Gly Gly Ser Leu Trp Leu Asp Pro Glu Met Thr Ser	
230 235 240 245	
cca tac gct tgg tac cag tac ttc atc aac gca tcc gac gct gac gtg	883
Pro Tyr Ala Trp Tyr Gln Tyr Phe Ile Asn Ala Ser Asp Ala Asp Val	
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Ile Arg Tyr Leu Arg Trp Phe Thr Phe Leu Thr Gln Glu Glu Leu Ala	
265 270 275	
gag ttg gaa gtt gaa gtt gca gag cgc cca ttc aag cgc gaa gca cag	979
Glu Leu Glu Val Glu Val Ala Glu Arg Pro Phe Lys Arg Glu Ala Gln	
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cgt cgt ctt gca cgc gaa atg acc aac ttg gtt cac gga acc gaa gca	1027
Arg Arg Leu Ala Arg Glu Met Thr Asn Leu Val His Gly Thr Glu Ala	
295 300 305	
acc gaa gca gtc gag ctt gct gct caa gca ctg ttc ggc cgc gca gaa	1075
Thr Glu Ala Val Glu Leu Ala Ala Gln Ala Leu Phe Gly Arg Ala Glu	
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Leu Arg Asp Leu Asp Glu Lys Thr Leu Ala Ala Ser Val Ser Glu Thr	
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Ala Val Ala Glu Ile Lys Ala Gly Glu Pro Arg Thr Ile Ile Asp Leu	
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Leu Val Ala Ser Gly Leu Ala Asp Ser Lys Gly Ala Ala Lys Arg Ala	
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Val Lys Glu Gly Gly Ala Tyr Val Asn Asn Glu Arg Ile Glu Ser Asp	
375 380 385	
gat tgg gag cct ttc gct gaa gat ctt ctt cac ggt tca tgg cta gta	1315
Asp Trp Glu Pro Phe Ala Glu Asp Leu Leu His Gly Ser Trp Leu Val	
390 395 400 405	
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&lt;211&gt; 420

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

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Tyr Cys Gly Phe Asp Pro Thr Gly Pro Ser Leu His Ala Gly His Leu  
 35 40 45

Val Pro Leu Leu Met Leu Arg Arg Phe Gln Gln Ala Gly His Asn Pro  
 50 55 60

Ile Val Leu Ala Gly Gly Ala Thr Gly Met Ile Gly Asp Pro Arg Asp  
 65 70 75 80

Val Gly Glu Arg Thr Met Asn Ser Ala Asp Thr Val Ser Asp Trp Ala  
 85 90 95

Glu Arg Ile Ser Gly Gln Leu Ser Arg Phe Val Asp Phe Asp Gly Glu  
 100 105 110

His Ala Ala Arg Leu Val Asn Asn Ala Glu Trp Thr Asn Glu Met Ser  
 115 120 125

Val Val Thr Phe Leu Arg Asp Val Gly Lys His Phe Ser Leu Asn Thr  
 130 135 140

Met Leu Ala Arg Asp Thr Val Lys Arg Arg Leu Glu Ser Asp Gly Ile  
 145 150 155 160

Ser Tyr Thr Glu Phe Ser Tyr Met Leu Leu Gln Ala Asn Asp Tyr Val  
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Glu Leu Asn Lys Arg Phe Gly Cys Thr Leu Gln Val Gly Gly Gly Asp  
 180 185 190

Gln Trp Gly Asn Ile Val Ser Gly Val Asp Leu Asn Arg Arg Val Asn  
 195 200 205

Gly Thr Ser Val His Ala Val Thr Val Pro Leu Val Thr Asp Ser Asp  
 210 215 220

Gly Lys Lys Phe Gly Lys Ser Thr Gly Gly Gly Ser Leu Trp Leu Asp  
 225 230 235 240

Pro Glu Met Thr Ser Pro Tyr Ala Trp Tyr Gln Tyr Phe Ile Asn Ala  
 245 250 255

Ser Asp Ala Asp Val Ile Arg Tyr Leu Arg Trp Phe Thr Phe Leu Thr  
 260 265 270

Gln Glu Glu Leu Ala Glu Leu Glu Val Glu Val Ala Glu Arg Pro Phe  
 275 280 285

Lys Arg Glu Ala Gln Arg Arg Leu Ala Arg Glu Met Thr Asn Leu Val  
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 His Gly Thr Glu Ala Thr Glu Ala Val Glu Leu Ala Ala Gln Ala Leu  
 305 310 315 320  
 Phe Gly Arg Ala Glu Leu Arg Asp Leu Asp Glu Lys Thr Leu Ala Ala  
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 Ser Val Ser Glu Thr Ala Val Ala Glu Ile Lys Ala Gly Glu Pro Arg  
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 Thr Ile Ile Asp Leu Leu Val Ala Ser Gly Leu Ala Asp Ser Lys Gly  
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 Ala Ala Lys Arg Ala Val Lys Glu Gly Gly Ala Tyr Val Asn Asn Glu  
 370 375 380  
 Arg Ile Glu Ser Asp Asp Trp Glu Pro Phe Ala Glu Asp Leu Leu His  
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 Glu Gly Gln Leu Lys Asp Leu Ser His Val Pro Glu Thr Thr Ala Thr  
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 Phe Thr Ala Val Pro Ala Asn Thr Asp Asp Gly Arg Ala Val Ile Arg  
 35 40 45  
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 His Ser Cys Ala His Val Leu Ala Gln Ala Val Gln Ala Glu Phe Pro  
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 Gly Thr Lys Leu Gly Ile Gly Pro Ala Ile Glu Asn Gly Phe Tyr Tyr  
 65 70 75 80  
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gaa	aag	cgg	atg	aag	aag	atc	atc	aag	acc	ggc	cag	aag	ttt	gag	cgc	336
Glu	Lys	Arg	Met	Lys	Lys	Ile	Ile	Lys	Thr	Gly	Gln	Lys	Phe	Glu	Arg	
			100					105					110			
cgc	gtc	tat	gaa	tcc	gct	gaa	gct	gca	gcg	gaa	gag	ttg	aag	aac	gag	384
Arg	Val	Tyr	Glu	Ser	Ala	Glu	Ala	Ala	Ala	Glu	Glu	Leu	Lys	Asn	Glu	
		115					120					125				
cct	tac	aag	ctg	gaa	ctt	atc	cag	gac	aag	ggc	aac	gtt	gat	ccc	aac	432
Pro	Tyr	Lys	Leu	Glu	Leu	Ile	Gln	Asp	Lys	Gly	Asn	Val	Asp	Pro	Asn	
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Ser	Asp	Glu	Ala	Thr	Glu	Val	Gly	Ala	Gly	Glu	Leu	Thr	Ala	Tyr	Asp	
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aac	gtc	aac	cct	cgc	acc	agt	gag	gtg	gag	tgg	tct	gat	ctt	tgc	cgt	528
Asn	Val	Asn	Pro	Arg	Thr	Ser	Glu	Val	Glu	Trp	Ser	Asp	Leu	Cys	Arg	
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gga	cca	cac	atc	cca	acc	acc	cgc	tac	att	cca	gca	ttc	gca	ttg	acc	576
Gly	Pro	His	Ile	Pro	Thr	Thr	Arg	Tyr	Ile	Pro	Ala	Phe	Ala	Leu	Thr	
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cga	tca	tcc	gct	gct	tat	tgg	cgt	ggc	gat	cag	gat	aat	gct	ggc	ctg	624
Arg	Ser	Ser	Ala	Ala	Tyr	Trp	Arg	Gly	Asp	Gln	Asp	Asn	Ala	Gly	Leu	
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cag	cgc	atc	tac	ggc	acc	gcg	tgg	gag	gat	aag	gaa	tcc	ctc	gat	gct	672
Gln	Arg	Ile	Tyr	Gly	Thr	Ala	Trp	Glu	Asp	Lys	Glu	Ser	Leu	Asp	Ala	
	210					215					220					
tac	cag	acc	atg	ctc	gct	gag	gca	gaa	aag	cgc	gat	cac	cgc	cgt	cta	720
Tyr	Gln	Thr	Met	Leu	Ala	Glu	Ala	Glu	Lys	Arg	Asp	His	Arg	Arg	Leu	
225					230					235					240	
ggc	act	gaa	ctt	gat	ttg	ttc	tcc	ttc	cca	gat	gat	ctg	ggc	tct	ggc	768
Gly	Thr	Glu	Leu	Asp	Leu	Phe	Ser	Phe	Pro	Asp	Asp	Leu	Gly	Ser	Gly	
				245					250					255		
ctg	cca	gta	ttc	cat	ccc	aac	ggc	ggc	atc	gtg	cgc	aat	gag	atg	gaa	816
Leu	Pro	Val	Phe	His	Pro	Asn	Gly	Gly	Ile	Val	Arg	Asn	Glu	Met	Glu	
			260					265					270			
gat	cac	tcc	cgt	cgc	cgc	cac	atc	gca	gcg	ggc	tac	tcc	ttt	gtg	aac	864
Asp	His	Ser	Arg	Arg	Arg	His	Ile	Ala	Ala	Gly	Tyr	Ser	Phe	Val	Asn	
			275				280					285				
acc	ccg	cac	atc	acc	aag	cag	gat	ctc	ttt	gag	cgt	tcc	ggc	cac	ctt	912
Thr	Pro	His	Ile	Thr	Lys	Gln	Asp	Leu	Phe	Glu	Arg	Ser	Gly	His	Leu	
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Gly	Phe	Tyr	Lys	Asp	Gly	Met	Phe	Pro	Pro	Met	Gln	Val	Asp	Ala	Glu	
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ttc	gac	gaa	gac	ggc	aat	gtg	acc	aag	ccg	ggc	caa	gag	tac	tac	ctc	1008
Phe	Asp	Glu	Asp	Gly	Asn	Val	Thr	Lys	Pro	Gly	Gln	Glu	Tyr	Tyr	Leu	

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cgt	tct	tac	cgt	gag	ctt	cca	ctg	cgt	ctt	ttt	gag	ttc	ggc	aac	gtc	1104				
Arg	Ser	Tyr	Arg	Glu	Leu	Pro	Leu	Arg	Leu	Phe	Glu	Phe	Gly	Asn	Val					
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tac	cgc	tac	gaa	aag	tcc	ggt	gtg	atc	cac	ggc	ctg	acc	cgt	gcc	cgt	1152				
Tyr	Arg	Tyr	Glu	Lys	Ser	Gly	Val	Ile	His	Gly	Leu	Thr	Arg	Ala	Arg					
	370					375					380									
ggc	ttc	acc	cag	gac	gat	gct	cac	atc	tac	tgc	acc	gag	gat	cag	ctg	1200				
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385					390					395					400					
gaa	gca	gag	ctc	acc	tct	gtg	ctg	gac	ttc	atc	ctg	tcg	ctg	ctg	cgc	1248				
Glu	Ala	Glu	Leu	Thr	Ser	Val	Leu	Asp	Phe	Ile	Leu	Ser	Leu	Leu	Arg					
			405						410					415						
gat	tac	ggt	ttg	gat	gat	ttc	tac	ctg	gag	ctc	tcc	acc	cgc	gat	cct	1296				
Asp	Tyr	Gly	Leu	Asp	Asp	Phe	Tyr	Leu	Glu	Leu	Ser	Thr	Arg	Asp	Pro					
			420					425					430							
aag	aag	tca	gtc	ggt	tct	gat	gag	atc	tgg	gag	cgt	tcc	act	gaa	atc	1344				
Lys	Lys	Ser	Val	Gly	Ser	Asp	Glu	Ile	Trp	Glu	Arg	Ser	Thr	Glu	Ile					
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ttg	aac	cgt	gtg	gcc	acc	aat	tct	ggc	ctg	gaa	ctt	gtt	cca	gac	cca	1392				
Leu	Asn	Arg	Val	Ala	Thr	Asn	Ser	Gly	Leu	Glu	Leu	Val	Pro	Asp	Pro					
	450					455					460									
gaa	ggt	gcc	gca	ttc	tac	ggc	cct	aag	att	tct	gtt	cag	gca	cgc	gac	1440				
Glu	Gly	Ala	Ala	Phe	Tyr	Gly	Pro	Lys	Ile	Ser	Val	Gln	Ala	Arg	Asp					
465					470					475					480					
gcg	att	ggc	cgt	acc	tgg	cag	atg	tcc	acc	gtg	cag	ctg	gac	ttc	aac	1488				
Ala	Ile	Gly	Arg	Thr	Trp	Gln	Met	Ser	Thr	Val	Gln	Leu	Asp	Phe	Asn					
				485					490					495						
atg	cct	gag	cgc	ttc	aac	ttg	gaa	tac	acc	tca	tct	gat	ggt	tcc	aag	1536				
Met	Pro	Glu	Arg	Phe	Asn	Leu	Glu	Tyr	Thr	Ser	Ser	Asp	Gly	Ser	Lys					
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Gln	Gln	Pro	Ile	Met	Ile	His	Arg	Ala	Leu	Phe	Gly	Ser	Ile	Glu	Arg					
		515					520					525								
ttc	ttt	ggc	gtg	ttg	ttg	gag	cac	tac	gct	ggt	gct	ttc	cca	gca	tgg	1632				
Phe	Phe	Gly	Val	Leu	Leu	Glu	His	Tyr	Ala	Gly	Ala	Phe	Pro	Ala	Trp					
	530					535					540									
ctg	gca	cct	cac	cag	gtc	atg	ggt	att	cca	gtt	gct	gat	gat	tgc	att	1680				
Leu	Ala	Pro	His	Gln	Val	Met	Gly	Ile	Pro	Val	Ala	Asp	Asp	Cys	Ile					
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cca	cac	ctg	gag	aca	atc	acc	gca	cag	ctg	cgt	gaa	aag	ggt	atc	cgc	1728				
Pro	His	Leu	Glu	Thr	Ile	Thr	Ala	Gln	Leu	Arg	Glu	Lys	Gly	Ile	Arg					
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gca gac gtg gac acc tcc gat gat cgc atg cag aag aag atc cgc aac 1776  
 Ala Asp Val Asp Thr Ser Asp Asp Arg Met Gln Lys Lys Ile Arg Asn  
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cac acc acc ggc aag gtt cca ttc atg ctg ctt gcc ggt gcc cgc gat 1824  
 His Thr Thr Gly Lys Val Pro Phe Met Leu Leu Ala Gly Ala Arg Asp  
                   595                  600                  605

gtg gaa gca aac gca gtg agc ttc cgt ttc ttg gac ggc acc cag gtc 1872  
 Val Glu Ala Asn Ala Val Ser Phe Arg Phe Leu Asp Gly Thr Gln Val  
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aac ggc gtg ccc gtc gat gag gca atc gct gtg att tct tcc tgg att 1920  
 Asn Gly Val Pro Val Asp Glu Ala Ile Ala Val Ile Ser Ser Trp Ile  
                   625                  630                  635                  640

ggg gac cgc atc aat gat cag ccg agc gag gac tcc att gca gct cgc 1968  
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Phe Thr Ala Val Pro Ala Asn Thr Asp Asp Gly Arg Ala Val Ile Arg  
                   35                  40                  45

His Ser Cys Ala His Val Leu Ala Gln Ala Val Gln Ala Glu Phe Pro  
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Gly Thr Lys Leu Gly Ile Gly Pro Ala Ile Glu Asn Gly Phe Tyr Tyr  
                   65                  70                  75                  80

Asp Phe Asp Ala Ala Glu Pro Phe Thr Pro Glu Asp Leu Lys Thr Ile  
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Glu Lys Arg Met Lys Lys Ile Ile Lys Thr Gly Gln Lys Phe Glu Arg  
                   100                  105                  110

Arg Val Tyr Glu Ser Ala Glu Ala Ala Ala Glu Glu Leu Lys Asn Glu  
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Pro Tyr Lys Leu Glu Leu Ile Gln Asp Lys Gly Asn Val Asp Pro Asn  
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Ser Asp Glu Ala Thr Glu Val Gly Ala Gly Glu Leu Thr Ala Tyr Asp  
                   145                  150                  155                  160

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Gly	Thr	Glu	Leu	Asp	Leu	Phe	Ser	Phe	Pro	Asp	Asp	Leu	Gly	Ser	Gly	
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Leu	Pro	Val	Phe	His	Pro	Asn	Gly	Gly	Ile	Val	Arg	Asn	Glu	Met	Glu	
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Phe	Asp	Glu	Asp	Gly	Asn	Val	Thr	Lys	Pro	Gly	Gln	Glu	Tyr	Tyr	Leu	
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Lys	Pro	Met	Asn	Cys	Pro	Met	His	Asn	Leu	Ile	Phe	Asp	Ser	Arg	Gly	
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Tyr	Arg	Tyr	Glu	Lys	Ser	Gly	Val	Ile	His	Gly	Leu	Thr	Arg	Ala	Arg	
	370					375					380					
Gly	Phe	Thr	Gln	Asp	Asp	Ala	His	Ile	Tyr	Cys	Thr	Glu	Asp	Gln	Leu	
385					390					395					400	
Glu	Ala	Glu	Leu	Thr	Ser	Val	Leu	Asp	Phe	Ile	Leu	Ser	Leu	Leu	Arg	
				405					410					415		
Asp	Tyr	Gly	Leu	Asp	Asp	Phe	Tyr	Leu	Glu	Leu	Ser	Thr	Arg	Asp	Pro	
			420					425					430			
Lys	Lys	Ser	Val	Gly	Ser	Asp	Glu	Ile	Trp	Glu	Arg	Ser	Thr	Glu	Ile	
		435					440					445				
Leu	Asn	Arg	Val	Ala	Thr	Asn	Ser	Gly	Leu	Glu	Leu	Val	Pro	Asp	Pro	
	450					455					460					
Glu	Gly	Ala	Ala	Phe	Tyr	Gly	Pro	Lys	Ile	Ser	Val	Gln	Ala	Arg	Asp	
465					470					475					480	

Ala Ile Gly Arg Thr Trp Gln Met Ser Thr Val Gln Leu Asp Phe Asn  
                             485                            490                            495

Met Pro Glu Arg Phe Asn Leu Glu Tyr Thr Ser Ser Asp Gly Ser Lys  
                             500                            505                            510

Gln Gln Pro Ile Met Ile His Arg Ala Leu Phe Gly Ser Ile Glu Arg  
                             515                            520                            525

Phe Phe Gly Val Leu Leu Glu His Tyr Ala Gly Ala Phe Pro Ala Trp  
                             530                            535                            540

Leu Ala Pro His Gln Val Met Gly Ile Pro Val Ala Asp Asp Cys Ile  
 545                            550                            555                            560

Pro His Leu Glu Thr Ile Thr Ala Gln Leu Arg Glu Lys Gly Ile Arg  
                             565                            570                            575

Ala Asp Val Asp Thr Ser Asp Asp Arg Met Gln Lys Lys Ile Arg Asn  
                             580                            585                            590

His Thr Thr Gly Lys Val Pro Phe Met Leu Leu Ala Gly Ala Arg Asp  
                             595                            600                            605

Val Glu Ala Asn Ala Val Ser Phe Arg Phe Leu Asp Gly Thr Gln Val  
 610                            615                            620

Asn Gly Val Pro Val Asp Glu Ala Ile Ala Val Ile Ser Ser Trp Ile  
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Gly Asp Arg Ile Asn Asp Gln Pro Ser Glu Asp Ser Ile Ala Ala Arg  
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Arg

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 Asp Leu Gln Asn Pro Thr Ala Lys Met Ser Lys Ser Gly Asp Asn Pro  
   1                            5                            10                            15

aag ggc atc atc aac ctg ctt gat gat cca aag gtg tcc acc aag cgc 96  
 Lys Gly Ile Ile Asn Leu Leu Asp Asp Pro Lys Val Ser Thr Lys Arg  
                             20                            25                            30

atc aag tcc gca gtc acc gac aac gac ggc gtc atc gcc tac gat cca 144  
 Ile Lys Ser Ala Val Thr Asp Asn Asp Gly Val Ile Ala Tyr Asp Pro  
                             35                            40                            45

gaa aac aag cct ggc gtg tcc aac ttg ctg gtc atc cag tct gcg ctg 192

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Lys	Gly	Ile	Ile 20	Asn	Leu	Leu	Asp	Asp 25	Pro	Lys	Val	Ser	Thr 30	Lys	Arg
Ile	Lys	Ser 35	Ala	Val	Thr	Asp	Asn 40	Asp	Gly	Val	Ile	Ala 45	Tyr	Asp	Pro
Glu	Asn 50	Lys	Pro	Gly	Val	Ser 55	Asn	Leu	Leu	Val	Ile 60	Gln	Ser	Ala	Leu
Thr 65	Gly	Thr	Ser	Ile	Asp 70	Ser	Leu	Val	Asp	Gly 75	Tyr	Gln	Gly	Ala	Gly 80
Tyr	Gly	Ala	Leu	Lys 85	Gly	Asp	Thr	Ala	Asp 90	Ala	Leu	Glu	Ala	Phe 95	Thr
Thr	Pro	Leu	Lys 100	Ala	Lys	Tyr	Asp	Glu 105	Tyr	Met	Asn	Asp	Arg 110	Gly	Glu
Leu	Glu	Arg 115	Val	Leu	Ala	Ile	Gly 120	Ala	Glu	Arg	Ala	Thr 125	Glu	Val	Ala
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aag ggc atc atc aac ctg ctt gat gat cca aag gtg tcc acc aag cgc 96  
Lys Gly Ile Ile Asn Leu Leu Asp Asp Pro Lys Val Ser Thr Lys Arg  
20 25 30  
  
atc aag tcc gca gtc acc gac aac gac ggc gtc atc gcc tac gat cca 144  
Ile Lys Ser Ala Val Thr Asp Asn Asp Gly Val Ile Ala Tyr Asp Pro  
35 40 45  
  
gaa aac aag cct ggc gtg tcc aac ttg ctg gtc atc cag tct gcg ctg 192  
Glu Asn Lys Pro Gly Val Ser Asn Leu Leu Val Ile Gln Ser Ala Leu  
50 55 60  
  
acg ggt acc tcc atc gat tgc ctt gtc gac ggc tac cag ggc gct ggc 240  
Thr Gly Thr Ser Ile Asp Ser Leu Val Asp Gly Tyr Gln Gly Ala Gly  
65 70 75 80  
  
tac ggt gcg ttg aag ggt gac acc gcc gac gcg ctt gag gct ttc acc 288  
Tyr Gly Ala Leu Lys Gly Asp Thr Ala Asp Ala Leu Glu Ala Phe Thr  
85 90 95  
  
act cct ttg aag gca aag tac gac gag tac atg aat gac cgc ggc gag 336  
Thr Pro Leu Lys Ala Lys Tyr Asp Glu Tyr Met Asn Asp Arg Gly Glu  
100 105 110  
  
ctc gaa cga gtc ttg gct atc ggt gct gag cgc gcc acc gaa gtt gcc 384  
Leu Glu Arg Val Leu Ala Ile Gly Ala Glu Arg Ala Thr Glu Val Ala  
115 120 125  
  
aac gaa acc ttg gct gat gtg tac gac aag att ggt ttc ttg gcg tct 432  
Asn Glu Thr Leu Ala Asp Val Tyr Asp Lys Ile Gly Phe Leu Ala Ser  
130 135 140  
  
cgt cgc taacaactag accctcgatt att 461  
Arg Arg  
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<210> 338  
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&lt;400&gt; 338

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 Lys Gly Ile Ile Asn Leu Leu Asp Asp Pro Lys Val Ser Thr Lys Arg  
 20 25 30  
 Ile Lys Ser Ala Val Thr Asp Asn Asp Gly Val Ile Ala Tyr Asp Pro  
 35 40 45  
 Glu Asn Lys Pro Gly Val Ser Asn Leu Leu Val Ile Gln Ser Ala Leu  
 50 55 60  
 Thr Gly Thr Ser Ile Asp Ser Leu Val Asp Gly Tyr Gln Gly Ala Gly  
 65 70 75 80  
 Tyr Gly Ala Leu Lys Gly Asp Thr Ala Asp Ala Leu Glu Ala Phe Thr  
 85 90 95  
 Thr Pro Leu Lys Ala Lys Tyr Asp Glu Tyr Met Asn Asp Arg Gly Glu  
 100 105 110  
 Leu Glu Arg Val Leu Ala Ile Gly Ala Glu Arg Ala Thr Glu Val Ala  
 115 120 125  
 Asn Glu Thr Leu Ala Asp Val Tyr Asp Lys Ile Gly Phe Leu Ala Ser  
 130 135 140  
 Arg Arg  
 145

&lt;210&gt; 339

&lt;211&gt; 580

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(580)

&lt;223&gt; RXN03078

&lt;400&gt; 339

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 accggaaaag gtctgtccaa ggtgactaca ctgatacagc atg acg acg cag gat 115  
 Met Thr Thr Gln Asp  
 1 5  
 aaa gat ctc acc gca caa acc gct tcc aga gtc ctt tct gga att cag 163  
 Lys Asp Leu Thr Ala Gln Thr Ala Ser Arg Val Leu Ser Gly Ile Gln  
 10 15 20  
 ccc acc gcc gat tcc tat cac ctg ggc aat tac ttg gga gca gtc aag 211  
 Pro Thr Ala Asp Ser Tyr His Leu Gly Asn Tyr Leu Gly Ala Val Lys  
 25 30 35  
 cag tgg att gac ctg caa gat tcc tac gat gcc ttc tac ttc att cca 259  
 Gln Trp Ile Asp Leu Gln Asp Ser Tyr Asp Ala Phe Tyr Phe Ile Pro  
 40 45 50

gat ctc cac gcg att acc gtc gat cag gaa cca gaa gag ctg cgc aac 307  
Asp Leu His Ala Ile Thr Val Asp Gln Glu Pro Glu Glu Leu Arg Asn  
55 60 65

cgc acc att tcc ggc gcc gca cag ctg ctg gcc ctg ggc att gat cca 355  
Arg Thr Ile Ser Gly Ala Ala Gln Leu Leu Ala Leu Gly Ile Asp Pro  
70 75 80 85

gaa cgc tcc acc ttg ttt gtg cag tcg cat gtt ccc gca cat gca gaa 403  
Glu Arg Ser Thr Leu Phe Val Gln Ser His Val Pro Ala His Ala Glu  
90 95 100

ctg tca tgg gtt ctg acc tgc ctg acc ggt ttc ggc gag gca tcc cgc 451  
Leu Ser Trp Val Leu Thr Cys Leu Thr Gly Phe Gly Glu Ala Ser Arg  
105 110 115

atg acc cag ttc aag gac aag tcc tcc aag cgt ggc gcc gac cgt acc 499  
Met Thr Gln Phe Lys Asp Lys Ser Ser Lys Arg Gly Ala Asp Arg Thr  
120 125 130

tca gct ggt ctg ttc acc tac ccg atg ctg atg gca gca gat att ttg 547  
Ser Ala Gly Leu Phe Thr Tyr Pro Met Leu Met Ala Ala Asp Ile Leu  
135 140 145

ctg tac cgc cca cat ctt gtc cca gtc ggt gaa 580  
Leu Tyr Arg Pro His Leu Val Pro Val Gly Glu  
150 155 160

&lt;210&gt; 340

&lt;211&gt; 160

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 340

Met Thr Thr Gln Asp Lys Asp Leu Thr Ala Gln Thr Ala Ser Arg Val  
1 5 10 15

Leu Ser Gly Ile Gln Pro Thr Ala Asp Ser Tyr His Leu Gly Asn Tyr  
20 25 30

Leu Gly Ala Val Lys Gln Trp Ile Asp Leu Gln Asp Ser Tyr Asp Ala  
35 40 45

Phe Tyr Phe Ile Pro Asp Leu His Ala Ile Thr Val Asp Gln Glu Pro  
50 55 60

Glu Glu Leu Arg Asn Arg Thr Ile Ser Gly Ala Ala Gln Leu Leu Ala  
65 70 75 80

Leu Gly Ile Asp Pro Glu Arg Ser Thr Leu Phe Val Gln Ser His Val  
85 90 95

Pro Ala His Ala Glu Leu Ser Trp Val Leu Thr Cys Leu Thr Gly Phe  
100 105 110

Gly Glu Ala Ser Arg Met Thr Gln Phe Lys Asp Lys Ser Ser Lys Arg  
115 120 125

Gly Ala Asp Arg Thr Ser Ala Gly Leu Phe Thr Tyr Pro Met Leu Met  
130 135 140

Ala Ala Asp Ile Leu Leu Tyr Arg Pro His Leu Val Pro Val Gly Glu  
 145 150 155 160

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 <223> FRXA02866

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 Met Thr Thr Gln Asp  
 1 5  
 aaa gat ctc acc gca caa acc gct tcc aga gtc ctt tct gga att cag 163  
 Lys Asp Leu Thr Ala Gln Thr Ala Ser Arg Val Leu Ser Gly Ile Gln  
 10 15 20  
 ccc acc gcc gat tcc tat cac ctg ggc aat tac ttg gga gca gtc aag 211  
 Pro Thr Ala Asp Ser Tyr His Leu Gly Asn Tyr Leu Gly Ala Val Lys  
 25 30 35  
 cag tgg att gac ctg caa gat tcc tac gat gcc ttc tac ttc att cca 259  
 Gln Trp Ile Asp Leu Gln Asp Ser Tyr Asp Ala Phe Tyr Phe Ile Pro  
 40 45 50  
 gat ctc cac gcg att acc gtc gat cag gaa cca gaa gag ctg cgc aac 307  
 Asp Leu His Ala Ile Thr Val Asp Gln Glu Pro Glu Glu Leu Arg Asn  
 55 60 65  
 cgc acc att tcc ggc gcc gca cag ctg ctg gcc ctg ggc att gat cca 355  
 Arg Thr Ile Ser Gly Ala Ala Gln Leu Leu Ala Leu Gly Ile Asp Pro  
 70 75 80 85  
 gaa cgc tcc acc ttg ttt gtg cag tcg cat gtt ccc gca cat gca gaa 403  
 Glu Arg Ser Thr Leu Phe Val Gln Ser His Val Pro Ala His Ala Glu  
 90 95 100  
 ctg tca tgg gtt ctg acc tgc ctg acc ggt ttc ggc gag gca tcc cgc 451  
 Leu Ser Trp Val Leu Thr Cys Leu Thr Gly Phe Gly Glu Ala Ser Arg  
 105 110 115  
 atg acc cag ttc aag gac aag tcc tcc aag cgt ggc gcc gac cgt acc 499  
 Met Thr Gln Phe Lys Asp Lys Ser Ser Lys Arg Gly Ala Asp Arg Thr  
 120 125 130  
 tca gct ggt ctg ttc acc tac ccg atg ctg atg gca gca gat att ttg 547  
 Ser Ala Gly Leu Phe Thr Tyr Pro Met Leu Met Ala Ala Asp Ile Leu  
 135 140 145  
 ctg tac cgc cca cat ctt gtc cca gtc ggt gaa 580  
 Leu Tyr Arg Pro His Leu Val Pro Val Gly Glu  
 150 155 160

&lt;210&gt; 342

&lt;211&gt; 160

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 342

Met Thr Thr Gln Asp Lys Asp Leu Thr Ala Gln Thr Ala Ser Arg Val  
 1 5 10 15

Leu Ser Gly Ile Gln Pro Thr Ala Asp Ser Tyr His Leu Gly Asn Tyr  
 20 25 30

Leu Gly Ala Val Lys Gln Trp Ile Asp Leu Gln Asp Ser Tyr Asp Ala  
 35 40 45

Phe Tyr Phe Ile Pro Asp Leu His Ala Ile Thr Val Asp Gln Glu Pro  
 50 55 60

Glu Glu Leu Arg Asn Arg Thr Ile Ser Gly Ala Ala Gln Leu Leu Ala  
 65 70 75 80

Leu Gly Ile Asp Pro Glu Arg Ser Thr Leu Phe Val Gln Ser His Val  
 85 90 95

Pro Ala His Ala Glu Leu Ser Trp Val Leu Thr Cys Leu Thr Gly Phe  
 100 105 110

Gly Glu Ala Ser Arg Met Thr Gln Phe Lys Asp Lys Ser Ser Lys Arg  
 115 120 125

Gly Ala Asp Arg Thr Ser Ala Gly Leu Phe Thr Tyr Pro Met Leu Met  
 130 135 140

Ala Ala Asp Ile Leu Leu Tyr Arg Pro His Leu Val Pro Val Gly Glu  
 145 150 155 160

&lt;210&gt; 343

&lt;211&gt; 2832

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2809)

&lt;223&gt; RXN00985

&lt;400&gt; 343

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cctaaatccg gataacttgat aaacaagttac aggggttaag atg gtc tgc gtg act 115  
 Met Val Cys Val Thr  
 1 5

gac cag aat aat gag acc acc agc cag aac cgc gca gac aag ctg ccc 163  
 Asp Gln Asn Asn Glu Thr Thr Ser Gln Asn Arg Ala Asp Lys Leu Pro  
 10 15 20

aag tcc tgg gat cct aaa gct gta gaa gct gat ttg tac cag ggc tgg 211

Lys	Ser	Trp	Asp	Pro	Lys	Ala	Val	Glu	Ala	Asp	Leu	Tyr	Gln	Gly	Trp		
			25					30					35				
gta	gac	gcc	ggg	tat	ttc	act	gcc	gat	cct	gct	agc	gac	aag	cca	gga	259	
Val	Asp	Ala	Gly	Tyr	Phe	Thr	Ala	Asp	Pro	Ala	Ser	Asp	Lys	Pro	Gly		
		40					45					50					
ttc	tcc	att	gtt	ctg	cct	cca	cca	aac	gtg	acc	ggc	cag	ctg	cac	atg	307	
Phe	Ser	Ile	Val	Leu	Pro	Pro	Pro	Asn	Val	Thr	Gly	Gln	Leu	His	Met		
	55					60					65						
gga	cac	gca	ctt	gac	cac	acc	ctg	atg	gat	gct	ctt	gca	cgt	cgc	aag	355	
Gly	His	Ala	Leu	Asp	His	Thr	Leu	Met	Asp	Ala	Leu	Ala	Arg	Arg	Lys		
70					75					80					85		
cgc	atg	cag	ggc	ttt	gag	gtt	ttg	tgg	ctg	cca	ggg	atg	gac	cac	gcg	403	
Arg	Met	Gln	Gly	Phe	Glu	Val	Leu	Trp	Leu	Pro	Gly	Met	Asp	His	Ala		
				90					95					100			
ggg	atc	gcg	acc	cag	acc	aag	gtc	gag	gag	atg	ctg	aag	gaa	act	gaa	451	
Gly	Ile	Ala	Thr	Gln	Thr	Lys	Val	Glu	Glu	Met	Leu	Lys	Glu	Thr	Glu		
			105					110					115				
ggc	aaa	act	cgc	tac	gac	tat	gac	cgc	gaa	gag	ttc	atc	gcc	aag	gtc	499	
Gly	Lys	Thr	Arg	Tyr	Asp	Tyr	Asp	Arg	Glu	Glu	Phe	Ile	Ala	Lys	Val		
		120					125					130					
tgg	gag	tgg	aag	caa	gaa	tat	ggg	gga	aag	atc	ggc	gag	cag	atg	cgc	547	
Trp	Glu	Trp	Lys	Gln	Glu	Tyr	Gly	Gly	Lys	Ile	Gly	Glu	Gln	Met	Arg		
	135					140					145						
gcc	atc	ggc	gat	tcc	gtg	gac	tgg	tcc	cgc	gag	cgt	ttc	acc	ttg	gat	595	
Ala	Ile	Gly	Asp	Ser	Val	Asp	Trp	Ser	Arg	Glu	Arg	Phe	Thr	Leu	Asp		
150					155					160					165		
gac	ggc	ttg	tcc	cgc	gcc	gtc	caa	acg	att	ttc	aag	aag	ctt	ttc	gac	643	
Asp	Gly	Leu	Ser	Arg	Ala	Val	Gln	Thr	Ile	Phe	Lys	Lys	Leu	Phe	Asp		
				170					175					180			
gcc	ggc	ctc	atc	tat	cag	gcc	aac	cgc	ctc	gtc	aac	tgg	tcg	ccc	gta	691	
Ala	Gly	Leu	Ile	Tyr	Gln	Ala	Asn	Arg	Leu	Val	Asn	Trp	Ser	Pro	Val		
			185					190					195				
cta	gaa	acc	gcg	gtt	tct	gac	atc	gaa	gtt	atc	tac	aag	gat	gtc	gaa	739	
Leu	Glu	Thr	Ala	Val	Ser	Asp	Ile	Glu	Val	Ile	Tyr	Lys	Asp	Val	Glu		
		200					205					210					
ggc	gaa	ctg	gta	tcc	att	cgc	tat	ggg	tcc	ctc	aac	gac	gat	gaa	cca	787	
Gly	Glu	Leu	Val	Ser	Ile	Arg	Tyr	Gly	Ser	Leu	Asn	Asp	Asp	Glu	Pro		
	215					220					225						
cat	gtc	att	gtt	gcc	acc	acc	cgt	gtg	gaa	acc	atg	ctc	ggc	gac	gtc	835	
His	Val	Ile	Val	Ala	Thr	Thr	Arg	Val	Glu	Thr	Met	Leu	Gly	Asp	Val		
230					235					240					245		
gct	gtt	gcc	gtg	cac	cca	gac	gat	gag	cgc	tac	aag	gat	ttg	gtc	gga	883	
Ala	Val	Ala	Val	His	Pro	Asp	Asp	Glu	Arg	Tyr	Lys	Asp	Leu	Val	Gly		
				250				255						260			
cag	acc	ctg	cct	cac	cca	ttc	cgc	gat	gac	ctg	agc	ctg	aag	gtt	gtt	931	
Gln	Thr	Leu	Pro	His	Pro	Phe	Arg	Asp	Asp	Leu	Ser	Leu	Lys	Val	Val		

265						270						275						
gct	gat	gat	tac	gtc	gac	cca	gag	ttc	ggc	tcc	ggt	gcc	gtc	aag	atc	979		
Ala	Asp	Asp	Tyr	Val	Asp	Pro	Glu	Phe	Gly	Ser	Gly	Ala	Val	Lys	Ile			
		280					285					290						
acc	cca	gca	cac	gac	cct	aat	gac	tac	gct	ctt	ggc	ctg	cgc	cac	aac	1027		
Thr	Pro	Ala	His	Asp	Pro	Asn	Asp	Tyr	Ala	Leu	Gly	Leu	Arg	His	Asn			
	295					300					305							
ctg	gac	atg	cct	acc	atc	atg	gac	aag	acc	gga	cgc	att	gcc	gat	acc	1075		
Leu	Asp	Met	Pro	Thr	Ile	Met	Asp	Lys	Thr	Gly	Arg	Ile	Ala	Asp	Thr			
310					315					320					325			
gga	acc	cag	ttt	gat	ggc	ctg	acc	cgc	gaa	gaa	gca	cgc	atc	aag	gtc	1123		
Gly	Thr	Gln	Phe	Asp	Gly	Leu	Thr	Arg	Glu	Glu	Ala	Arg	Ile	Lys	Val			
				330					335					340				
cgc	gaa	gaa	ctc	gca	gcc	cag	ggt	cgc	att	gtc	aag	gaa	att	cgc	cca	1171		
Arg	Glu	Glu	Leu	Ala	Ala	Gln	Gly	Arg	Ile	Val	Lys	Glu	Ile	Arg	Pro			
			345				350						355					
tac	gtc	cac	tcc	gtc	gga	cac	tcc	gag	cgt	tcc	ggc	gaa	gct	att	gag	1219		
Tyr	Val	His	Ser	Val	Gly	His	Ser	Glu	Arg	Ser	Gly	Glu	Ala	Ile	Glu			
		360					365					370						
cct	cgt	ctg	tct	ctg	cag	tgg	ttc	gtc	aag	gtc	gaa	gag	ctg	gcc	aag	1267		
Pro	Arg	Leu	Ser	Leu	Gln	Trp	Phe	Val	Lys	Val	Glu	Glu	Leu	Ala	Lys			
	375					380					385							
atg	tcc	ggc	gat	gcc	gtg	cgc	gaa	ggc	gac	acc	acc	atc	cac	ccg	aag	1315		
Met	Ser	Gly	Asp	Ala	Val	Arg	Glu	Gly	Asp	Thr	Thr	Ile	His	Pro	Lys			
390					395					400					405			
tcc	ctg	gag	cct	cgc	tac	ttt	gac	tgg	gtt	gac	aac	atg	cat	gac	tgg	1363		
Ser	Leu	Glu	Pro	Arg	Tyr	Phe	Asp	Trp	Val	Asp	Asn	Met	His	Asp	Trp			
				410					415					420				
acc	att	tcc	cgt	cag	ctg	tgg	tgg	gga	cac	cgc	atc	cca	att	tgg	tat	1411		
Thr	Ile	Ser	Arg	Gln	Leu	Trp	Trp	Gly	His	Arg	Ile	Pro	Ile	Trp	Tyr			
			425					430					435					
gga	cca	aac	gat	gaa	atc	atc	tgc	gtt	ggg	cct	gat	gag	cag	gca	cct	1459		
Gly	Pro	Asn	Asp	Glu	Ile	Ile	Cys	Val	Gly	Pro	Asp	Glu	Gln	Ala	Pro			
		440					445					450						
gag	ggc	tac	gtc	caa	gac	cca	gat	gtt	cta	gat	acc	tgg	ttc	tct	tct	1507		
Glu	Gly	Tyr	Val	Gln	Asp	Pro	Asp	Val	Leu	Asp	Thr	Trp	Phe	Ser	Ser			
	455					460					465							
gcg	ctg	tgg	cca	ttt	tct	aca	atg	ggt	tgg	cca	gaa	aag	acc	cct	gag	1555		
Ala	Leu	Trp	Pro	Phe	Ser	Thr	Met	Gly	Trp	Pro	Glu	Lys	Thr	Pro	Glu			
470					475					480					485			
ctg	gag	aag	ttc	tac	cca	acc	tcc	gtg	ctg	gtc	acc	gcc	tac	gac	atc	1603		
Leu	Glu	Lys	Phe	Tyr	Pro	Thr	Ser	Val	Leu	Val	Thr	Ala	Tyr	Asp	Ile			
				490					495					500				
ctg	ttc	ttc	tgg	gtt	gcc	cgc	atg	atg	atg	ttc	ggc	acc	ttt	gca	gcc	1651		
Leu	Phe	Phe	Trp	Val	Ala	Arg	Met	Met	Met	Phe	Gly	Thr	Phe	Ala	Ala			
			505					510					515					

aag gaa acc cca gaa ctt ctg ggc gaa ggc aag gat gga cgc cca cag	1699
Lys Glu Thr Pro Glu Leu Leu Gly Glu Gly Lys Asp Gly Arg Pro Gln	
520 525 530	
ggt cca ttc acc gac ctc ttc ctg cac ggc ctg gtt cgc gat gag cac	1747
Val Pro Phe Thr Asp Leu Phe Leu His Gly Leu Val Arg Asp Glu His	
535 540 545	
ggc cgc aag atg tcc aag tct ttg ggc aac ggc atc gat ccg atg gat	1795
Gly Arg Lys Met Ser Lys Ser Leu Gly Asn Gly Ile Asp Pro Met Asp	
550 555 560 565	
tgg gtg gag aac tac ggc gcg gat gcg ttg cgc ttc acc ctt gcc cgt	1843
Trp Val Glu Asn Tyr Gly Ala Asp Ala Leu Arg Phe Thr Leu Ala Arg	
570 575 580	
ggc gct aac cca ggc gtc gac ctg cct gtc ggt gaa gac tct gca cag	1891
Gly Ala Asn Pro Gly Val Asp Leu Pro Val Gly Glu Asp Ser Ala Gln	
585 590 595	
agc tcc cgt aac ttt gcc acc aag ctg ttc aac gca acc aag ttt gcg	1939
Ser Ser Arg Asn Phe Ala Thr Lys Leu Phe Asn Ala Thr Lys Phe Ala	
600 605 610	
ctg atg aac ggt gca gtg tcc gaa ggc ctg cca gca cgt gaa gaa ctc	1987
Leu Met Asn Gly Ala Val Ser Glu Gly Leu Pro Ala Arg Glu Glu Leu	
615 620 625	
acc gac gct gac cgc tgg atc gtg gac ctc ctt gag cag gtt cgc ctc	2035
Thr Asp Ala Asp Arg Trp Ile Val Asp Leu Leu Glu Gln Val Arg Leu	
630 635 640 645	
gac gtt gat gct tac ctg gac aac tac cag ttc gcg aag gcc aac gag	2083
Asp Val Asp Ala Tyr Leu Asp Asn Tyr Gln Phe Ala Lys Ala Asn Glu	
650 655 660	
gag ctc tac cac ttt gcg tgg aac gag ttc tgt gac tgg tac ctg gaa	2131
Glu Leu Tyr His Phe Ala Trp Asn Glu Phe Cys Asp Trp Tyr Leu Glu	
665 670 675	
atc gcg aag gtt cag atc cca cgc gaa ggc acc tcc gct cag ggt gaa	2179
Ile Ala Lys Val Gln Ile Pro Arg Glu Gly Thr Ser Ala Gln Gly Glu	
680 685 690	
aac acc caa aag gtg ctt ggc cat gtc ttg gat gca ctg ctt cgt ctg	2227
Asn Thr Gln Lys Val Leu Gly His Val Leu Asp Ala Leu Leu Arg Leu	
695 700 705	
ctg cac cca gct atg cct ttc gtc acc gaa gtt ctg tgg cag gca ctt	2275
Leu His Pro Ala Met Pro Phe Val Thr Glu Val Leu Trp Gln Ala Leu	
710 715 720 725	
act gat cgc acc tcc atc gtg gtg gcc tcc tgg cca acc gca gct gac	2323
Thr Asp Arg Thr Ser Ile Val Val Ala Ser Trp Pro Thr Ala Ala Asp	
730 735 740	
acc aac ggc gga gtc gcc gtg gac gct gat gca gct agg cgc att ggc	2371
Thr Asn Gly Gly Val Ala Val Asp Ala Asp Ala Ala Arg Arg Ile Gly	
745 750 755	

gac gtc gag aag ctt gtt act gag gtt cgt cgt ttc cgc gct gac cag 2419  
 Asp Val Glu Lys Leu Val Thr Glu Val Arg Arg Phe Arg Ala Asp Gln  
 760 765 770

ggt gtg aag cct tcc cag aag gtt cca gca cgc ctt gat ttc gtg gca 2467  
 Gly Val Lys Pro Ser Gln Lys Val Pro Ala Arg Leu Asp Phe Val Ala  
 775 780 785

tgt gac ctg cag gat ctg gaa gat tcc gtg cgc tcc ctg gtt cgc atc 2515  
 Cys Asp Leu Gln Asp Leu Glu Asp Ser Val Arg Ser Leu Val Arg Ile  
 790 795 800 805

gag caa cca gaa gat gat ttc gca gct tct gcc agc ctg gag atc cgc 2563  
 Glu Gln Pro Glu Asp Asp Phe Ala Ala Ser Ala Ser Leu Glu Ile Arg  
 810 815 820

ctg agc caa gca acc atc acg gtg gag ctt gac acc tct gga act gtt 2611  
 Leu Ser Gln Ala Thr Ile Thr Val Glu Leu Asp Thr Ser Gly Thr Val  
 825 830 835

gac gtt gca gca gag cgc aag cgc ctg gaa aag gac ctg gct aac gca 2659  
 Asp Val Ala Ala Glu Arg Lys Arg Leu Glu Lys Asp Leu Ala Asn Ala  
 840 845 850

cag aag gaa ttg gaa acc acc gca aag aag ctg ggt aat gag gct ttc 2707  
 Gln Lys Glu Leu Glu Thr Thr Ala Lys Lys Leu Gly Asn Glu Ala Phe  
 855 860 865

ctg tcc aag gca cct gat gca gtg gta gac aag atc cgt ggc cgt gcg 2755  
 Leu Ser Lys Ala Pro Asp Ala Val Val Asp Lys Ile Arg Gly Arg Ala  
 870 875 880 885

cag att gcc caa gaa gaa gtt gag cgc att aac aag cgt ctg gag gaa 2803  
 Gln Ile Ala Gln Glu Glu Val Glu Arg Ile Asn Lys Arg Leu Glu Glu  
 890 895 900

ttg gcc tagtggttaa caacgacgga atc 2832  
 Leu Ala

&lt;210&gt; 344

&lt;211&gt; 903

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 344

Met Val Cys Val Thr Asp Gln Asn Asn Glu Thr Thr Ser Gln Asn Arg  
 1 5 10 15

Ala Asp Lys Leu Pro Lys Ser Trp Asp Pro Lys Ala Val Glu Ala Asp  
 20 25 30

Leu Tyr Gln Gly Trp Val Asp Ala Gly Tyr Phe Thr Ala Asp Pro Ala  
 35 40 45

Ser Asp Lys Pro Gly Phe Ser Ile Val Leu Pro Pro Pro Asn Val Thr  
 50 55 60

Gly Gln Leu His Met Gly His Ala Leu Asp His Thr Leu Met Asp Ala  
 65 70 75 80

Leu Ala Arg Arg Lys Arg Met Gln Gly Phe Glu Val Leu Trp Leu Pro  
                                   85                                  90                                  95  
 Gly Met Asp His Ala Gly Ile Ala Thr Gln Thr Lys Val Glu Glu Met  
                                   100                                  105                                  110  
 Leu Lys Glu Thr Glu Gly Lys Thr Arg Tyr Asp Tyr Asp Arg Glu Glu  
                                   115                                  120                                  125  
 Phe Ile Ala Lys Val Trp Glu Trp Lys Gln Glu Tyr Gly Gly Lys Ile  
                                   130                                  135                                  140  
 Gly Glu Gln Met Arg Ala Ile Gly Asp Ser Val Asp Trp Ser Arg Glu  
                                   145                                  150                                  155                                  160  
 Arg Phe Thr Leu Asp Asp Gly Leu Ser Arg Ala Val Gln Thr Ile Phe  
                                   165                                  170                                  175  
 Lys Lys Leu Phe Asp Ala Gly Leu Ile Tyr Gln Ala Asn Arg Leu Val  
                                   180                                  185                                  190  
 Asn Trp Ser Pro Val Leu Glu Thr Ala Val Ser Asp Ile Glu Val Ile  
                                   195                                  200                                  205  
 Tyr Lys Asp Val Glu Gly Glu Leu Val Ser Ile Arg Tyr Gly Ser Leu  
                                   210                                  215                                  220  
 Asn Asp Asp Glu Pro His Val Ile Val Ala Thr Thr Arg Val Glu Thr  
                                   225                                  230                                  235                                  240  
 Met Leu Gly Asp Val Ala Val Ala Val His Pro Asp Asp Glu Arg Tyr  
                                   245                                  250                                  255  
 Lys Asp Leu Val Gly Gln Thr Leu Pro His Pro Phe Arg Asp Asp Leu  
                                   260                                  265                                  270  
 Ser Leu Lys Val Val Ala Asp Asp Tyr Val Asp Pro Glu Phe Gly Ser  
                                   275                                  280                                  285  
 Gly Ala Val Lys Ile Thr Pro Ala His Asp Pro Asn Asp Tyr Ala Leu  
                                   290                                  295                                  300  
 Gly Leu Arg His Asn Leu Asp Met Pro Thr Ile Met Asp Lys Thr Gly  
                                   305                                  310                                  315                                  320  
 Arg Ile Ala Asp Thr Gly Thr Gln Phe Asp Gly Leu Thr Arg Glu Glu  
                                   325                                  330                                  335  
 Ala Arg Ile Lys Val Arg Glu Glu Leu Ala Ala Gln Gly Arg Ile Val  
                                   340                                  345                                  350  
 Lys Glu Ile Arg Pro Tyr Val His Ser Val Gly His Ser Glu Arg Ser  
                                   355                                  360                                  365  
 Gly Glu Ala Ile Glu Pro Arg Leu Ser Leu Gln Trp Phe Val Lys Val  
                                   370                                  375                                  380  
 Glu Glu Leu Ala Lys Met Ser Gly Asp Ala Val Arg Glu Gly Asp Thr  
                                   385                                  390                                  395                                  400

Thr Ile His Pro Lys Ser Leu Glu Pro Arg Tyr Phe Asp Trp Val Asp  
 405 410 415  
 Asn Met His Asp Trp Thr Ile Ser Arg Gln Leu Trp Trp Gly His Arg  
 420 425 430  
 Ile Pro Ile Trp Tyr Gly Pro Asn Asp Glu Ile Ile Cys Val Gly Pro  
 435 440 445  
 Asp Glu Gln Ala Pro Glu Gly Tyr Val Gln Asp Pro Asp Val Leu Asp  
 450 455 460  
 Thr Trp Phe Ser Ser Ala Leu Trp Pro Phe Ser Thr Met Gly Trp Pro  
 465 470 475 480  
 Glu Lys Thr Pro Glu Leu Glu Lys Phe Tyr Pro Thr Ser Val Leu Val  
 485 490 495  
 Thr Ala Tyr Asp Ile Leu Phe Phe Trp Val Ala Arg Met Met Met Phe  
 500 505 510  
 Gly Thr Phe Ala Ala Lys Glu Thr Pro Glu Leu Leu Gly Glu Gly Lys  
 515 520 525  
 Asp Gly Arg Pro Gln Val Pro Phe Thr Asp Leu Phe Leu His Gly Leu  
 530 535 540  
 Val Arg Asp Glu His Gly Arg Lys Met Ser Lys Ser Leu Gly Asn Gly  
 545 550 555 560  
 Ile Asp Pro Met Asp Trp Val Glu Asn Tyr Gly Ala Asp Ala Leu Arg  
 565 570 575  
 Phe Thr Leu Ala Arg Gly Ala Asn Pro Gly Val Asp Leu Pro Val Gly  
 580 585 590  
 Glu Asp Ser Ala Gln Ser Ser Arg Asn Phe Ala Thr Lys Leu Phe Asn  
 595 600 605  
 Ala Thr Lys Phe Ala Leu Met Asn Gly Ala Val Ser Glu Gly Leu Pro  
 610 615 620  
 Ala Arg Glu Glu Leu Thr Asp Ala Asp Arg Trp Ile Val Asp Leu Leu  
 625 630 635 640  
 Glu Gln Val Arg Leu Asp Val Asp Ala Tyr Leu Asp Asn Tyr Gln Phe  
 645 650 655  
 Ala Lys Ala Asn Glu Glu Leu Tyr His Phe Ala Trp Asn Glu Phe Cys  
 660 665 670  
 Asp Trp Tyr Leu Glu Ile Ala Lys Val Gln Ile Pro Arg Glu Gly Thr  
 675 680 685  
 Ser Ala Gln Gly Glu Asn Thr Gln Lys Val Leu Gly His Val Leu Asp  
 690 695 700  
 Ala Leu Leu Arg Leu Leu His Pro Ala Met Pro Phe Val Thr Glu Val  
 705 710 715 720  
 Leu Trp Gln Ala Leu Thr Asp Arg Thr Ser Ile Val Val Ala Ser Trp

725										730					735				
Pro	Thr	Ala	Ala	Asp	Thr	Asn	Gly	Gly	Val	Ala	Val	Asp	Ala	Asp	Ala				
			740					745					750						
Ala	Arg	Arg	Ile	Gly	Asp	Val	Glu	Lys	Leu	Val	Thr	Glu	Val	Arg	Arg				
		755					760					765							
Phe	Arg	Ala	Asp	Gln	Gly	Val	Lys	Pro	Ser	Gln	Lys	Val	Pro	Ala	Arg				
	770					775					780								
Leu	Asp	Phe	Val	Ala	Cys	Asp	Leu	Gln	Asp	Leu	Glu	Asp	Ser	Val	Arg				
785					790					795					800				
Ser	Leu	Val	Arg	Ile	Glu	Gln	Pro	Glu	Asp	Asp	Phe	Ala	Ala	Ser	Ala				
				805					810						815				
Ser	Leu	Glu	Ile	Arg	Leu	Ser	Gln	Ala	Thr	Ile	Thr	Val	Glu	Leu	Asp				
			820					825					830						
Thr	Ser	Gly	Thr	Val	Asp	Val	Ala	Ala	Glu	Arg	Lys	Arg	Leu	Glu	Lys				
		835					840					845							
Asp	Leu	Ala	Asn	Ala	Gln	Lys	Glu	Leu	Glu	Thr	Thr	Ala	Lys	Lys	Leu				
	850					855					860								
Gly	Asn	Glu	Ala	Phe	Leu	Ser	Lys	Ala	Pro	Asp	Ala	Val	Val	Asp	Lys				
865					870					875					880				
Ile	Arg	Gly	Arg	Ala	Gln	Ile	Ala	Gln	Glu	Glu	Val	Glu	Arg	Ile	Asn				
				885				890						895					
Lys	Arg	Leu	Glu	Glu	Leu	Ala													
			900																

&lt;210&gt; 345

&lt;211&gt; 590

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (96)..(590)

&lt;223&gt; FRXA00985

&lt;400&gt; 345

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aaggcacctc cgctcagggt gaaaacaccc aaaag gtg ctt ggc cat gtc ttg gat 116

Val	Leu	Gly	His	Val	Leu	Asp
1				5		

gca ctg ctt cgt ctg ctg cac cca gct atg cct ttc gtc acc gaa gtt 164

Ala	Leu	Leu	Arg	Leu	Leu	His	Pro	Ala	Met	Pro	Phe	Val	Thr	Glu	Val
		10					15					20			

ctg tgg cag gca ctt act gat cgc acc tcc atc gtg gtg gcc tcc tgg 212

Leu	Trp	Gln	Ala	Leu	Thr	Asp	Arg	Thr	Ser	Ile	Val	Val	Ala	Ser	Trp
	25					30				35					

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cca acc gca gct gac acc aac ggc gga gtc gcc gtg gac gct gat gca 260
Pro Thr Ala Ala Asp Thr Asn Gly Gly Val Ala Val Asp Ala Asp Ala
40 45 50 55

gct agg cgc att ggc gac gtc gag aag ctt gtt act gag gtt cgt cgt 308
Ala Arg Arg Ile Gly Asp Val Glu Lys Leu Val Thr Glu Val Arg Arg
60 65 70

ttc cgc gct gac cag ggt gtg aag cct tcc cag aag gtt cca gca cgc 356
Phe Arg Ala Asp Gln Gly Val Lys Pro Ser Gln Lys Val Pro Ala Arg
75 80 85

ctt gat ttc gtg gca tgt gac ctg cag gat ctg gaa gat tcc gtg cgc 404
Leu Asp Phe Val Ala Cys Asp Leu Gln Asp Leu Glu Asp Ser Val Arg
90 95 100

tcc ctg gtt cgc atc gag caa cca gaa gat gat ttc gca gct tct gcc 452
Ser Leu Val Arg Ile Glu Gln Pro Glu Asp Asp Phe Ala Ala Ser Ala
105 110 115

agc ctg gag atc cgc ctg agc caa gca acc atc acg gtg gag ctt gac 500
Ser Leu Glu Ile Arg Leu Ser Gln Ala Thr Ile Thr Val Glu Leu Asp
120 125 130 135

acc tct gga act gtt gac gtt gca gca gag cgc aag cgc ctg gaa aag 548
Thr Ser Gly Thr Val Asp Val Ala Ala Glu Arg Lys Arg Leu Glu Lys
140 145 150

gac ctg gct aac gca cag aag gaa ttg gaa acc acc gca aag 590
Asp Leu Ala Asn Ala Gln Lys Glu Leu Glu Thr Thr Ala Lys
155 160 165

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&lt;210&gt; 346

&lt;211&gt; 165

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 346

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Val Leu Gly His Val Leu Asp Ala Leu Leu Arg Leu Leu His Pro Ala
1 5 10 15

Met Pro Phe Val Thr Glu Val Leu Trp Gln Ala Leu Thr Asp Arg Thr
20 25 30

Ser Ile Val Val Ala Ser Trp Pro Thr Ala Ala Asp Thr Asn Gly Gly
35 40 45

Val Ala Val Asp Ala Asp Ala Ala Arg Arg Ile Gly Asp Val Glu Lys
50 55 60

Leu Val Thr Glu Val Arg Arg Phe Arg Ala Asp Gln Gly Val Lys Pro
65 70 75 80

Ser Gln Lys Val Pro Ala Arg Leu Asp Phe Val Ala Cys Asp Leu Gln
85 90 95

Asp Leu Glu Asp Ser Val Arg Ser Leu Val Arg Ile Glu Gln Pro Glu
100 105 110

Asp Asp Phe Ala Ala Ser Ala Ser Leu Glu Ile Arg Leu Ser Gln Ala

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      115              120              125
Thr Ile Thr Val Glu Leu Asp Thr Ser Gly Thr Val Asp Val Ala Ala
  130              135              140

Glu Arg Lys Arg Leu Glu Lys Asp Leu Ala Asn Ala Gln Lys Glu Leu
  145              150              155              160

Glu Thr Thr Ala Lys
      165

<210> 347
<211> 2149
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2149)
<223> FRXA01347

<400> 347
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cctaaatccg gatacttgat aaacaagttac aggggttaag atg gtc tgc gtg act 115
              Met Val Cys Val Thr
              1              5

gac cag aat aat gag acc acc agc cag aac cgc gca gac aag ctg ccc 163
Asp Gln Asn Asn Glu Thr Thr Ser Gln Asn Arg Ala Asp Lys Leu Pro
              10              15              20

aag tcc tgg gat cct aaa gct gta gaa gct gat ttg tac cag ggc tgg 211
Lys Ser Trp Asp Pro Lys Ala Val Glu Ala Asp Leu Tyr Gln Gly Trp
              25              30              35

gta gac gcc ggt tat ttc act gcc gat cct gct agc gac aag cca gga 259
Val Asp Ala Gly Tyr Phe Thr Ala Asp Pro Ala Ser Asp Lys Pro Gly
              40              45              50

ttc tcc att gtt ctg cct cca cca aac gtg acc ggc cag ctg cac atg 307
Phe Ser Ile Val Leu Pro Pro Pro Asn Val Thr Gly Gln Leu His Met
              55              60              65

gga cac gca ctt gac cac acc ctg atg gat gct ctt gca cgt cgc aag 355
Gly His Ala Leu Asp His Thr Leu Met Asp Ala Leu Ala Arg Arg Lys
              70              75              80              85

cgc atg cag ggc ttt gag gtt ttg tgg ctg cca ggt atg gac cac gcg 403
Arg Met Gln Gly Phe Glu Val Leu Trp Leu Pro Gly Met Asp His Ala
              90              95              100

ggt atc gcg acc cag acc aag gtc gag gag atg ctg aag gaa act gaa 451
Gly Ile Ala Thr Gln Thr Lys Val Glu Glu Met Leu Lys Glu Thr Glu
              105              110              115

ggc aaa act cgc tac gac tat gac cgc gaa gag ttc atc gcc aag gtc 499
Gly Lys Thr Arg Tyr Asp Tyr Asp Arg Glu Glu Phe Ile Ala Lys Val
              120              125              130

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tgg gag tgg aag caa gaa tat ggt gga aag atc ggc gag cag atg cgc	547
Trp Glu Trp Lys Gln Glu Tyr Gly Gly Lys Ile Gly Glu Gln Met Arg	
135 140 145	
gcc atc ggc gat tcc gtg gac tgg tcc cgc gag cgt ttc acc ttg gat	595
Ala Ile Gly Asp Ser Val Asp Trp Ser Arg Glu Arg Phe Thr Leu Asp	
150 155 160 165	
gac ggc ttg tcc cgc gcc gtc caa acg att ttc aag aag ctt ttc gac	643
Asp Gly Leu Ser Arg Ala Val Gln Thr Ile Phe Lys Lys Leu Phe Asp	
170 175 180	
gcc ggc ctc atc tat cag gcc aac cgc ctc gtc aac tgg tcg ccc gta	691
Ala Gly Leu Ile Tyr Gln Ala Asn Arg Leu Val Asn Trp Ser Pro Val	
185 190 195	
cta gaa acc gcg gtt tct gac atc gaa gtt atc tac aag gat gtc gaa	739
Leu Glu Thr Ala Val Ser Asp Ile Glu Val Ile Tyr Lys Asp Val Glu	
200 205 210	
ggc gaa ctg gta tcc att cgc tat ggt tcc ctc aac gac gat gaa cca	787
Gly Glu Leu Val Ser Ile Arg Tyr Gly Ser Leu Asn Asp Asp Glu Pro	
215 220 225	
cat gtc att gtt gcc acc acc cgt gtg gaa acc atg ctc ggc gac gtc	835
His Val Ile Val Ala Thr Thr Arg Val Glu Thr Met Leu Gly Asp Val	
230 235 240 245	
gct gtt gcc gtg cac cca gac gat gag cgc tac aag gat ttg gtc gga	883
Ala Val Ala Val His Pro Asp Asp Glu Arg Tyr Lys Asp Leu Val Gly	
250 255 260	
cag acc ctg cct cac cca ttc cgc gat gac ctg agc ctg aag gtt gtt	931
Gln Thr Leu Pro His Pro Phe Arg Asp Asp Leu Ser Leu Lys Val Val	
265 270 275	
gct gat gat tac gtc gac cca gag ttc ggc tcc ggt gcc gtc aag atc	979
Ala Asp Asp Tyr Val Asp Pro Glu Phe Gly Ser Gly Ala Val Lys Ile	
280 285 290	
acc cca gca cac gac cct aat gac tac gct ctt ggc ctg cgc cac aac	1027
Thr Pro Ala His Asp Pro Asn Asp Tyr Ala Leu Gly Leu Arg His Asn	
295 300 305	
ctg gac atg cct acc atc atg gac aag acc gga cgc att gcc gat acc	1075
Leu Asp Met Pro Thr Ile Met Asp Lys Thr Gly Arg Ile Ala Asp Thr	
310 315 320 325	
gga acc cag ttt gat ggc ctg acc cgc gaa gaa gca cgc atc aag gtc	1123
Gly Thr Gln Phe Asp Gly Leu Thr Arg Glu Glu Ala Arg Ile Lys Val	
330 335 340	
cgc gaa gaa ctc gca gcc cag ggt cgc att gtc aag gaa att cgc cca	1171
Arg Glu Glu Leu Ala Ala Gln Gly Arg Ile Val Lys Glu Ile Arg Pro	
345 350 355	
tac gtc cac tcc gtc gga cac tcc gag cgt tcc ggc gaa gct att gag	1219
Tyr Val His Ser Val Gly His Ser Glu Arg Ser Gly Glu Ala Ile Glu	
360 365 370	
cct cgt ctg tct ctg cag tgg ttc gtc aag gtc gaa gag ctg gcc aag	1267

Pro	Arg	Leu	Ser	Leu	Gln	Trp	Phe	Val	Lys	Val	Glu	Glu	Leu	Ala	Lys	
	375					380					385					
atg	tcc	ggc	gat	gcc	gtg	cgc	gaa	ggc	gac	acc	acc	atc	cac	ccg	aag	1315
Met	Ser	Gly	Asp	Ala	Val	Arg	Glu	Gly	Asp	Thr	Thr	Ile	His	Pro	Lys	
390					395				400						405	
tcc	ctg	gag	cct	cgc	tac	ttt	gac	tgg	gtt	gac	aac	atg	cat	gac	tgg	1363
Ser	Leu	Glu	Pro	Arg	Tyr	Phe	Asp	Trp	Val	Asp	Asn	Met	His	Asp	Trp	
				410					415					420		
acc	att	tcc	cgt	cag	ctg	tgg	tgg	gga	cac	cgc	atc	cca	att	tgg	tat	1411
Thr	Ile	Ser	Arg	Gln	Leu	Trp	Trp	Gly	His	Arg	Ile	Pro	Ile	Trp	Tyr	
			425					430					435			
gga	cca	aac	gat	gaa	atc	atc	tgc	gtt	ggg	cct	gat	gag	cag	gca	cct	1459
Gly	Pro	Asn	Asp	Glu	Ile	Ile	Cys	Val	Gly	Pro	Asp	Glu	Gln	Ala	Pro	
		440					445					450				
gag	ggc	tac	gtc	caa	gac	cca	gat	gtt	cta	gat	acc	tgg	ttc	tct	tct	1507
Glu	Gly	Tyr	Val	Gln	Asp	Pro	Asp	Val	Leu	Asp	Thr	Trp	Phe	Ser	Ser	
	455					460					465					
gcg	ctg	tgg	cca	ttt	tct	aca	atg	ggt	tgg	cca	gaa	aag	acc	cct	gag	1555
Ala	Leu	Trp	Pro	Phe	Ser	Thr	Met	Gly	Trp	Pro	Glu	Lys	Thr	Pro	Glu	
470					475					480					485	
ctg	gag	aag	ttc	tac	cca	acc	tcc	gtg	ctg	gtc	acc	gcc	tac	gac	atc	1603
Leu	Glu	Lys	Phe	Tyr	Pro	Thr	Ser	Val	Leu	Val	Thr	Ala	Tyr	Asp	Ile	
				490					495					500		
ctg	ttc	ttc	tgg	gtt	gcc	cgc	atg	atg	atg	ttc	ggc	acc	ttt	gca	gcc	1651
Leu	Phe	Phe	Trp	Val	Ala	Arg	Met	Met	Met	Phe	Gly	Thr	Phe	Ala	Ala	
			505					510					515			
aag	gaa	acc	cca	gaa	ctt	ctg	ggc	gaa	ggc	aag	gat	gga	cgc	cca	cag	1699
Lys	Glu	Thr	Pro	Glu	Leu	Leu	Gly	Glu	Gly	Lys	Asp	Gly	Arg	Pro	Gln	
		520					525					530				
gtt	cca	ttc	acc	gac	ctc	ttc	ctg	cac	ggc	ctg	gtt	cgc	gat	gag	cac	1747
Val	Pro	Phe	Thr	Asp	Leu	Phe	Leu	His	Gly	Leu	Val	Arg	Asp	Glu	His	
	535					540					545					
ggc	cgc	aag	atg	tcc	aag	tct	ttg	ggc	aac	ggc	atc	gat	ccg	atg	gat	1795
Gly	Arg	Lys	Met	Ser	Lys	Ser	Leu	Gly	Asn	Gly	Ile	Asp	Pro	Met	Asp	
550					555					560					565	
tgg	gtg	gag	aac	tac	ggc	gcg	gat	gcg	ttg	cgc	ttc	acc	ctt	gcc	cgt	1843
Trp	Val	Glu	Asn	Tyr	Gly	Ala	Asp	Ala	Leu	Arg	Phe	Thr	Leu	Ala	Arg	
				570					575					580		
ggc	gct	aac	cca	ggc	gtc	gac	ctg	cct	gtc	ggt	gaa	gac	tct	gca	cag	1891
Gly	Ala	Asn	Pro	Gly	Val	Asp	Leu	Pro	Val	Gly	Glu	Asp	Ser	Ala	Gln	
			585					590					595			
agc	tcc	cgt	aac	ttt	gcc	acc	aag	ctg	ttc	aac	gca	acc	aag	ttt	gcg	1939
Ser	Ser	Arg	Asn	Phe	Ala	Thr	Lys	Leu	Phe	Asn	Ala	Thr	Lys	Phe	Ala	
		600					605					610				
ctg	atg	aac	ggt	gca	gtg	tcc	gaa	ggc	ctg	cca	gca	cgt	gaa	gaa	ctc	1987
Leu	Met	Asn	Gly	Ala	Val	Ser	Glu	Gly	Leu	Pro	Ala	Arg	Glu	Glu	Leu	

615	620	625	
acc gac gct gac cgc tgg atc gtg gac ctc ctt gag cag gtt cgc ctc			2035
Thr Asp Ala Asp Arg Trp Ile Val Asp Leu Leu Glu Gln Val Arg Leu			
630	635	640	645
gac gtt gat gct tac ctg gac aac tac cag ttc gcg aag gcc aac gag			2083
Asp Val Asp Ala Tyr Leu Asp Asn Tyr Gln Phe Ala Lys Ala Asn Glu			
	650	655	660
gag ctc tac cac ttt gcg tgg aac gag ttc tgt gac tgg tac ctg gaa			2131
Glu Leu Tyr His Phe Ala Trp Asn Glu Phe Cys Asp Trp Tyr Leu Glu			
	665	670	675
atc gcg aag gtt cag atc			2149
Ile Ala Lys Val Gln Ile			
	680		

&lt;210&gt; 348

&lt;211&gt; 683

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 348

Met Val Cys Val Thr Asp Gln Asn Asn Glu Thr Thr Ser Gln Asn Arg			
1	5	10	15
Ala Asp Lys Leu Pro Lys Ser Trp Asp Pro Lys Ala Val Glu Ala Asp			
	20	25	30
Leu Tyr Gln Gly Trp Val Asp Ala Gly Tyr Phe Thr Ala Asp Pro Ala			
	35	40	45
Ser Asp Lys Pro Gly Phe Ser Ile Val Leu Pro Pro Pro Asn Val Thr			
	50	55	60
Gly Gln Leu His Met Gly His Ala Leu Asp His Thr Leu Met Asp Ala			
	65	70	75
Leu Ala Arg Arg Lys Arg Met Gln Gly Phe Glu Val Leu Trp Leu Pro			
	85	90	95
Gly Met Asp His Ala Gly Ile Ala Thr Gln Thr Lys Val Glu Glu Met			
	100	105	110
Leu Lys Glu Thr Glu Gly Lys Thr Arg Tyr Asp Tyr Asp Arg Glu Glu			
	115	120	125
Phe Ile Ala Lys Val Trp Glu Trp Lys Gln Glu Tyr Gly Gly Lys Ile			
	130	135	140
Gly Glu Gln Met Arg Ala Ile Gly Asp Ser Val Asp Trp Ser Arg Glu			
	145	150	155
Arg Phe Thr Leu Asp Asp Gly Leu Ser Arg Ala Val Gln Thr Ile Phe			
	165	170	175
Lys Lys Leu Phe Asp Ala Gly Leu Ile Tyr Gln Ala Asn Arg Leu Val			
	180	185	190

Asn Trp Ser Pro Val Leu Glu Thr Ala Val Ser Asp Ile Glu Val Ile  
 195 200 205  
 Tyr Lys Asp Val Glu Gly Glu Leu Val Ser Ile Arg Tyr Gly Ser Leu  
 210 215 220  
 Asn Asp Asp Glu Pro His Val Ile Val Ala Thr Thr Arg Val Glu Thr  
 225 230 235 240  
 Met Leu Gly Asp Val Ala Val Ala Val His Pro Asp Asp Glu Arg Tyr  
 245 250 255  
 Lys Asp Leu Val Gly Gln Thr Leu Pro His Pro Phe Arg Asp Asp Leu  
 260 265 270  
 Ser Leu Lys Val Val Ala Asp Asp Tyr Val Asp Pro Glu Phe Gly Ser  
 275 280 285  
 Gly Ala Val Lys Ile Thr Pro Ala His Asp Pro Asn Asp Tyr Ala Leu  
 290 295 300  
 Gly Leu Arg His Asn Leu Asp Met Pro Thr Ile Met Asp Lys Thr Gly  
 305 310 315 320  
 Arg Ile Ala Asp Thr Gly Thr Gln Phe Asp Gly Leu Thr Arg Glu Glu  
 325 330 335  
 Ala Arg Ile Lys Val Arg Glu Glu Leu Ala Ala Gln Gly Arg Ile Val  
 340 345 350  
 Lys Glu Ile Arg Pro Tyr Val His Ser Val Gly His Ser Glu Arg Ser  
 355 360 365  
 Gly Glu Ala Ile Glu Pro Arg Leu Ser Leu Gln Trp Phe Val Lys Val  
 370 375 380  
 Glu Glu Leu Ala Lys Met Ser Gly Asp Ala Val Arg Glu Gly Asp Thr  
 385 390 395 400  
 Thr Ile His Pro Lys Ser Leu Glu Pro Arg Tyr Phe Asp Trp Val Asp  
 405 410 415  
 Asn Met His Asp Trp Thr Ile Ser Arg Gln Leu Trp Trp Gly His Arg  
 420 425 430  
 Ile Pro Ile Trp Tyr Gly Pro Asn Asp Glu Ile Ile Cys Val Gly Pro  
 435 440 445  
 Asp Glu Gln Ala Pro Glu Gly Tyr Val Gln Asp Pro Asp Val Leu Asp  
 450 455 460  
 Thr Trp Phe Ser Ser Ala Leu Trp Pro Phe Ser Thr Met Gly Trp Pro  
 465 470 475 480  
 Glu Lys Thr Pro Glu Leu Glu Lys Phe Tyr Pro Thr Ser Val Leu Val  
 485 490 495  
 Thr Ala Tyr Asp Ile Leu Phe Phe Trp Val Ala Arg Met Met Met Phe  
 500 505 510  
 Gly Thr Phe Ala Ala Lys Glu Thr Pro Glu Leu Leu Gly Glu Gly Lys

515	520	525
Asp Gly Arg Pro Gln Val	Pro Phe Thr Asp Leu Phe Leu His Gly Leu	
530	535	540
Val Arg Asp Glu His Gly Arg Lys Met Ser Lys Ser Leu Gly Asn Gly		
545	550	555
Ile Asp Pro Met Asp Trp Val Glu Asn Tyr Gly Ala Asp Ala Leu Arg		
	565	570
Phe Thr Leu Ala Arg Gly Ala Asn Pro Gly Val Asp Leu Pro Val Gly		
	580	585
Glu Asp Ser Ala Gln Ser Ser Arg Asn Phe Ala Thr Lys Leu Phe Asn		
	595	600
Ala Thr Lys Phe Ala Leu Met Asn Gly Ala Val Ser Glu Gly Leu Pro		
	610	615
Ala Arg Glu Glu Leu Thr Asp Ala Asp Arg Trp Ile Val Asp Leu Leu		
	625	630
Glu Gln Val Arg Leu Asp Val Asp Ala Tyr Leu Asp Asn Tyr Gln Phe		
	645	650
Ala Lys Ala Asn Glu Glu Leu Tyr His Phe Ala Trp Asn Glu Phe Cys		
	660	665
Asp Trp Tyr Leu Glu Ile Ala Lys Val Gln Ile		
	675	680

&lt;210&gt; 349

&lt;211&gt; 1416

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1393)

&lt;223&gt; RXN00454

&lt;400&gt; 349

cgctcgatggt cctgatgggc aaggccacgt ggtggatgcc taagtggctg gatcgaattc 60

tgccaagttt	ggacattgaa	ggcaccgcac	tgagagaagga	atg gga gga gaa gca	115
				Met Gly Gly Glu Ala	
				1	5

ggc tgc acg tta gac ttg gca cct atg tca gat ctt tca ttc acc ctc	163
Gly Cys Thr Leu Asp Leu Ala Pro Met Ser Asp Leu Ser Phe Thr Leu	
	10
	15
	20

aac aac aag ctt gcc gat gac gcc ccc ggc aag cat ggt cgt aca ggt	211
Asn Asn Lys Leu Ala Asp Asp Ala Pro Gly Lys His Gly Arg Thr Gly	
	25
	30
	35

gta atc cac aca cct cac ggt gat att gcc acc cct gct ttc att cct	259
Val Ile His Thr Pro His Gly Asp Ile Ala Thr Pro Ala Phe Ile Pro	
	40
	45
	50

gtg gct acc aaa gcc acg gtg aaa acc ctt acc cct gag cag att cgg	307
Val Ala Thr Lys Ala Thr Val Lys Thr Leu Thr Pro Glu Gln Ile Arg	
55 60 65	
gag acc ggc gca cag gct att ttg tcc aac gcc tac cac ctg tat ctg	355
Glu Thr Gly Ala Gln Ala Ile Leu Ser Asn Ala Tyr His Leu Tyr Leu	
70 75 80 85	
cag cct ggc ccc gac atc gtg gac gag gct ggc ggt gtg tct gcc ttt	403
Gln Pro Gly Pro Asp Ile Val Asp Glu Ala Gly Gly Val Ser Ala Phe	
90 95 100	
gag aac tgg cac ggc ccc acc tac acc gac tcc ggc gga ttc cag gtc	451
Glu Asn Trp His Gly Pro Thr Tyr Thr Asp Ser Gly Gly Phe Gln Val	
105 110 115	
atg agc ctg ggc tcc ggc ttt aaa aag gtg ctg gcc atg gac acc acc	499
Met Ser Leu Gly Ser Gly Phe Lys Lys Val Leu Ala Met Asp Thr Thr	
120 125 130	
aac ttg acg cgc aac gat atc aag gcg gct aaa aaa gag cgc atg gcg	547
Asn Leu Thr Arg Asn Asp Ile Lys Ala Ala Lys Lys Glu Arg Met Ala	
135 140 145	
ctt gtc gac gaa gac ggc gtg gat ttc aaa tct gtt atc gat ggc tca	595
Leu Val Asp Glu Asp Gly Val Asp Phe Lys Ser Val Ile Asp Gly Ser	
150 155 160 165	
aag cac cga ttc acc cca gaa gtc tcc atg cag att cag cac caa ttg	643
Lys His Arg Phe Thr Pro Glu Val Ser Met Gln Ile Gln His Gln Leu	
170 175 180	
ggc gca gac atc atc ttt gct ttt gat gaa ctg acc acc ttg gtt gat	691
Gly Ala Asp Ile Ile Phe Ala Phe Asp Glu Leu Thr Thr Leu Val Asp	
185 190 195	
acc tat gac tac cag gtg gaa tct gtg gaa cgt acc cgc agg tgg gca	739
Thr Tyr Asp Tyr Gln Val Glu Ser Val Glu Arg Thr Arg Arg Trp Ala	
200 205 210	
cag cgc tgc ctc ctg gag cat gaa cgt ttg act cag gaa cgt gtg gat	787
Gln Arg Cys Leu Leu Glu His Glu Arg Leu Thr Gln Glu Arg Val Asp	
215 220 225	
aaa cca ctg caa tcc cta tgg gga gtg gtg cag ggc ggc cag ttc gag	835
Lys Pro Leu Gln Ser Leu Trp Gly Val Val Gln Gly Ala Gln Phe Glu	
230 235 240 245	
gat ttg cgt cga caa gca gta aaa ggc ctg ttg gac ctg gat cgc cag	883
Asp Leu Arg Arg Gln Ala Val Lys Gly Leu Leu Asp Leu Asp Arg Gln	
250 255 260	
gcc gcc gac gaa ggc cgt cgc ggc ttc ggc ggt ttc ggc atc ggt ggc	931
Ala Ala Asp Glu Gly Arg Arg Gly Phe Gly Gly Phe Gly Ile Gly Gly	
265 270 275	
gcc cta gag aag gaa aac ctg ggc acc atc gtg ggc tgg gtg tgc gat	979
Ala Leu Glu Lys Glu Asn Leu Gly Thr Ile Val Gly Trp Val Cys Asp	
280 285 290	

gag ctg ccc gag gac aag cca cgt cac ctg ctg ggc att tcc gag ccg 1027  
 Glu Leu Pro Glu Asp Lys Pro Arg His Leu Leu Gly Ile Ser Glu Pro  
 295 300 305  
  
 gac gat ctg ttc gtg gct gtc gaa gcc ggt gcg gac acc ttt gac tgc 1075  
 Asp Asp Leu Phe Val Ala Val Glu Ala Gly Ala Asp Thr Phe Asp Cys  
 310 315 320 325  
  
 gtg gcg ccg act cgt ttg ggt cga cgc ggc ggt gtc tac acg ctt gat 1123  
 Val Ala Pro Thr Arg Leu Gly Arg Arg Gly Gly Val Tyr Thr Leu Asp  
 330 335 340  
  
 gga cgc atg aat ttg acc ggt gcg cgt ttc aag cgt gac ttc aag gga 1171  
 Gly Arg Met Asn Leu Thr Gly Ala Arg Phe Lys Arg Asp Phe Lys Gly  
 345 350 355  
  
 atc gat gag gaa gtc ggc gga tac gcc agc gag aac tac tcc cgc gcg 1219  
 Ile Asp Glu Glu Val Gly Gly Tyr Ala Ser Glu Asn Tyr Ser Arg Ala  
 360 365 370  
  
 tac att cat cac ctg ctc aaa gcg aag gaa ttt ttg gcc ggc acg ctg 1267  
 Tyr Ile His His Leu Leu Lys Ala Lys Glu Phe Leu Ala Gly Thr Leu  
 375 380 385  
  
 tgc acc atg cac aat ctg cac ttc atg atc acc ttg gtg gat aag att 1315  
 Cys Thr Met His Asn Leu His Phe Met Ile Thr Leu Val Asp Lys Ile  
 390 395 400 405  
  
 cgt gcc agc atc gat gat ggc acg tac tac gaa ttc aag gaa gaa ttc 1363  
 Arg Ala Ser Ile Asp Asp Gly Thr Tyr Tyr Glu Phe Lys Glu Glu Phe  
 410 415 420  
  
 tta ggc cgg tac tac gcg tcg aag gtt tca taaccttcgc ggcgtttcac cca 1416  
 Leu Gly Arg Tyr Tyr Ala Ser Lys Val Ser  
 425 430

&lt;210&gt; 350

&lt;211&gt; 431

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 350

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 1 5 10 15  
  
 Leu Ser Phe Thr Leu Asn Asn Lys Leu Ala Asp Asp Ala Pro Gly Lys  
 20 25 30  
  
 His Gly Arg Thr Gly Val Ile His Thr Pro His Gly Asp Ile Ala Thr  
 35 40 45  
  
 Pro Ala Phe Ile Pro Val Ala Thr Lys Ala Thr Val Lys Thr Leu Thr  
 50 55 60  
  
 Pro Glu Gln Ile Arg Glu Thr Gly Ala Gln Ala Ile Leu Ser Asn Ala  
 65 70 75 80  
  
 Tyr His Leu Tyr Leu Gln Pro Gly Pro Asp Ile Val Asp Glu Ala Gly  
 85 90 95

Gly Val Ser Ala Phe Glu Asn Trp His Gly Pro Thr Tyr Thr Asp Ser  
 100 105 110  
 Gly Gly Phe Gln Val Met Ser Leu Gly Ser Gly Phe Lys Lys Val Leu  
 115 120 125  
 Ala Met Asp Thr Thr Asn Leu Thr Arg Asn Asp Ile Lys Ala Ala Lys  
 130 135 140  
 Lys Glu Arg Met Ala Leu Val Asp Glu Asp Gly Val Asp Phe Lys Ser  
 145 150 155 160  
 Val Ile Asp Gly Ser Lys His Arg Phe Thr Pro Glu Val Ser Met Gln  
 165 170 175  
 Ile Gln His Gln Leu Gly Ala Asp Ile Ile Phe Ala Phe Asp Glu Leu  
 180 185 190  
 Thr Thr Leu Val Asp Thr Tyr Asp Tyr Gln Val Glu Ser Val Glu Arg  
 195 200 205  
 Thr Arg Arg Trp Ala Gln Arg Cys Leu Leu Glu His Glu Arg Leu Thr  
 210 215 220  
 Gln Glu Arg Val Asp Lys Pro Leu Gln Ser Leu Trp Gly Val Val Gln  
 225 230 235 240  
 Gly Ala Gln Phe Glu Asp Leu Arg Arg Gln Ala Val Lys Gly Leu Leu  
 245 250 255  
 Asp Leu Asp Arg Gln Ala Ala Asp Glu Gly Arg Arg Gly Phe Gly Gly  
 260 265 270  
 Phe Gly Ile Gly Gly Ala Leu Glu Lys Glu Asn Leu Gly Thr Ile Val  
 275 280 285  
 Gly Trp Val Cys Asp Glu Leu Pro Glu Asp Lys Pro Arg His Leu Leu  
 290 295 300  
 Gly Ile Ser Glu Pro Asp Asp Leu Phe Val Ala Val Glu Ala Gly Ala  
 305 310 315 320  
 Asp Thr Phe Asp Cys Val Ala Pro Thr Arg Leu Gly Arg Arg Gly Gly  
 325 330 335  
 Val Tyr Thr Leu Asp Gly Arg Met Asn Leu Thr Gly Ala Arg Phe Lys  
 340 345 350  
 Arg Asp Phe Lys Gly Ile Asp Glu Glu Val Gly Gly Tyr Ala Ser Glu  
 355 360 365  
 Asn Tyr Ser Arg Ala Tyr Ile His His Leu Leu Lys Ala Lys Glu Phe  
 370 375 380  
 Leu Ala Gly Thr Leu Cys Thr Met His Asn Leu His Phe Met Ile Thr  
 385 390 395 400  
 Leu Val Asp Lys Ile Arg Ala Ser Ile Asp Asp Gly Thr Tyr Tyr Glu  
 405 410 415  
 Phe Lys Glu Glu Phe Leu Gly Arg Tyr Tyr Ala Ser Lys Val Ser

420

425

430

<210> 351  
 <211> 864  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(864)  
 <223> FRXA00454

<400> 351  
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 Gly Asp Ile Ala Thr Pro Ala Phe Ile Pro Val Ala Thr Lys Ala Thr  
 1 5 10 15  
 gtg aaa acc ctt acc cct gag cag att cgg gag acc ggc gca cag gct 96  
 Val Lys Thr Leu Thr Pro Glu Gln Ile Arg Glu Thr Gly Ala Gln Ala  
 20 25 30  
 att ttg tcc aac gcc tac cac ctg tat ctg cag cct ggc ccc gac atc 144  
 Ile Leu Ser Asn Ala Tyr His Leu Tyr Leu Gln Pro Gly Pro Asp Ile  
 35 40 45  
 gtg gac gag gct ggc ggt gtg tct gcc ttt gag aac tgg cac ggc ccc 192  
 Val Asp Glu Ala Gly Gly Val Ser Ala Phe Glu Asn Trp His Gly Pro  
 50 55 60  
 acc tac acc gac tcc ggc gga ttc cag gtc atg agc ctg ggc tcc ggc 240  
 Thr Tyr Thr Asp Ser Gly Gly Phe Gln Val Met Ser Leu Gly Ser Gly  
 65 70 75 80  
 ttt aaa aag gtg ctg gcc atg gac acc acc aac ttg acg cgc aac gat 288  
 Phe Lys Lys Val Leu Ala Met Asp Thr Thr Asn Leu Thr Arg Asn Asp  
 85 90 95  
 atc aag gcg gct aaa aaa gag cgc atg gcg ctt gtc gac gaa gac ggc 336  
 Ile Lys Ala Ala Lys Lys Glu Arg Met Ala Leu Val Asp Glu Asp Gly  
 100 105 110  
 gtg gat ttc aaa tct gtt atc gat ggc tca aag cac cga ttc acc cca 384  
 Val Asp Phe Lys Ser Val Ile Asp Gly Ser Lys His Arg Phe Thr Pro  
 115 120 125  
 gaa gtc tcc atg cag att cag cac caa ttg ggc gca gac atc atc ttt 432  
 Glu Val Ser Met Gln Ile Gln His Gln Leu Gly Ala Asp Ile Ile Phe  
 130 135 140  
 gct ttt gat gaa ctg acc acc ttg gtt gat acc tat gac tac cag gtg 480  
 Ala Phe Asp Glu Leu Thr Thr Leu Val Asp Thr Tyr Asp Tyr Gln Val  
 145 150 155 160  
 gaa tct gtg gaa cgt acc cgc agg tgg gca cag cgc tgc ctc ctg gag 528  
 Glu Ser Val Glu Arg Thr Arg Arg Trp Ala Gln Arg Cys Leu Leu Glu  
 165 170 175  
 cat gaa cgt ttg act cag gaa cgt gtg gat aaa cca ctg caa tcc cta 576  
 His Glu Arg Leu Thr Gln Glu Arg Val Asp Lys Pro Leu Gln Ser Leu  
 180 185 190

<400> 352															
Gly 1	Asp	Ile	Ala	Thr 5	Pro	Ala	Phe	Ile	Pro 10	Val	Ala	Thr	Lys	Ala 15	Thr
Val	Lys	Thr	Leu 20	Thr	Pro	Glu	Gln	Ile 25	Arg	Glu	Thr	Gly	Ala 30	Gln	Ala
Ile	Leu	Ser 35	Asn	Ala	Tyr	His	Leu 40	Tyr	Leu	Gln	Pro	Gly 45	Pro	Asp	Ile
Val	Asp 50	Glu	Ala	Gly	Gly	Val 55	Ser	Ala	Phe	Glu	Asn 60	Trp	His	Gly	Pro
Thr 65	Tyr	Thr	Asp	Ser	Gly 70	Gly	Phe	Gln	Val	Met 75	Ser	Leu	Gly	Ser	Gly 80
Phe	Lys	Lys	Val	Leu 85	Ala	Met	Asp	Thr	Thr 90	Asn	Leu	Thr	Arg	Asn 95	Asp
Ile	Lys	Ala	Ala 100	Lys	Lys	Glu	Arg	Met 105	Ala	Leu	Val	Asp	Glu 110	Asp	Gly
Val	Asp	Phe 115	Lys	Ser	Val	Ile	Asp 120	Gly	Ser	Lys	His	Arg 125	Phe	Thr	Pro
Glu 130	Val	Ser	Met	Gln	Ile	Gln 135	His	Gln	Leu	Gly	Ala 140	Asp	Ile	Ile	Phe
Ala 145	Phe	Asp	Glu	Leu 150	Thr	Thr	Leu	Val	Asp 155	Thr	Tyr	Asp	Tyr	Gln	Val 160

<400> 353																
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aatatccact gtttttagact acggcataga ctcaacagac																
											atg	aat	gct	cct	gcc	115
											Met	Asn	Ala	Pro	Ala	
											1				5	
cct aaa cct gga ctc gtg atc gtc gac aag ccc gcc gga atg aca tcc															163	
Pro	Lys	Pro	Gly	Leu	Val	Ile	Val	Asp	Lys	Pro	Ala	Gly	Met	Thr	Ser	
				10					15					20		
cat gac gtg gtg tcc aaa ttg cgc cgc gca ttt tcc acc cgc aaa gta															211	
His	Asp	Val	Val	Ser	Lys	Leu	Arg	Arg	Ala	Phe	Ser	Thr	Arg	Lys	Val	
				25					30					35		
ggc cac gca ggc acc ctc gac ccc atg gca acc ggc gtg tta gtc gtc															259	
Gly	His	Ala	Gly	Thr	Leu	Asp	Pro	Met	Ala	Thr	Gly	Val	Leu	Val	Val	
				40					45					50		
gga att gag cgc gga acc cgc ttc ctg gca cac atg gtg gcc tcc acc															307	
Gly	Ile	Glu	Arg	Gly	Thr	Arg	Phe	Leu	Ala	His	Met	Val	Ala	Ser	Thr	
				55					60					65		
aaa gcc tac gac gcc acc att cga ctc ggc gcc gcc acc agc acc gat															355	
Lys	Ala	Tyr	Asp	Ala	Thr	Ile	Arg	Leu	Gly	Ala	Ala	Thr	Ser	Thr	Asp	

70	75	80	85	
gat gca gaa ggc gag gtt atc tcc aca aca gac gca tcc ggc ctc gac				403
Asp Ala Glu Gly Glu Val Ile Ser Thr Thr Asp Ala Ser Gly Leu Asp	90	95	100	
cac agc acc atc ctt gct gaa atc gtc aac ctc acc ggc gac atc atg				451
His Ser Thr Ile Leu Ala Glu Ile Val Asn Leu Thr Gly Asp Ile Met	105	110	115	
caa aaa ccc acc aaa gtc tcc gcc atc aaa atc gac ggc aaa cgc gcc				499
Gln Lys Pro Thr Lys Val Ser Ala Ile Lys Ile Asp Gly Lys Arg Ala	120	125	130	
cac gaa cgc gtc cgc gac ggc gaa gaa gta gac att ccc gca cgt ccc				547
His Glu Arg Val Arg Asp Gly Glu Glu Val Asp Ile Pro Ala Arg Pro	135	140	145	
gtc acc gtc agc gtc ttt gac gtg ctc gac tac cac gtc gac ggt gaa				595
Val Thr Val Ser Val Phe Asp Val Leu Asp Tyr His Val Asp Gly Glu	150	155	160	165
ttt tat gac tta gat gtg cgc gtc cac tgc tcc tcc ggc acc tac atc				643
Phe Tyr Asp Leu Asp Val Arg Val His Cys Ser Ser Gly Thr Tyr Ile	170	175	180	
cgc gcg ctc gcc cgc gac ctc ggc aac gct ttg cag gtc ggc ggc cac				691
Arg Ala Leu Ala Arg Asp Leu Gly Asn Ala Leu Gln Val Gly Gly His	185	190	195	
ctg acc gcg ctt agg cgc aca gag gtc ggc cct ttt acg ctt aac gac				739
Leu Thr Ala Leu Arg Arg Thr Glu Val Gly Pro Phe Thr Leu Asn Asp	200	205	210	
gcg acc ccc ctc tcc aaa ctc caa gag aat cca gaa ctc tcc ctc aac				787
Ala Thr Pro Leu Ser Lys Leu Gln Glu Asn Pro Glu Leu Ser Leu Asn	215	220	225	
ctc gac cag gca ctc acc cgc agt tac cca gtc ctt gac atc acc gaa				835
Leu Asp Gln Ala Leu Thr Arg Ser Tyr Pro Val Leu Asp Ile Thr Glu	230	235	240	245
gac gaa ggc gtt gac ctg tcc atg ggc aaa tgg ttg gaa cct cgc gga				883
Asp Glu Gly Val Asp Leu Ser Met Gly Lys Trp Leu Glu Pro Arg Gly	250	255	260	
ctg aaa ggc gtc cac gct gca gta aca cca tca gga aaa gcc gtg gcg				931
Leu Lys Gly Val His Ala Ala Val Thr Pro Ser Gly Lys Ala Val Ala	265	270	275	
ctc atc gaa gaa aag ggc aaa cgc ctg gcc acc gtg ttt gtt gct cac				979
Leu Ile Glu Glu Lys Gly Lys Arg Leu Ala Thr Val Phe Val Ala His	280	285	290	
ccc aac act ctt tagttggtct gccagaagcc gat				1014
Pro Asn Thr Leu	295			

&lt;210&gt; 354

&lt;211&gt; 297

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 354

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Met Asn Ala Pro Ala Pro Lys Pro Gly Leu Val Ile Val Asp Lys Pro
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Ala Gly Met Thr Ser His Asp Val Val Ser Lys Leu Arg Arg Ala Phe
          20              25              30

Ser Thr Arg Lys Val Gly His Ala Gly Thr Leu Asp Pro Met Ala Thr
          35              40              45

Gly Val Leu Val Val Gly Ile Glu Arg Gly Thr Arg Phe Leu Ala His
 50              55              60

Met Val Ala Ser Thr Lys Ala Tyr Asp Ala Thr Ile Arg Leu Gly Ala
 65              70              75              80

Ala Thr Ser Thr Asp Asp Ala Glu Gly Glu Val Ile Ser Thr Thr Asp
          85              90              95

Ala Ser Gly Leu Asp His Ser Thr Ile Leu Ala Glu Ile Val Asn Leu
          100              105              110

Thr Gly Asp Ile Met Gln Lys Pro Thr Lys Val Ser Ala Ile Lys Ile
 115              120              125

Asp Gly Lys Arg Ala His Glu Arg Val Arg Asp Gly Glu Glu Val Asp
 130              135              140

Ile Pro Ala Arg Pro Val Thr Val Ser Val Phe Asp Val Leu Asp Tyr
 145              150              155              160

His Val Asp Gly Glu Phe Tyr Asp Leu Asp Val Arg Val His Cys Ser
          165              170              175

Ser Gly Thr Tyr Ile Arg Ala Leu Ala Arg Asp Leu Gly Asn Ala Leu
          180              185              190

Gln Val Gly Gly His Leu Thr Ala Leu Arg Arg Thr Glu Val Gly Pro
 195              200              205

Phe Thr Leu Asn Asp Ala Thr Pro Leu Ser Lys Leu Gln Glu Asn Pro
 210              215              220

Glu Leu Ser Leu Asn Leu Asp Gln Ala Leu Thr Arg Ser Tyr Pro Val
 225              230              235              240

Leu Asp Ile Thr Glu Asp Glu Gly Val Asp Leu Ser Met Gly Lys Trp
          245              250              255

Leu Glu Pro Arg Gly Leu Lys Gly Val His Ala Ala Val Thr Pro Ser
          260              265              270

Gly Lys Ala Val Ala Leu Ile Glu Glu Lys Gly Lys Arg Leu Ala Thr
          275              280              285

Val Phe Val Ala His Pro Asn Thr Leu
 290              295

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aatatccact gtttttagact acggcataga ctcaacagac											atg aat gct cct gcc			115		
											Met Asn Ala Pro Ala			5		
											1					
cct aaa cct gga ctc gtg atc gtc gac aag ccc gcc gga atg aca tcc 163																
Pro Lys Pro Gly Leu Val Ile Val Asp Lys Pro Ala Gly Met Thr Ser																
10 15 20																
cat gac gtg gtg tcc aaa ttg cgc cgc gca ttt tcc acc cgc aaa gta 211																
His Asp Val Val Ser Lys Leu Arg Arg Ala Phe Ser Thr Arg Lys Val																
25 30 35																
ggc cac gca ggc acc ctc gac ccc atg gca acc ggc gtg tta gtc gtc 259																
Gly His Ala Gly Thr Leu Asp Pro Met Ala Thr Gly Val Leu Val Val																
40 45 50																
gga att gag cgc gga acc cgc ttc ctg gca cac atg gtg gcc tcc acc 307																
Gly Ile Glu Arg Gly Thr Arg Phe Leu Ala His Met Val Ala Ser Thr																
55 60 65																
aaa gcc tac gac gcc acc att cga ctc ggc gcc gcc acc agc acc gat 355																
Lys Ala Tyr Asp Ala Thr Ile Arg Leu Gly Ala Ala Thr Ser Thr Asp																
70 75 80 85																
gat gca gaa ggc gag gtt atc tcc aca aca gac gca tcc ggc ctc gac 403																
Asp Ala Glu Gly Glu Val Ile Ser Thr Thr Asp Ala Ser Gly Leu Asp																
90 95 100																
cac agc acc atc ctt gct gaa atc gtc aac ctc acc ggc gac atc atg 451																
His Ser Thr Ile Leu Ala Glu Ile Val Asn Leu Thr Gly Asp Ile Met																
105 110 115																
caa aaa ccc acc aaa gtc tcc gcc atc aaa atc gac ggc aaa cgc gcc 499																
Gln Lys Pro Thr Lys Val Ser Ala Ile Lys Ile Asp Gly Lys Arg Ala																
120 125 130																
cac gaa cgc gtc cgc gac ggc gaa gaa gta gac att ccc gca cgt ccc 547																
His Glu Arg Val Arg Asp Gly Glu Glu Val Asp Ile Pro Ala Arg Pro																
135 140 145																
gtc acc gtc agc gtc ttt gac gtg ctc gac tac cac gtc gac ggt gaa 595																
Val Thr Val Ser Val Phe Asp Val Leu Asp Tyr His Val Asp Gly Glu																
150 155 160 165																
ttt tat gac tta gat gtg cgc gtc cac tgc tcc tcc ggc acc tac atc 643																
Phe Tyr Asp Leu Asp Val Arg Val His Cys Ser Ser Gly Thr Tyr Ile																
170 175 180																

cgc gcg ctc gcc cgc gac ctc ggc aac gct ttg cag gtc ggc ggc cac 691  
 Arg Ala Leu Ala Arg Asp Leu Gly Asn Ala Leu Gln Val Gly Gly His  
 185 190 195

ctg acc gcg ctt agg cgc aca gag gtc ggc cct ttt acg ctt aac gac 739  
 Leu Thr Ala Leu Arg Arg Thr Glu Val Gly Pro Phe Thr Leu Asn Asp  
 200 205 210

gcg acc ccc ctc tcc aaa ctc caa gag aat cca gaa ctc tcc ctc aac 787  
 Ala Thr Pro Leu Ser Lys Leu Gln Glu Asn Pro Glu Leu Ser Leu Asn  
 215 220 225

ctc gac cag gca ctc acc cgc agt tac cca gtc ctt gac atc acc gaa 835  
 Leu Asp Gln Ala Leu Thr Arg Ser Tyr Pro Val Leu Asp Ile Thr Glu  
 230 235 240 245

gac gaa ggc gtt gac ctg tcc atg ggc aaa tgg ttg gaa cct cgc gga 883  
 Asp Glu Gly Val Asp Leu Ser Met Gly Lys Trp Leu Glu Pro Arg Gly  
 250 255 260

ctg aaa ggc gtc cac gct gca gta aca cca tca gga aaa gcc gtg gcg 931  
 Leu Lys Gly Val His Ala Ala Val Thr Pro Ser Gly Lys Ala Val Ala  
 265 270 275

ctc atc gaa gaa aag ggc aaa cgc ctg gcc acc gtg ttt gtt gct cac 979  
 Leu Ile Glu Glu Lys Gly Lys Arg Leu Ala Thr Val Phe Val Ala His  
 280 285 290

ccc aac act ctt tagttggtct gccagaagcc gat 1014  
 Pro Asn Thr Leu  
 295

&lt;210&gt; 356

&lt;211&gt; 297

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 356

Met Asn Ala Pro Ala Pro Lys Pro Gly Leu Val Ile Val Asp Lys Pro  
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Ala Gly Met Thr Ser His Asp Val Val Ser Lys Leu Arg Arg Ala Phe  
 20 25 30

Ser Thr Arg Lys Val Gly His Ala Gly Thr Leu Asp Pro Met Ala Thr  
 35 40 45

Gly Val Leu Val Val Gly Ile Glu Arg Gly Thr Arg Phe Leu Ala His  
 50 55 60

Met Val Ala Ser Thr Lys Ala Tyr Asp Ala Thr Ile Arg Leu Gly Ala  
 65 70 75 80

Ala Thr Ser Thr Asp Asp Ala Glu Gly Glu Val Ile Ser Thr Thr Asp  
 85 90 95

Ala Ser Gly Leu Asp His Ser Thr Ile Leu Ala Glu Ile Val Asn Leu  
 100 105 110

Thr Gly Asp Ile Met Gln Lys Pro Thr Lys Val Ser Ala Ile Lys Ile  
 115 120 125  
 Asp Gly Lys Arg Ala His Glu Arg Val Arg Asp Gly Glu Glu Val Asp  
 130 135 140  
 Ile Pro Ala Arg Pro Val Thr Val Ser Val Phe Asp Val Leu Asp Tyr  
 145 150 155 160  
 His Val Asp Gly Glu Phe Tyr Asp Leu Asp Val Arg Val His Cys Ser  
 165 170 175  
 Ser Gly Thr Tyr Ile Arg Ala Leu Ala Arg Asp Leu Gly Asn Ala Leu  
 180 185 190  
 Gln Val Gly Gly His Leu Thr Ala Leu Arg Arg Thr Glu Val Gly Pro  
 195 200 205  
 Phe Thr Leu Asn Asp Ala Thr Pro Leu Ser Lys Leu Gln Glu Asn Pro  
 210 215 220  
 Glu Leu Ser Leu Asn Leu Asp Gln Ala Leu Thr Arg Ser Tyr Pro Val  
 225 230 235 240  
 Leu Asp Ile Thr Glu Asp Glu Gly Val Asp Leu Ser Met Gly Lys Trp  
 245 250 255  
 Leu Glu Pro Arg Gly Leu Lys Gly Val His Ala Ala Val Thr Pro Ser  
 260 265 270  
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 Val Phe Val Ala His Pro Asn Thr Leu  
 290 295

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<220>  
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 Val Asp Gln Glu Val 5  
 1  
 gac cgc ctt gct tta atg gcg cgc gct cac cag gca att ggt gag ctt 163  
 Asp Arg Leu Ala Leu Met Ala Arg Ala His Gln Ala Ile Gly Glu Leu 20  
 10 15  
 tca gac atc ctt gtg ccc cta gcg gca gca ttt tcc agc aag gga cac 211  
 Ser Asp Ile Leu Val Pro Leu Ala Ala Phe Ser Ser Lys Gly His 35  
 25 30

tcc cta tat ttg gtg ggc ggt tcc gtg agg gat gct ttc tta ggt gag	259
Ser Leu Tyr Leu Val Gly Gly Ser Val Arg Asp Ala Phe Leu Gly Glu	
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Leu Gly His Asp Leu Asp Phe Thr Thr Ser Ala Arg Pro Glu Glu Thr	
55 60 65	
aag gcg atc ctg gat gat tac gcc gat gtg gtg tgg gat acc gga att	355
Lys Ala Ile Leu Asp Asp Tyr Ala Asp Val Val Trp Asp Thr Gly Ile	
70 75 80 85	
gcg ttt ggc acc ctt tct gca gaa aag cat ggt cag cag atc gaa atc	403
Ala Phe Gly Thr Leu Ser Ala Glu Lys His Gly Gln Gln Ile Glu Ile	
90 95 100	
acg aca ttc cgt tct gat ctc tat gac gga aac tcc cgc aac cct gaa	451
Thr Thr Phe Arg Ser Asp Leu Tyr Asp Gly Asn Ser Arg Asn Pro Glu	
105 110 115	
gtg acc ttc ggt gac acc ttg gaa ggc gat ctg att agg cgc gat ttc	499
Val Thr Phe Gly Asp Thr Leu Glu Gly Asp Leu Ile Arg Arg Asp Phe	
120 125 130	
aag gtc aac gcc atg gct gtg gag atc caa gcc gat ggt gaa tta act	547
Lys Val Asn Ala Met Ala Val Glu Ile Gln Ala Asp Gly Glu Leu Thr	
135 140 145	
ttc cac gat cca gtg ggt ggc ttg gaa gat cta ctt acc cac act ttg	595
Phe His Asp Pro Val Gly Gly Leu Glu Asp Leu Leu Thr His Thr Leu	
150 155 160 165	
gat acc cca gct act ccg gaa caa tca ttc aat gat gat cct ctg cga	643
Asp Thr Pro Ala Thr Pro Glu Gln Ser Phe Asn Asp Asp Pro Leu Arg	
170 175 180	
atg ctg cgc gct gcc cgc ttt gtt tcc caa ctg aat ttc acc ctt gca	691
Met Leu Arg Ala Ala Arg Phe Val Ser Gln Leu Asn Phe Thr Leu Ala	
185 190 195	
cca cga gtt att acc gcc atg act gaa atg gcg cag cag att act cgc	739
Pro Arg Val Ile Thr Ala Met Thr Glu Met Ala Gln Gln Ile Thr Arg	
200 205 210	
atc act gtg gaa cgc atg cag gtt gag ttg gac aaa atg atc ctt ggc	787
Ile Thr Val Glu Arg Met Gln Val Glu Leu Asp Lys Met Ile Leu Gly	
215 220 225	
aaa aac cct gag gct ggc att gac ctc atg gtg gag tcc ggt atc gcg	835
Lys Asn Pro Glu Ala Gly Ile Asp Leu Met Val Glu Ser Gly Ile Ala	
230 235 240 245	
cag att att tat ccg gag atc cct gcg atg cag atg act caa gat gaa	883
Gln Ile Ile Tyr Pro Glu Ile Pro Ala Met Gln Met Thr Gln Asp Glu	
250 255 260	
cac atg cag cac aag gat gtg tac gcg cac tcg ttg cag gtg atg cgc	931
His Met Gln His Lys Asp Val Tyr Ala His Ser Leu Gln Val Met Arg	
265 270 275	

caa gcg att gat cag gaa gaa gat ggc cct gac ctg gtg ctt cgt tgg	979
Gln Ala Ile Asp Gln Glu Glu Asp Gly Pro Asp Leu Val Leu Arg Trp	
280 285 290	
gct gct ctg ctt cat gat tgc ggt aag cca gat act cgt gac ttc aat	1027
Ala Ala Leu Leu His Asp Cys Gly Lys Pro Asp Thr Arg Asp Phe Asn	
295 300 305	
gag gaa ggc cgc gtg agc ttc cat cag cat gag gta gtt ggc gcc aag	1075
Glu Glu Gly Arg Val Ser Phe His Gln His Glu Val Val Gly Ala Lys	
310 315 320 325	
ctg gtg agg cga cgg atg cgc aag ctg aag tac tca aag caa atg gtc	1123
Leu Val Arg Arg Arg Met Arg Lys Leu Lys Tyr Ser Lys Gln Met Val	
330 335 340	
ggc gat gtc ggg cag ttg gtg ttc ctg cac atg cgt ttc cat ggt ttc	1171
Gly Asp Val Gly Gln Leu Val Phe Leu His Met Arg Phe His Gly Phe	
345 350 355	
agc gaa ggc cag tgg acg gat tct gca gtg cgt agg tat gcc gca gat	1219
Ser Glu Gly Gln Trp Thr Asp Ser Ala Val Arg Arg Tyr Ala Ala Asp	
360 365 370	
gcg ggt gaa ttg ctg cca cgt ttg cac aag tta gtg cgt gct gat tgc	1267
Ala Gly Glu Leu Leu Pro Arg Leu His Lys Leu Val Arg Ala Asp Cys	
375 380 385	
acc aca aga aat aaa agg aag gca gca cga ctg caa gcc acc tac gat	1315
Thr Thr Arg Asn Lys Arg Lys Ala Ala Arg Leu Gln Ala Thr Tyr Asp	
390 395 400 405	
cat ttg gaa gag cgc atc gcg gag atc gcc gca aag gaa gat ctt gcc	1363
His Leu Glu Glu Arg Ile Ala Glu Ile Ala Ala Lys Glu Asp Leu Ala	
410 415 420	
agg gtg cgc cca gat ttg gat ggc aat gag atc atg gag att ctg aac	1411
Arg Val Arg Pro Asp Leu Asp Gly Asn Glu Ile Met Glu Ile Leu Asn	
425 430 435	
atc caa gcc gga cct gaa gtg ggt aag gcg tgg gcg ttt ttg aag gag	1459
Ile Gln Ala Gly Pro Glu Val Gly Lys Ala Trp Ala Phe Leu Lys Glu	
440 445 450	
ctt cgt ttg gag cgc ggt cct ttg gat cgt gaa gtt gcc atc gca gag	1507
Leu Arg Leu Glu Arg Gly Pro Leu Asp Arg Glu Val Ala Ile Ala Glu	
455 460 465	
ctg aag agc tgg tgg gaa gga gaa aac aat gag tgatttttat gccgacaggt	1560
Leu Lys Ser Trp Trp Glu Gly Glu Asn Asn Glu	
470 475 480	
tgt	1563
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<213> Corynebacterium glutamicum	
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Ala	Ile	Gly	Glu 20	Leu	Ser	Asp	Ile	Leu 25	Val	Pro	Leu	Ala	Ala 30	Ala	Phe
Ser	Ser	Lys 35	Gly	His	Ser	Leu	Tyr 40	Leu	Val	Gly	Gly	Ser 45	Val	Arg	Asp
Ala	Phe 50	Leu	Gly	Glu	Leu	Gly 55	His	Asp	Leu	Asp	Phe	Thr 60	Thr	Ser	Ala
Arg 65	Pro	Glu	Glu	Thr	Lys 70	Ala	Ile	Leu	Asp	Asp 75	Tyr	Ala	Asp	Val	Val 80
Trp	Asp	Thr	Gly	Ile 85	Ala	Phe	Gly	Thr	Leu 90	Ser	Ala	Glu	Lys	His 95	Gly
Gln	Gln	Ile	Glu 100	Ile	Thr	Thr	Phe	Arg 105	Ser	Asp	Leu	Tyr	Asp 110	Gly	Asn
Ser	Arg	Asn 115	Pro	Glu	Val	Thr	Phe	Gly 120	Asp	Thr	Leu	Glu	Gly 125	Asp	Leu
Ile 130	Arg	Arg	Asp	Phe	Lys	Val 135	Asn	Ala	Met	Ala	Val 140	Glu	Ile	Gln	Ala
Asp 145	Gly	Glu	Leu	Thr	Phe 150	His	Asp	Pro	Val	Gly 155	Gly	Leu	Glu	Asp	Leu 160
Leu	Thr	His	Thr	Leu 165	Asp	Thr	Pro	Ala	Thr 170	Pro	Glu	Gln	Ser	Phe 175	Asn
Asp	Asp	Pro	Leu 180	Arg	Met	Leu	Arg	Ala 185	Ala	Arg	Phe	Val	Ser 190	Gln	Leu
Asn	Phe	Thr 195	Leu	Ala	Pro	Arg	Val 200	Ile	Thr	Ala	Met	Thr 205	Glu	Met	Ala
Gln 210	Gln	Ile	Thr	Arg	Ile	Thr 215	Val	Glu	Arg	Met	Gln 220	Val	Glu	Leu	Asp
Lys 225	Met	Ile	Leu	Gly	Lys 230	Asn	Pro	Glu	Ala	Gly 235	Ile	Asp	Leu	Met	Val 240
Glu	Ser	Gly	Ile	Ala 245	Gln	Ile	Ile	Tyr	Pro 250	Glu	Ile	Pro	Ala	Met 255	Gln
Met	Thr	Gln 260	Asp	Glu	His	Met	Gln 265	His	Lys	Asp	Val	Tyr	Ala 270	His	Ser
Leu	Gln	Val 275	Met	Arg	Gln	Ala	Ile 280	Asp	Gln	Glu	Glu	Asp 285	Gly	Pro	Asp
Leu	Val	Leu 290	Arg	Trp	Ala	Ala 295	Leu	Leu	His	Asp	Cys 300	Gly	Lys	Pro	Asp
Thr 305	Arg	Asp	Phe	Asn 310	Glu	Gly	Arg	Val	Ser 315	Phe	His	Gln	His	Glu 320	
Val	Val	Gly	Ala	Lys	Leu	Val	Arg	Arg	Arg	Met	Arg	Lys	Leu	Lys	Tyr

				325						330						335
Ser	Lys	Gln	Met	Val	Gly	Asp	Val	Gly	Gln	Leu	Val	Phe	Leu	His	Met	
			340					345					350			
Arg	Phe	His	Gly	Phe	Ser	Glu	Gly	Gln	Trp	Thr	Asp	Ser	Ala	Val	Arg	
		355					360					365				
Arg	Tyr	Ala	Ala	Asp	Ala	Gly	Glu	Leu	Leu	Pro	Arg	Leu	His	Lys	Leu	
	370					375					380					
Val	Arg	Ala	Asp	Cys	Thr	Thr	Arg	Asn	Lys	Arg	Lys	Ala	Ala	Arg	Leu	
385					390					395					400	
Gln	Ala	Thr	Tyr	Asp	His	Leu	Glu	Glu	Arg	Ile	Ala	Glu	Ile	Ala	Ala	
				405					410					415		
Lys	Glu	Asp	Leu	Ala	Arg	Val	Arg	Pro	Asp	Leu	Asp	Gly	Asn	Glu	Ile	
			420					425					430			
Met	Glu	Ile	Leu	Asn	Ile	Gln	Ala	Gly	Pro	Glu	Val	Gly	Lys	Ala	Trp	
		435					440					445				
Ala	Phe	Leu	Lys	Glu	Leu	Arg	Leu	Glu	Arg	Gly	Pro	Leu	Asp	Arg	Glu	
	450					455					460					
Val	Ala	Ile	Ala	Glu	Leu	Lys	Ser	Trp	Trp	Glu	Gly	Glu	Asn	Asn	Glu	
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(1077)  
 <223> RXN01704

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gct gat cgt gtc gat tcc cgg tgc cca gca gcg gca gca ggt gct ggt	96
Ala Asp Arg Val Asp Ser Arg Cys Pro Ala Ala Ala Ala Gly Ala Gly	
20 25 30	
tgc tgt gac tat gca gaa ctc aac cca act gtg gag ctt gag atc aag	144
Cys Cys Asp Tyr Ala Glu Leu Asn Pro Thr Val Glu Leu Glu Ile Lys	
35 40 45	
tcc cgc gtg ctt cgt gat cag ttg gag cgc atc ggt gga atc gat gag	192
Ser Arg Val Leu Arg Asp Gln Leu Glu Arg Ile Gly Gly Ile Asp Glu	
50 55 60	
ctt cct gaa ttt gag ctt caa gat ctg gag cca aca gct ggt tgg cgt	240
Leu Pro Glu Phe Glu Leu Gln Asp Leu Glu Pro Thr Ala Gly Trp Arg	
65 70 75 80	

acc cgc gtt cgc ctc ggc gtt gat gcg tct ggt cgt gcc ggg ttc cgc	288
Thr Arg Val Arg Leu Gly Val Asp Ala Ser Gly Arg Ala Gly Phe Arg	
85 90 95	
aag ctg aag tcc aat gag ttg gtt act gag gtt gcg tgt tct cag gtt	336
Lys Leu Lys Ser Asn Glu Leu Val Thr Glu Val Ala Cys Ser Gln Val	
100 105 110	
gtg cca gag ctt ctt gag ggc ctt gtg ggt gag ggc gct cgt cgt ttc	384
Val Pro Glu Leu Leu Glu Gly Leu Val Gly Glu Gly Ala Arg Arg Phe	
115 120 125	
acc cct ggc gtg gag atc att gca gct att gat gat gcg ggt cag cgc	432
Thr Pro Gly Val Glu Ile Ile Ala Ala Ile Asp Asp Ala Gly Gln Arg	
130 135 140	
cac gtt gtg gaa tcc cgt aag gct cct cgt ggt cgt cgt act gaa act	480
His Val Val Glu Ser Arg Lys Ala Pro Arg Gly Arg Arg Thr Glu Thr	
145 150 155 160	
gtg ttg aag gtg ctg gaa ggc act ggc gag gtg gag cag aag gta ggc	528
Val Leu Lys Val Leu Glu Gly Thr Gly Glu Val Glu Gln Lys Val Gly	
165 170 175	
gat tac acc tgg aag ttc cca gtt tct tcc ttc tgg cag gcg cac acc	576
Asp Tyr Thr Trp Lys Phe Pro Val Ser Ser Phe Trp Gln Ala His Thr	
180 185 190	
aag gcc cct gcg gcg tat tca gag ttc atc gcc gaa gcg tta acc gga	624
Lys Ala Pro Ala Ala Tyr Ser Glu Phe Ile Ala Glu Ala Leu Thr Gly	
195 200 205	
ttg gaa ctg gtt gac gtc gat aag cgt ggc cct gtt gcg tgg gac ctt	672
Leu Glu Leu Val Asp Val Asp Lys Arg Gly Pro Val Ala Trp Asp Leu	
210 215 220	
tat ggc ggc gtc ggc ctg ttc gcg ccg att atc acc agc aag ctg cag	720
Tyr Gly Gly Val Gly Leu Phe Ala Pro Ile Ile Thr Ser Lys Leu Gln	
225 230 235 240	
gca gct gtc cac tct gtg gag ctg tcc cca ggt tca gcg gag gct ggc	768
Ala Ala Val His Ser Val Glu Leu Ser Pro Gly Ser Ala Glu Ala Gly	
245 250 255	
gaa gag gcg ttg gct ggt ttg cct gtc act ttc cac act ggt cgg gta	816
Glu Glu Ala Leu Ala Gly Leu Pro Val Thr Phe His Thr Gly Arg Val	
260 265 270	
gag ggc atg gcg tcc cag ctg cct tcg cca aac gtg gtt gtt ttg gat	864
Glu Gly Met Ala Ser Gln Leu Pro Ser Pro Asn Val Val Leu Asp	
275 280 285	
cct cct cgc acc ggt gca ggc agt gac gtg ttg aag agc atc gcg gag	912
Pro Pro Arg Thr Gly Ala Gly Ser Asp Val Leu Lys Ser Ile Ala Glu	
290 295 300	
gct aag cct cag ctg gtt atc cac att ggt tgt gac ccg gcg act ttc	960
Ala Lys Pro Gln Leu Val Ile His Ile Gly Cys Asp Pro Ala Thr Phe	
305 310 315 320	
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Ala	Asp	Arg	Val	Asp	Ser	Arg	Cys	Pro	Ala	Ala	Ala	Ala	Gly	Ala	Gly
			20					25					30		
Cys	Cys	Asp	Tyr	Ala	Glu	Leu	Asn	Pro	Thr	Val	Glu	Leu	Glu	Ile	Lys
		35					40					45			
Ser	Arg	Val	Leu	Arg	Asp	Gln	Leu	Glu	Arg	Ile	Gly	Gly	Ile	Asp	Glu
	50					55					60				
Leu	Pro	Glu	Phe	Glu	Leu	Gln	Asp	Leu	Glu	Pro	Thr	Ala	Gly	Trp	Arg
65					70					75					80
Thr	Arg	Val	Arg	Leu	Gly	Val	Asp	Ala	Ser	Gly	Arg	Ala	Gly	Phe	Arg
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Lys	Leu	Lys	Ser	Asn	Glu	Leu	Val	Thr	Glu	Val	Ala	Cys	Ser	Gln	Val
			100					105					110		
Val	Pro	Glu	Leu	Leu	Glu	Gly	Leu	Val	Gly	Glu	Gly	Ala	Arg	Arg	Phe
		115					120					125			
Thr	Pro	Gly	Val	Glu	Ile	Ile	Ala	Ala	Ile	Asp	Asp	Ala	Gly	Gln	Arg
	130					135					140				
His	Val	Val	Glu	Ser	Arg	Lys	Ala	Pro	Arg	Gly	Arg	Arg	Thr	Glu	Thr
145					150					155					160
Val	Leu	Lys	Val	Leu	Glu	Gly	Thr	Gly	Glu	Val	Glu	Gln	Lys	Val	Gly
				165					170					175	
Asp	Tyr	Thr	Trp	Lys	Phe	Pro	Val	Ser	Ser	Phe	Trp	Gln	Ala	His	Thr
			180					185					190		
Lys	Ala	Pro	Ala	Ala	Tyr	Ser	Glu	Phe	Ile	Ala	Glu	Ala	Leu	Thr	Gly
		195					200					205			
Leu	Glu	Leu	Val	Asp	Val	Asp	Lys	Arg	Gly	Pro	Val	Ala	Trp	Asp	Leu
	210					215					220				
Tyr	Gly	Gly	Val	Gly	Leu	Phe	Ala	Pro	Ile	Ile	Thr	Ser	Lys	Leu	Gln

225	230	235	240
Ala Ala Val His Ser Val Glu Leu Ser Pro Gly Ser Ala Glu Ala Gly	245	250	255
Glu Glu Ala Leu Ala Gly Leu Pro Val Thr Phe His Thr Gly Arg Val	260	265	270
Glu Gly Met Ala Ser Gln Leu Pro Ser Pro Asn Val Val Val Leu Asp	275	280	285
Pro Pro Arg Thr Gly Ala Gly Ser Asp Val Leu Lys Ser Ile Ala Glu	290	295	300
Ala Lys Pro Gln Leu Val Ile His Ile Gly Cys Asp Pro Ala Thr Phe	305	310	315
Ala Arg Asp Val Ala Asp Trp Lys Leu Asn Gly Tyr Glu Met Asp Gln	325	330	335
Leu Ala Val Phe Asn Ala Phe Pro Gly Thr His His Phe Glu Thr Ile	340	345	350
Gly Val Phe Val Arg Val Ser	355		

&lt;210&gt; 361

&lt;211&gt; 839

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(816)

&lt;223&gt; FRXA01704

&lt;400&gt; 361

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Asp Ala Ser Gly Arg Ala Gly Phe Arg Lys Leu Lys Ser Asn Glu Leu	
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ggt act gag gtt gcg tgt tct cag gtt gtg cca gag ctt ctt gag ggc	96
Val Thr Glu Val Ala Cys Ser Gln Val Val Pro Glu Leu Leu Glu Gly	
20 25 30	
ctt gtg ggt gag ggc gct cgt cgt ttc acc cct ggc gtg gag atc att	144
Leu Val Gly Glu Gly Ala Arg Arg Phe Thr Pro Gly Val Glu Ile Ile	
35 40 45	
gca gct att gat gat gcg ggt cag cgc cac gtt gtg gaa tcc cgt aag	192
Ala Ala Ile Asp Asp Ala Gly Gln Arg His Val Val Glu Ser Arg Lys	
50 55 60	
gct cct cgt ggt cgt cgt act gaa act gtg ttg aag gtg ctg gaa ggc	240
Ala Pro Arg Gly Arg Arg Thr Glu Thr Val Leu Lys Val Leu Glu Gly	
65 70 75 80	
act ggc gag gtg gag cag aag gta ggc gat tac acc tgg aag ttc cca	288
Thr Gly Glu Val Glu Gln Lys Val Gly Asp Tyr Thr Trp Lys Phe Pro	
85 90 95	

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 Val Ser Ser Phe Trp Gln Ala His Thr Lys Ala Pro Ala Ala Tyr Ser  
 100 105 110

gag ttc atc gcc gaa gcg tta acc gga ttg gaa ctg gtt gac gtc gat 384  
 Glu Phe Ile Ala Glu Ala Leu Thr Gly Leu Glu Leu Val Asp Val Asp  
 115 120 125

aag cgt ggc cct gtt gcg tgg gac ctt tat ggc ggc gtc ggc ctg ttc 432  
 Lys Arg Gly Pro Val Ala Trp Asp Leu Tyr Gly Gly Val Gly Leu Phe  
 130 135 140

gcg ccg att atc acc agc aag ctg cag gca gct gtc cac tct gtg gag 480  
 Ala Pro Ile Ile Thr Ser Lys Leu Gln Ala Ala Val His Ser Val Glu  
 145 150 155 160

ctg tcc cca ggt tca gcg gag gct ggc gaa gag gcg ttg gct ggt ttg 528  
 Leu Ser Pro Gly Ser Ala Glu Ala Gly Glu Glu Ala Leu Ala Gly Leu  
 165 170 175

cct gtc act ttc cac act ggt cgg gta gag ggc atg gcg tcc cag ctg 576  
 Pro Val Thr Phe His Thr Gly Arg Val Glu Gly Met Ala Ser Gln Leu  
 180 185 190

cct tcg cca aac gtg gtt gtt ttg gat cct cct cgc acc ggt gca ggc 624  
 Pro Ser Pro Asn Val Val Val Leu Asp Pro Pro Arg Thr Gly Ala Gly  
 195 200 205

agt gac gtg ttg aag agc atc gcg gag gct aag cct cag ctg gtt atc 672  
 Ser Asp Val Leu Lys Ser Ile Ala Glu Ala Lys Pro Gln Leu Val Ile  
 210 215 220

cac att ggt tgt gac ccg gcg act ttc gct cgc gac gtt gcc gat tgg 720  
 His Ile Gly Cys Asp Pro Ala Thr Phe Ala Arg Asp Val Ala Asp Trp  
 225 230 235 240

aag ctc aac ggc tac gaa atg gat caa ttg gct gtt ttt aac gcg ttc 768  
 Lys Leu Asn Gly Tyr Glu Met Asp Gln Leu Ala Val Phe Asn Ala Phe  
 245 250 255

cct gga act cac cac ttt gag acg att ggt gta ttt gtc cgc gtt tcc 816  
 Pro Gly Thr His His Phe Glu Thr Ile Gly Val Phe Val Arg Val Ser  
 260 265 270

taaggcggat taagccttgg cta 839

&lt;210&gt; 362

&lt;211&gt; 272

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 362

Asp Ala Ser Gly Arg Ala Gly Phe Arg Lys Leu Lys Ser Asn Glu Leu  
 1 5 10 15

Val Thr Glu Val Ala Cys Ser Gln Val Val Pro Glu Leu Leu Glu Gly  
 20 25 30

Leu Val Gly Glu Gly Ala Arg Arg Phe Thr Pro Gly Val Glu Ile Ile

ctccgaaaat cttgattccc accgtctgcg gcttgatgtc gtg acc att ttc ccc 115  
Val Thr Ile Phe Pro  
1 5

gaa tac ctg gat cct ctg cgc cat gcc ctg ctg ggt aag gcg att gag	163
Glu Tyr Leu Asp Pro Leu Arg His Ala Leu Leu Gly Lys Ala Ile Glu	
10 15 20	
gat ggc att ttg gaa gtc ggt gtt cat gat ctt cgg aat tgg gcg acc	211
Asp Gly Ile Leu Glu Val Gly Val His Asp Leu Arg Asn Trp Ala Thr	
25 30 35	
ggc gga cac aag gcc gtc gac gat acc ccg tat ggc ggt ggc ccg ggc	259
Gly Gly His Lys Ala Val Asp Asp Thr Pro Tyr Gly Gly Gly Pro Gly	
40 45 50	
atg gtg atg aag cca gag gtc tgg ggg cca gcg ctt gat gat gtc gcc	307
Met Val Met Lys Pro Glu Val Trp Gly Pro Ala Leu Asp Asp Val Ala	
55 60 65	
gca ggc cgg gtg agc ggt gcg gaa ctc gat tcg gcc tcg ctg cac ctg	355
Ala Gly Arg Val Ser Gly Ala Glu Leu Asp Ser Ala Ser Leu His Leu	
70 75 80 85	
aaa aat gtg cgc cat gat gag ctg ggt ggc gtc gaa aag cgt gct tat	403
Lys Asn Val Arg His Asp Glu Leu Gly Gly Val Glu Lys Arg Ala Tyr	
90 95 100	
gtc gtg gaa gaa gac cgc gac ctg ccg ctg ttg ctg gtg ccc acc ccg	451
Val Val Glu Glu Asp Arg Asp Leu Pro Leu Leu Leu Val Pro Thr Pro	
105 110 115	
gct ggc aag ccg ttc acg cag gcg gat gcg cag gcg tgg tcc aac gag	499
Ala Gly Lys Pro Phe Thr Gln Ala Asp Ala Gln Ala Trp Ser Asn Glu	
120 125 130	
gag cac att gtg ttc gcg tgc ggg cgc tac gag ggc att gac cag cgc	547
Glu His Ile Val Phe Ala Cys Gly Arg Tyr Glu Gly Ile Asp Gln Arg	
135 140 145	
gtt att gat gat gcc gcc aac cgc tac cgc gtg cgc gag gta tcg atc	595
Val Ile Asp Asp Ala Ala Asn Arg Tyr Arg Val Arg Glu Val Ser Ile	
150 155 160 165	
ggc gat tat gtg ctg atc ggc ggg gaa gtg gca gtc ctg gtc atc gcg	643
Gly Asp Tyr Val Leu Ile Gly Gly Glu Val Ala Val Leu Val Ile Ala	
170 175 180	
gaa gcc gtc gtg cgc ctg atc cct ggc gtg ctc gga aac cgt cgt agc	691
Glu Ala Val Val Arg Leu Ile Pro Gly Val Leu Gly Asn Arg Arg Ser	
185 190 195	
cac gaa gaa gac agc ttc tcc gat ggc ctg ctc gaa ggc ccg tcg tac	739
His Glu Glu Asp Ser Phe Ser Asp Gly Leu Leu Glu Gly Pro Ser Tyr	
200 205 210	
aca aag ccg cgc acc tgg cgc gga ctt gac gtc ccc gaa gta cta ttc	787
Thr Lys Pro Arg Thr Trp Arg Gly Leu Asp Val Pro Glu Val Leu Phe	
215 220 225	
tcg ggc aac cac gcc aag gtc gat cgc tgg cga cgc gat cag gcg ctc	835
Ser Gly Asn His Ala Lys Val Asp Arg Trp Arg Arg Asp Gln Ala Leu	
230 235 240 245	

cta cgc acc cag gca att agg cct gag ctt atc gac gca tcc ctc ctc 883  
 Leu Arg Thr Gln Ala Ile Arg Pro Glu Leu Ile Asp Ala Ser Leu Leu  
                   250                  255                  260

gat tcc acc gac ctc aaa gta ttg gga ctg gac aaa tgacagagac 929  
 Asp Ser Thr Asp Leu Lys Val Leu Gly Leu Asp Lys  
                   265                  270

cacacctcaa ccc 942

<210> 364

<211> 273

<212> PRT

<213> Corynebacterium glutamicum

<400> 364

Val Thr Ile Phe Pro Glu Tyr Leu Asp Pro Leu Arg His Ala Leu Leu  
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Gly Lys Ala Ile Glu Asp Gly Ile Leu Glu Val Gly Val His Asp Leu  
                   20                  25                  30

Arg Asn Trp Ala Thr Gly Gly His Lys Ala Val Asp Asp Thr Pro Tyr  
                   35                  40                  45

Gly Gly Gly Pro Gly Met Val Met Lys Pro Glu Val Trp Gly Pro Ala  
                   50                  55                  60

Leu Asp Asp Val Ala Ala Gly Arg Val Ser Gly Ala Glu Leu Asp Ser  
   65                  70                  75                  80

Ala Ser Leu His Leu Lys Asn Val Arg His Asp Glu Leu Gly Gly Val  
                   85                  90                  95

Glu Lys Arg Ala Tyr Val Val Glu Glu Asp Arg Asp Leu Pro Leu Leu  
                   100                  105                  110

Leu Val Pro Thr Pro Ala Gly Lys Pro Phe Thr Gln Ala Asp Ala Gln  
                   115                  120                  125

Ala Trp Ser Asn Glu Glu His Ile Val Phe Ala Cys Gly Arg Tyr Glu  
                   130                  135                  140

Gly Ile Asp Gln Arg Val Ile Asp Asp Ala Ala Asn Arg Tyr Arg Val  
   145                  150                  155                  160

Arg Glu Val Ser Ile Gly Asp Tyr Val Leu Ile Gly Gly Glu Val Ala  
                   165                  170                  175

Val Leu Val Ile Ala Glu Ala Val Val Arg Leu Ile Pro Gly Val Leu  
                   180                  185                  190

Gly Asn Arg Arg Ser His Glu Glu Asp Ser Phe Ser Asp Gly Leu Leu  
                   195                  200                  205

Glu Gly Pro Ser Tyr Thr Lys Pro Arg Thr Trp Arg Gly Leu Asp Val  
                   210                  215                  220

Pro Glu Val Leu Phe Ser Gly Asn His Ala Lys Val Asp Arg Trp Arg  
   225                  230                  235                  240

Arg Asp Gln Ala Leu Leu Arg Thr Gln Ala Ile Arg Pro Glu Leu Ile  
 245 250 255

Asp Ala Ser Leu Leu Asp Ser Thr Asp Leu Lys Val Leu Gly Leu Asp  
 260 265 270

Lys

<210> 365

<211> 1068

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1045)

<223> RXA02243

<400> 365

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 tctgcatggt ttaacaaata atgagtggaa agggcacttc atg cgc cta gtt ttt 115  
 Met Arg Leu Val Phe  
 1 5  
 gcc gga act ccg gaa cct gca gtg gtg gca ctg caa aag ctc att gat 163  
 Ala Gly Thr Pro Glu Pro Ala Val Val Ala Leu Gln Lys Leu Ile Asp  
 10 15 20  
 tcc gat cat gag gtc gtc gct gtg ttg acg caa cca gat gca cgt cgc 211  
 Ser Asp His Glu Val Val Ala Val Leu Thr Gln Pro Asp Ala Arg Arg  
 25 30 35  
 ggc cgt ggt cgt acg ctg cat cct tca gct gtc gcg gag ctt gca cag 259  
 Gly Arg Gly Arg Thr Leu His Pro Ser Ala Val Ala Glu Leu Ala Gln  
 40 45 50  
 cag cac ggt att gag gtg tta aag ccc acc tcc ctg aag gct gat acg 307  
 Gln His Gly Ile Glu Val Leu Lys Pro Thr Ser Leu Lys Ala Asp Thr  
 55 60 65  
 gaa gat ggc caa gca atc cgt cag cgc ttg gct gag ctt gcc ccc gat 355  
 Glu Asp Gly Gln Ala Ile Arg Gln Arg Leu Ala Glu Leu Ala Pro Asp  
 70 75 80 85  
 tgc ttg ccg gtg gtg gca tac gga cag ctg atc acc aag gat ttg ctg 403  
 Cys Leu Pro Val Val Ala Tyr Gly Gln Leu Ile Thr Lys Asp Leu Leu  
 90 95 100  
 gat gtt gcg cca cac ggt tgg gtg aat ctg cac ttt tct ttg ctt cct 451  
 Asp Val Ala Pro His Gly Trp Val Asn Leu His Phe Ser Leu Leu Pro  
 105 110 115  
 gca tgg cgt ggg gcg gcg ccg gtt cag gcg tcg atc cgt gaa ggc gat 499  
 Ala Trp Arg Gly Ala Ala Pro Val Gln Ala Ser Ile Arg Glu Gly Asp  
 120 125 130  
 cag atc act ggt gcc acg acc ttc cgc att gat gag ggc ctg gat acc 547

Gln Ile Thr Gly Ala Thr Thr Phe Arg Ile Asp Glu Gly Leu Asp Thr  
 135 140 145  
 ggc gtg att ttg tcc acc atc gag gac aca att cag ccc acc gat act 595  
 Gly Val Ile Leu Ser Thr Ile Glu Asp Thr Ile Gln Pro Thr Asp Thr  
 150 155 160 165  
 gcg gat gat ctt ctt act cgc ctg gcg tat tca ggc ggt gac ctg ctg 643  
 Ala Asp Asp Leu Leu Thr Arg Leu Ala Tyr Ser Gly Gly Asp Leu Leu  
 170 175 180  
 gtt gag acc atg act ggc ctg gag cag ggc aca atc acc ccg cgc gcc 691  
 Val Glu Thr Met Thr Gly Leu Glu Gln Gly Thr Ile Thr Pro Arg Ala  
 185 190 195  
 cag gaa ggc gag gcc acg tac gcc tca aaa atc acc acc cag gac gcg 739  
 Gln Glu Gly Glu Ala Thr Tyr Ala Ser Lys Ile Thr Thr Gln Asp Ala  
 200 205 210  
 cag att gat tgg tcg aag ccc gcc gag gtc atc gac cgc cac atc agg 787  
 Gln Ile Asp Trp Ser Lys Pro Ala Glu Val Ile Asp Arg His Ile Arg  
 215 220 225  
 gca cat acc cca gga cct ggc gca tgg acc acg ctt gtc gac gcc cgc 835  
 Ala His Thr Pro Gly Pro Gly Ala Trp Thr Thr Leu Val Asp Ala Arg  
 230 235 240 245  
 ctc aag gtc ggg ccc atc agc cac tca ggc gag gtc gaa gta gca gcg 883  
 Leu Lys Val Gly Pro Ile Ser His Ser Gly Glu Val Glu Val Ala Ala  
 250 255 260  
 gac ttg gcg cct ggc gcc atc ctg gcg caa aag aac tcc gtg gtg gtc 931  
 Asp Leu Ala Pro Gly Ala Ile Leu Ala Gln Lys Asn Ser Val Val Val  
 265 270 275  
 gga acg ggc acc aca cca att gtt ctg ggc aat atc caa ccc ccg gga 979  
 Gly Thr Gly Thr Thr Pro Ile Val Leu Gly Asn Ile Gln Pro Pro Gly  
 280 285 290  
 aag aaa atg atg aat gca gca gac tgg gcg cgt ggt gtc caa ctt gat 1027  
 Lys Lys Met Met Asn Ala Ala Asp Trp Ala Arg Gly Val Gln Leu Asp  
 295 300 305  
 cag gaa gcg aaa ttc caa tgagcctaga aaaatccggc gga 1068  
 Gln Glu Ala Lys Phe Gln  
 310 315

&lt;210&gt; 366

&lt;211&gt; 315

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 366

Met Arg Leu Val Phe Ala Gly Thr Pro Glu Pro Ala Val Val Ala Leu  
 1 5 10 15

Gln Lys Leu Ile Asp Ser Asp His Glu Val Val Ala Val Leu Thr Gln  
 20 25 30

Pro Asp Ala Arg Arg Gly Arg Gly Arg Thr Leu His Pro Ser Ala Val

35					40					45					
Ala	Glu	Leu	Ala	Gln	Gln	His	Gly	Ile	Glu	Val	Leu	Lys	Pro	Thr	Ser
50						55					60				
Leu	Lys	Ala	Asp	Thr	Glu	Asp	Gly	Gln	Ala	Ile	Arg	Gln	Arg	Leu	Ala
65					70					75					80
Glu	Leu	Ala	Pro	Asp	Cys	Leu	Pro	Val	Val	Ala	Tyr	Gly	Gln	Leu	Ile
				85					90					95	
Thr	Lys	Asp	Leu	Leu	Asp	Val	Ala	Pro	His	Gly	Trp	Val	Asn	Leu	His
			100					105					110		
Phe	Ser	Leu	Leu	Pro	Ala	Trp	Arg	Gly	Ala	Ala	Pro	Val	Gln	Ala	Ser
		115					120					125			
Ile	Arg	Glu	Gly	Asp	Gln	Ile	Thr	Gly	Ala	Thr	Thr	Phe	Arg	Ile	Asp
	130					135					140				
Glu	Gly	Leu	Asp	Thr	Gly	Val	Ile	Leu	Ser	Thr	Ile	Glu	Asp	Thr	Ile
145					150					155					160
Gln	Pro	Thr	Asp	Thr	Ala	Asp	Asp	Leu	Leu	Thr	Arg	Leu	Ala	Tyr	Ser
				165					170					175	
Gly	Gly	Asp	Leu	Leu	Val	Glu	Thr	Met	Thr	Gly	Leu	Glu	Gln	Gly	Thr
			180					185					190		
Ile	Thr	Pro	Arg	Ala	Gln	Glu	Gly	Glu	Ala	Thr	Tyr	Ala	Ser	Lys	Ile
		195					200					205			
Thr	Thr	Gln	Asp	Ala	Gln	Ile	Asp	Trp	Ser	Lys	Pro	Ala	Glu	Val	Ile
		210				215					220				
Asp	Arg	His	Ile	Arg	Ala	His	Thr	Pro	Gly	Pro	Gly	Ala	Trp	Thr	Thr
225					230					235					240
Leu	Val	Asp	Ala	Arg	Leu	Lys	Val	Gly	Pro	Ile	Ser	His	Ser	Gly	Glu
				245					250					255	
Val	Glu	Val	Ala	Ala	Asp	Leu	Ala	Pro	Gly	Ala	Ile	Leu	Ala	Gln	Lys
			260					265					270		
Asn	Ser	Val	Val	Val	Gly	Thr	Gly	Thr	Thr	Pro	Ile	Val	Leu	Gly	Asn
		275					280					285			
Ile	Gln	Pro	Pro	Gly	Lys	Lys	Met	Met	Asn	Ala	Ala	Asp	Trp	Ala	Arg
	290					295					300				
Gly	Val	Gln	Leu	Asp	Gln	Glu	Ala	Lys	Phe	Gln					
305					310					315					

&lt;210&gt; 367

&lt;211&gt; 1218

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1195)

&lt;223&gt; RXA00217

&lt;400&gt; 367

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ccaaataaaaa gaaattcggg atttcgggaa catgcggata cgctacgttg ttgagattaa 60

ttaagtaaac gtaggcagaa agctttgtag aggggagatc atg cgg gtt ctt gca 115
                                         Met Arg Val Leu Ala
                                         1                               5

gca atg agt gga ggc gtt gat tcc gcc gtc gcg gcg tca cgc gcg gtc 163
Ala Met Ser Gly Gly Val Asp Ser Ala Val Ala Ala Ser Arg Ala Val
                        10                               15                               20

gca gct ggt cat gaa gtg gtt ggc gtg cat ttg gcg ttg tcg caa gat 211
Ala Ala Gly His Glu Val Val Gly Val His Leu Ala Leu Ser Gln Asp
                        25                               30                               35

ccg caa acg gtg cgt gag tct tcg cgc ggt tgc tgc tct ctg gaa gat 259
Pro Gln Thr Val Arg Glu Ser Ser Arg Gly Cys Cys Ser Leu Glu Asp
                        40                               45                               50

tcc gct gat gct cgt cgc gtg tgt gac aag ttg ggt atc ccg ttt tat 307
Ser Ala Asp Ala Arg Arg Val Cys Asp Lys Leu Gly Ile Pro Phe Tyr
                        55                               60                               65

gtc tgg gat ttc tcg gat cgt ttc aag gaa gat gtg atc gac aac ttc 355
Val Trp Asp Phe Ser Asp Arg Phe Lys Glu Asp Val Ile Asp Asn Phe
                        70                               75                               80                               85

att gat tct tac gcg atc ggt gag act cca aac cct tgc ctg cgt tgt 403
Ile Asp Ser Tyr Ala Ile Gly Glu Thr Pro Asn Pro Cys Leu Arg Cys
                        90                               95                               100

aat gag aaa atc aag ttt gcc gcc ttg ctt gag cgt ggc atc gcg ctt 451
Asn Glu Lys Ile Lys Phe Ala Ala Leu Leu Glu Arg Gly Ile Ala Leu
                        105                               110                               115

ggt ttc gat gca gtg gtt acc ggc cac tac gcg cgc ttg acc cag cct 499
Gly Phe Asp Ala Val Val Thr Gly His Tyr Ala Arg Leu Thr Gln Pro
                        120                               125                               130

gct gat ggt ggc gat ggc tac ttg cgt cgc gga gtt gat ccc aac aag 547
Ala Asp Gly Gly Asp Gly Tyr Leu Arg Arg Gly Val Asp Pro Asn Lys
                        135                               140                               145

gat cag tct tac gtg ctt ggt gtg ctt ggc gct cat gag atc gag cac 595
Asp Gln Ser Tyr Val Leu Gly Val Leu Gly Ala His Glu Ile Glu His
                        150                               155                               160                               165

tgc atg ttc cca gtc ggc gat acc atc aag cct gaa atc cgt gaa gaa 643
Cys Met Phe Pro Val Gly Asp Thr Ile Lys Pro Glu Ile Arg Glu Glu
                        170                               175                               180

gcc agt gct gca ggt ttc tct gtg gca aag aag cca gac tcc tac gac 691
Ala Ser Ala Ala Gly Phe Ser Val Ala Lys Lys Pro Asp Ser Tyr Asp
                        185                               190                               195

att tgc ttc att ccg gat ggc aac acc cag gcg ttc ttg ggc aag cac 739
Ile Cys Phe Ile Pro Asp Gly Asn Thr Gln Ala Phe Leu Gly Lys His
                        200                               205                               210

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atc ggt atg cgt ccg ggc atg atc gtg gat cag gaa ggc acg cat ctc 787  
 Ile Gly Met Arg Pro Gly Met Ile Val Asp Gln Glu Gly Thr His Leu  
 215 220 225  
  
 cgt gag cac gct ggt gtc cat gaa ttc acc att ggt cag cgc aag ggc 835  
 Arg Glu His Ala Gly Val His Glu Phe Thr Ile Gly Gln Arg Lys Gly  
 230 235 240 245  
  
 ctt gac att aag gct cca gca gcc gat ggt cgt cca cgt tac gtc acc 883  
 Leu Asp Ile Lys Ala Pro Ala Ala Asp Gly Arg Pro Arg Tyr Val Thr  
 250 255 260  
  
 gat att gat gcc aag acc ggc acc gtc acc gtt ggt act cgc gaa aac 931  
 Asp Ile Asp Ala Lys Thr Gly Thr Val Thr Val Gly Thr Arg Glu Asn  
 265 270 275  
  
 cta aag atc agc acc atc cac gcc gat cgt ttg aag ttc ctc cat cca 979  
 Leu Lys Ile Ser Thr Ile His Ala Asp Arg Leu Lys Phe Leu His Pro  
 280 285 290  
  
 gcg atg gac gga cag atc gat tgc gaa gtc cag gtc cgc gca cac ggt 1027  
 Ala Met Asp Gly Gln Ile Asp Cys Glu Val Gln Val Arg Ala His Gly  
 295 300 305  
  
 gga gta gtt tcc tgc tct gcg acg att gat cgt gac gct gat ttc atg 1075  
 Gly Val Val Ser Cys Ser Ala Thr Ile Asp Arg Asp Ala Asp Phe Met  
 310 315 320 325  
  
 gtg ctc aac ctc aat gaa cct ctt cag ggt gtt gct cgc ggc cag gca 1123  
 Val Leu Asn Leu Asn Glu Pro Leu Gln Gly Val Ala Arg Gly Gln Ala  
 330 335 340  
  
 gca gtg ctg tac ctg cct gac gcg gat ggt gac atc gtt ctt gga tca 1171  
 Ala Val Leu Tyr Leu Pro Asp Ala Asp Gly Asp Ile Val Leu Gly Ser  
 345 350 355  
  
 ggc acc atc tgc cac acg gag tct taagaaaatt gggcgcttat ggt 1218  
 Gly Thr Ile Cys His Thr Glu Ser  
 360 365

&lt;210&gt; 368

&lt;211&gt; 365

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 368

Met Arg Val Leu Ala Ala Met Ser Gly Gly Val Asp Ser Ala Val Ala  
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 Ala Ser Arg Ala Val Ala Ala Gly His Glu Val Val Gly Val His Leu  
 20 25 30  
  
 Ala Leu Ser Gln Asp Pro Gln Thr Val Arg Glu Ser Ser Arg Gly Cys  
 35 40 45  
  
 Cys Ser Leu Glu Asp Ser Ala Asp Ala Arg Arg Val Cys Asp Lys Leu  
 50 55 60  
  
 Gly Ile Pro Phe Tyr Val Trp Asp Phe Ser Asp Arg Phe Lys Glu Asp

65						70						75						80
Val	Ile	Asp	Asn	Phe	Ile	Asp	Ser	Tyr	Ala	Ile	Gly	Glu	Thr	Pro	Asn			
				85					90					95				
Pro	Cys	Leu	Arg	Cys	Asn	Glu	Lys	Ile	Lys	Phe	Ala	Ala	Leu	Leu	Glu			
			100					105					110					
Arg	Gly	Ile	Ala	Leu	Gly	Phe	Asp	Ala	Val	Val	Thr	Gly	His	Tyr	Ala			
		115					120					125						
Arg	Leu	Thr	Gln	Pro	Ala	Asp	Gly	Gly	Asp	Gly	Tyr	Leu	Arg	Arg	Gly			
		130				135					140							
Val	Asp	Pro	Asn	Lys	Asp	Gln	Ser	Tyr	Val	Leu	Gly	Val	Leu	Gly	Ala			
				150						155					160			
His	Glu	Ile	Glu	His	Cys	Met	Phe	Pro	Val	Gly	Asp	Thr	Ile	Lys	Pro			
				165					170					175				
Glu	Ile	Arg	Glu	Glu	Ala	Ser	Ala	Ala	Gly	Phe	Ser	Val	Ala	Lys	Lys			
			180					185					190					
Pro	Asp	Ser	Tyr	Asp	Ile	Cys	Phe	Ile	Pro	Asp	Gly	Asn	Thr	Gln	Ala			
		195					200					205						
Phe	Leu	Gly	Lys	His	Ile	Gly	Met	Arg	Pro	Gly	Met	Ile	Val	Asp	Gln			
		210				215					220							
Glu	Gly	Thr	His	Leu	Arg	Glu	His	Ala	Gly	Val	His	Glu	Phe	Thr	Ile			
				230						235					240			
Gly	Gln	Arg	Lys	Gly	Leu	Asp	Ile	Lys	Ala	Pro	Ala	Ala	Asp	Gly	Arg			
				245					250					255				
Pro	Arg	Tyr	Val	Thr	Asp	Ile	Asp	Ala	Lys	Thr	Gly	Thr	Val	Thr	Val			
			260					265					270					
Gly	Thr	Arg	Glu	Asn	Leu	Lys	Ile	Ser	Thr	Ile	His	Ala	Asp	Arg	Leu			
		275					280					285						
Lys	Phe	Leu	His	Pro	Ala	Met	Asp	Gly	Gln	Ile	Asp	Cys	Glu	Val	Gln			
		290				295					300							
Val	Arg	Ala	His	Gly	Gly	Val	Val	Ser	Cys	Ser	Ala	Thr	Ile	Asp	Arg			
				310						315					320			
Asp	Ala	Asp	Phe	Met	Val	Leu	Asn	Leu	Asn	Glu	Pro	Leu	Gln	Gly	Val			
				325					330					335				
Ala	Arg	Gly	Gln	Ala	Ala	Val	Leu	Tyr	Leu	Pro	Asp	Ala	Asp	Gly	Asp			
			340					345					350					
Ile	Val	Leu	Gly	Ser	Gly	Thr	Ile	Cys	His	Thr	Glu	Ser						
		355					360					365						

&lt;210&gt; 369

&lt;211&gt; 735

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

<223> RXA01223

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gcc gcc gag gca gtg gat ttg ctg ctg gcc cag gga tta tct gct gcg 691  
Ala Ala Glu Ala Val Asp Leu Leu Leu Ala Gln Gly Leu Ser Ala Ala  
185 190 195

caa aac gct atc cac agc cgc tagattgcta gagattcccg cac  
 Gln Asn Ala Ile His Ser Arg  
 200

735

<210> 370  
 <211> 204  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 370  
 Met Thr Ser Val Ser Phe Leu Ser Lys Ile Gln Ala Leu Phe Ala Pro  
 1 5 10 15  
 Lys Pro Glu Leu Pro Ala Ala Lys Trp Leu Val Val Gly Leu Gly Asn  
 20 25 30  
 Pro Gly Ala Lys Tyr Glu Ser Thr Arg His Asn Val Gly Tyr Met Cys  
 35 40 45  
 Gln Asp Met Leu Ile Asp Ala His Gln Gln Gln Pro Leu Thr Pro Ala  
 50 55 60  
 Thr Gly Tyr Lys Ala Leu Thr Thr Gln Leu Ala Pro Gly Val Leu Ala  
 65 70 75 80  
 Val Arg Ser Thr Thr Phe Met Asn His Ser Gly Gln Gly Val Ala Pro  
 85 90 95  
 Ile Ala Ala Ala Leu Gly Ile Pro Ala Glu Arg Ile Ile Val Ile His  
 100 105 110  
 Asp Glu Leu Asp Leu Pro Ala Gly Lys Val Arg Leu Lys Lys Gly Gly  
 115 120 125  
 Asn Glu Asn Gly His Asn Gly Leu Lys Ser Leu Thr Glu Glu Leu Gly  
 130 135 140  
 Thr Arg Asp Tyr Leu Arg Val Arg Ile Gly Ile Ser Arg Pro Pro Ala  
 145 150 155 160  
 Gly Met Ala Val Pro Asp Tyr Val Leu Glu Pro Val Asp His Asp Gln  
 165 170 175  
 Pro Gly Ile Glu Leu Ala Ala Glu Ala Val Asp Leu Leu Leu Ala Gln  
 180 185 190  
 Gly Leu Ser Ala Ala Gln Asn Ala Ile His Ser Arg  
 195 200

<210> 371  
 <211> 475  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (9)..(452)  
 <223> RXA01226

&lt;400&gt; 371

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ttgaggtt gca gaa gaa cta gtg tcg cgc agc ttt gga tca ttt agt gtg 50
      Ala Glu Glu Leu Val Ser Arg Ser Phe Gly Ser Phe Ser Val
        1              5              10

cac aag cgc tcc aac acc gat atc gcg cag ctt cct ggg cta att gtg 98
His Lys Arg Ser Asn Thr Asp Ile Ala Gln Leu Pro Gly Leu Ile Val
  15              20              25              30

gcc aag ccg cgc agc ttt atg aac ctg tcg gga act ccg att cgg gcg 146
Ala Lys Pro Arg Ser Phe Met Asn Leu Ser Gly Thr Pro Ile Arg Ala
              35              40              45

ctg tgt gac ttc ttt aag att tcc cca gcc aat gtc atc gtg gtg cat 194
Leu Cys Asp Phe Phe Lys Ile Ser Pro Ala Asn Val Ile Val Val His
              50              55              60

gat gaa ttg gag ctt gat ttc ggc tca gtg aag cta cgt cag ggt ggc 242
Asp Glu Leu Glu Leu Asp Phe Gly Ser Val Lys Leu Arg Gln Gly Gly
      65              70              75

ggg gat cat ggg cac aat ggt ctg aaa tcc acg tcc aaa tct ttg gga 290
Gly Asp His Gly His Asn Gly Leu Lys Ser Thr Ser Lys Ser Leu Gly
      80              85              90

act aag gac tat tgg aag ctc agc atg ggt atc ggt agg cca ccg ggt 338
Thr Lys Asp Tyr Trp Lys Leu Ser Met Gly Ile Gly Arg Pro Pro Gly
      95              100              105              110

cgg atg gat ccg gca agt ttt gtg ttg aag cct ttt ggc aag caa gaa 386
Arg Met Asp Pro Ala Ser Phe Val Leu Lys Pro Phe Gly Lys Gln Glu
              115              120              125

ctg gcg gat att ccc atc atg gcg gct gac gct gca gat ctc gtc gaa 434
Leu Ala Asp Ile Pro Ile Met Ala Ala Asp Ala Ala Asp Leu Val Glu
      130              135              140

aag cat ttg cag cag ggc tagctacttg cgccgcgcct ctt 475
Lys His Leu Gln Gln Gly
      145

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&lt;210&gt; 372

&lt;211&gt; 148

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 372

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Ala Glu Glu Leu Val Ser Arg Ser Phe Gly Ser Phe Ser Val His Lys
  1              5              10              15

Arg Ser Asn Thr Asp Ile Ala Gln Leu Pro Gly Leu Ile Val Ala Lys
      20              25              30

Pro Arg Ser Phe Met Asn Leu Ser Gly Thr Pro Ile Arg Ala Leu Cys
      35              40              45

Asp Phe Phe Lys Ile Ser Pro Ala Asn Val Ile Val Val His Asp Glu
      50              55              60

Leu Glu Leu Asp Phe Gly Ser Val Lys Leu Arg Gln Gly Gly Gly Asp

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65	70	75	80
His Gly His Asn Gly Leu Lys Ser Thr Ser Lys Ser Leu Gly Thr Lys	85	90	95
Asp Tyr Trp Lys Leu Ser Met Gly Ile Gly Arg Pro Pro Gly Arg Met	100	105	110
Asp Pro Ala Ser Phe Val Leu Lys Pro Phe Gly Lys Gln Glu Leu Ala	115	120	125
Asp Ile Pro Ile Met Ala Ala Asp Ala Ala Asp Leu Val Glu Lys His	130	135	140
Leu Gln Gln Gly			
145			
<210> 373			
<211> 1614			
<212> DNA			
<213> Corynebacterium glutamicum			
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<221> CDS			
<222> (101)..(1591)			
<223> RXA00209			
<400> 373			
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ttatggttcc gcagattctg ggtgagggcg actaataatt atg acc aac aag tac			115
		Met Thr Asn Lys Tyr	
		1 5	
ctg gtt gaa ggc tct gaa aac gag ctg acc aca aag acc gca gca gag			163
Leu Val Glu Gly Ser Glu Asn Glu Leu Thr Thr Lys Thr Ala Ala Glu	10	15	20
ctg gca ggt ctt att cat tcc cgc gag gta act tcc cgc gag gtt act			211
Leu Ala Gly Leu Ile His Ser Arg Glu Val Thr Ser Arg Glu Val Thr	25	30	35
caa gcg cac cta gat cgc att gct gcg gtt gac ggc gat att cat gca			259
Gln Ala His Leu Asp Arg Ile Ala Ala Val Asp Gly Asp Ile His Ala	40	45	50
ttt ctc cac gtt ggc cag gag gag gcc ctg aac gcg gcg gat gac gtc			307
Phe Leu His Val Gly Gln Glu Glu Ala Leu Asn Ala Ala Asp Asp Val	55	60	65
gat aag cgt cta gac gct gga gag gca cct gcc tcg gct ttg gct ggc			355
Asp Lys Arg Leu Asp Ala Gly Glu Ala Pro Ala Ser Ala Leu Ala Gly	70	75	80
			85
gtg ccg ctt gcg ctg aag gat gtc ttt acc acc act gat gcg ccg acc			403
Val Pro Leu Ala Leu Lys Asp Val Phe Thr Thr Thr Asp Ala Pro Thr	90	95	100
acg gcg gca tcg aag atg ctt gag ggc tac atg agc cct tat gac gcg			451
Thr Ala Ala Ser Lys Met Leu Glu Gly Tyr Met Ser Pro Tyr Asp Ala			

105										110					115					
act	gtg	acc	cgc	aag	atc	cgt	gag	gct	ggc	atc	cca	att	ttg	ggt	aag	499				
Thr	Val	Thr	Arg	Lys	Ile	Arg	Glu	Ala	Gly	Ile	Pro	Ile	Leu	Gly	Lys					
		120					125					130								
acc	aac	atg	gat	gag	ttt	gcg	atg	ggt	tcc	tcc	act	gag	aac	tcc	gca	547				
Thr	Asn	Met	Asp	Glu	Phe	Ala	Met	Gly	Ser	Ser	Thr	Glu	Asn	Ser	Ala					
	135					140					145									
tac	ggc	cca	acc	cac	aat	ccg	tgg	gat	ctg	gag	cgc	acc	gca	ggt	ggt	595				
Tyr	Gly	Pro	Thr	His	Asn	Pro	Trp	Asp	Leu	Glu	Arg	Thr	Ala	Gly	Gly					
150					155					160					165					
tct	ggt	ggt	ggc	tct	tca	gct	gct	ctt	gct	gca	ggt	cag	gcg	cca	ctt	643				
Ser	Gly	Gly	Gly	Ser	Ser	Ala	Ala	Leu	Ala	Ala	Gly	Gln	Ala	Pro	Leu					
				170					175					180						
gcg	att	ggt	act	gac	act	ggt	gga	tcc	atc	cgt	cag	cca	gct	gcg	ctg	691				
Ala	Ile	Gly	Thr	Asp	Thr	Gly	Gly	Ser	Ile	Arg	Gln	Pro	Ala	Ala	Leu					
			185					190					195							
acc	aac	act	gtc	ggt	gtg	aag	cca	acc	tac	gga	acc	gta	tcc	cgt	tac	739				
Thr	Asn	Thr	Val	Gly	Val	Lys	Pro	Thr	Tyr	Gly	Thr	Val	Ser	Arg	Tyr					
		200					205					210								
ggt	ctg	att	gcg	tgt	gcg	tcc	tcc	ctg	gat	cag	ggt	ggc	cca	acc	gct	787				
Gly	Leu	Ile	Ala	Cys	Ala	Ser	Ser	Leu	Asp	Gln	Gly	Gly	Pro	Thr	Ala					
	215					220					225									
cgt	act	gtt	ctg	gat	acc	gcg	ctt	ttg	cac	gag	gtt	atc	gca	ggc	cac	835				
Arg	Thr	Val	Leu	Asp	Thr	Ala	Leu	Leu	His	Glu	Val	Ile	Ala	Gly	His					
230					235					240					245					
gac	gct	ttt	gat	gcg	acc	tcc	gtg	aat	cgt	ccg	gtt	gct	cct	gtt	gtg	883				
Asp	Ala	Phe	Asp	Ala	Thr	Ser	Val	Asn	Arg	Pro	Val	Ala	Pro	Val	Val					
				250					255					260						
cag	gct	gcc	cgt	gaa	ggc	gcg	aac	ggt	gac	ctg	aaa	ggc	gtg	aag	gtc	931				
Gln	Ala	Ala	Arg	Glu	Gly	Ala	Asn	Gly	Asp	Leu	Lys	Gly	Val	Lys	Val					
			265					270					275							
ggt	gtg	gtc	aag	cag	ttc	gac	cgc	gac	ggc	tac	cag	cct	ggc	gtg	ctt	979				
Gly	Val	Val	Lys	Gln	Phe	Asp	Arg	Asp	Gly	Tyr	Gln	Pro	Gly	Val	Leu					
		280					285					290								
gag	gca	ttc	cac	gct	tct	gtt	gag	cag	atg	cgc	tcc	cag	ggt	gcg	gaa	1027				
Glu	Ala	Phe	His	Ala	Ser	Val	Glu	Gln	Met	Arg	Ser	Gln	Gly	Ala	Glu					
		295				300					305									
atc	gtc	gag	gtt	gat	tgc	cct	cac	ttt	gat	gac	gct	ctt	ggc	gcg	tac	1075				
Ile	Val	Glu	Val	Asp	Cys	Pro	His	Phe	Asp	Asp	Ala	Leu	Gly	Ala	Tyr					
310					315					320					325					
tac	ctg	att	ctt	cct	tgt	gaa	gtt	tcc	tcc	aac	ctc	gcg	cgt	ttt	gac	1123				
Tyr	Leu	Ile	Leu	Pro	Cys	Glu	Val	Ser	Ser	Asn	Leu	Ala	Arg	Phe	Asp					
				330					335					340						
ggc	atg	cgt	tac	ggt	ttg	cgc	gct	ggt	gat	gac	gga	act	cgt	tcc	gcc	1171				
Gly	Met	Arg	Tyr	Gly	Leu	Arg	Ala	Gly	Asp	Asp	Gly	Thr	Arg	Ser	Ala					
			345					350					355							

gat gag gtc atg gcg tac acc cgt gcg cag gga ttc ggc cct gag gtt 1219  
Asp Glu Val Met Ala Tyr Thr Arg Ala Gln Gly Phe Gly Pro Glu Val  
360 365 370  
  
aag cgc cgt atc atc ctc ggc act tac gcg ttg tct gtt ggt tac tac 1267  
Lys Arg Arg Ile Ile Leu Gly Thr Tyr Ala Leu Ser Val Gly Tyr Tyr  
375 380 385  
  
gac gcg tac tac ctg cag gct cag cgc gtt cgt acc ctc att gca cag 1315  
Asp Ala Tyr Tyr Leu Gln Ala Gln Arg Val Arg Thr Leu Ile Ala Gln  
390 395 400 405  
  
gac ttc gcc aag gct tac gag cag gtc gac atc ttg gtg tcc cca acc 1363  
Asp Phe Ala Lys Ala Tyr Glu Gln Val Asp Ile Leu Val Ser Pro Thr  
410 415 420  
  
act cca acc acc gcg ttc aag ctg ggg gag aag gtc acc gat ccg ctg 1411  
Thr Pro Thr Thr Ala Phe Lys Leu Gly Glu Lys Val Thr Asp Pro Leu  
425 430 435  
  
gag atg tac aac ttc gac ttg tgc acc ctg cca ctg aac ctg gct ggt 1459  
Glu Met Tyr Asn Phe Asp Leu Cys Thr Leu Pro Leu Asn Leu Ala Gly  
440 445 450  
  
ctc gcg ggc atg tcc ctg cct tcc ggc ttg gca tca gat act ggt ctg 1507  
Leu Ala Gly Met Ser Leu Pro Ser Gly Leu Ala Ser Asp Thr Gly Leu  
455 460 465  
  
cct gtt ggt ttg cag ctg atg gct cct gct ttc cag gac gat cgt ctc 1555  
Pro Val Gly Leu Gln Leu Met Ala Pro Ala Phe Gln Asp Asp Arg Leu  
470 475 480 485  
  
tac cgc gtc ggc gct gct ttt gaa gct gga cgc aag taggttctaa 1601  
Tyr Arg Val Gly Ala Ala Phe Glu Ala Gly Arg Lys  
490 495  
  
acccttttta aga 1614

&lt;210&gt; 374

&lt;211&gt; 497

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 374

Met Thr Asn Lys Tyr Leu Val Glu Gly Ser Glu Asn Glu Leu Thr Thr  
1 5 10 15  
  
Lys Thr Ala Ala Glu Leu Ala Gly Leu Ile His Ser Arg Glu Val Thr  
20 25 30  
  
Ser Arg Glu Val Thr Gln Ala His Leu Asp Arg Ile Ala Ala Val Asp  
35 40 45  
  
Gly Asp Ile His Ala Phe Leu His Val Gly Gln Glu Glu Ala Leu Asn  
50 55 60  
  
Ala Ala Asp Asp Val Asp Lys Arg Leu Asp Ala Gly Glu Ala Pro Ala  
65 70 75 80

Ser Ala Leu Ala Gly Val Pro Leu Ala Leu Lys Asp Val Phe Thr Thr  
 85 90 95  
 Thr Asp Ala Pro Thr Thr Ala Ala Ser Lys Met Leu Glu Gly Tyr Met  
 100 105 110  
 Ser Pro Tyr Asp Ala Thr Val Thr Arg Lys Ile Arg Glu Ala Gly Ile  
 115 120 125  
 Pro Ile Leu Gly Lys Thr Asn Met Asp Glu Phe Ala Met Gly Ser Ser  
 130 135 140  
 Thr Glu Asn Ser Ala Tyr Gly Pro Thr His Asn Pro Trp Asp Leu Glu  
 145 150 155 160  
 Arg Thr Ala Gly Gly Ser Gly Gly Gly Ser Ser Ala Ala Leu Ala Ala  
 165 170 175  
 Gly Gln Ala Pro Leu Ala Ile Gly Thr Asp Thr Gly Gly Ser Ile Arg  
 180 185 190  
 Gln Pro Ala Ala Leu Thr Asn Thr Val Gly Val Lys Pro Thr Tyr Gly  
 195 200 205  
 Thr Val Ser Arg Tyr Gly Leu Ile Ala Cys Ala Ser Ser Leu Asp Gln  
 210 215 220  
 Gly Gly Pro Thr Ala Arg Thr Val Leu Asp Thr Ala Leu Leu His Glu  
 225 230 235 240  
 Val Ile Ala Gly His Asp Ala Phe Asp Ala Thr Ser Val Asn Arg Pro  
 245 250 255  
 Val Ala Pro Val Val Gln Ala Ala Arg Glu Gly Ala Asn Gly Asp Leu  
 260 265 270  
 Lys Gly Val Lys Val Gly Val Val Lys Gln Phe Asp Arg Asp Gly Tyr  
 275 280 285  
 Gln Pro Gly Val Leu Glu Ala Phe His Ala Ser Val Glu Gln Met Arg  
 290 295 300  
 Ser Gln Gly Ala Glu Ile Val Glu Val Asp Cys Pro His Phe Asp Asp  
 305 310 315 320  
 Ala Leu Gly Ala Tyr Tyr Leu Ile Leu Pro Cys Glu Val Ser Ser Asn  
 325 330 335  
 Leu Ala Arg Phe Asp Gly Met Arg Tyr Gly Leu Arg Ala Gly Asp Asp  
 340 345 350  
 Gly Thr Arg Ser Ala Asp Glu Val Met Ala Tyr Thr Arg Ala Gln Gly  
 355 360 365  
 Phe Gly Pro Glu Val Lys Arg Arg Ile Ile Leu Gly Thr Tyr Ala Leu  
 370 375 380  
 Ser Val Gly Tyr Tyr Asp Ala Tyr Tyr Leu Gln Ala Gln Arg Val Arg  
 385 390 395 400  
 Thr Leu Ile Ala Gln Asp Phe Ala Lys Ala Tyr Glu Gln Val Asp Ile

	405		410		415
Leu Val Ser Pro Thr Thr Pro Thr Thr Ala Phe Lys Leu Gly Glu Lys					
	420		425		430
Val Thr Asp Pro Leu Glu Met Tyr Asn Phe Asp Leu Cys Thr Leu Pro					
	435		440		445
Leu Asn Leu Ala Gly Leu Ala Gly Met Ser Leu Pro Ser Gly Leu Ala					
	450		455		460
Ser Asp Thr Gly Leu Pro Val Gly Leu Gln Leu Met Ala Pro Ala Phe					
465	470		475		480
Gln Asp Asp Arg Leu Tyr Arg Val Gly Ala Ala Phe Glu Ala Gly Arg					
	485		490		495

Lys

<210> 375  
 <211> 420  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(397)  
 <223> RXA00210

<400> 375  
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 cttgtacca ttgtgactag cgaagaggat cagaaaccaa gtg cct gag att tcg 115  
 Val Pro Glu Ile Ser 5  
 1  
 cgc gac cag gtc gct cac ctt gcc aaa ctt tcc aga ctg gcg ctc act 163  
 Arg Asp Gln Val Ala His Leu Ala Lys Leu Ser Arg Leu Ala Leu Thr 20  
 10 15  
 gag gaa gaa ctc gag cag ttt gct gga cag atc gat gac att gtc gga 211  
 Glu Glu Glu Leu Glu Gln Phe Ala Gly Gln Ile Asp Asp Ile Val Gly 35  
 25 30  
 tat gtt tcc gca gtt caa aac gtc gac gcc gca ggt gtt gag cct atg 259  
 Tyr Val Ser Ala Val Gln Asn Val Asp Ala Ala Gly Val Glu Pro Met 50  
 40 45  
 agc cac ccg cac agc atc gcc acc acc atg cgt gaa gat gtc gtg cac 307  
 Ser His Pro His Ser Ile Ala Thr Met Arg Glu Asp Val Val His 65  
 55 60  
 aag acc ctc gat gct gcg gct gcg ttg gac caa gcg ccc gct gtc gag 355  
 Lys Thr Leu Asp Ala Ala Ala Ala Leu Asp Gln Ala Pro Ala Val Glu 85  
 70 75 80  
 gat gga cgt ttt atg gtt ccg cag att ctg ggt gag ggc gac 397  
 Asp Gly Arg Phe Met Val Pro Gln Ile Leu Gly Glu Gly Asp 95  
 90 95

taataattat gaccaacaag tac

420

<210> 376

<211> 99

<212> PRT

<213> Corynebacterium glutamicum

<400> 376

Val Pro Glu Ile Ser Arg Asp Gln Val Ala His Leu Ala Lys Leu Ser  
1 5 10 15

Arg Leu Ala Leu Thr Glu Glu Glu Leu Glu Gln Phe Ala Gly Gln Ile  
20 25 30

Asp Asp Ile Val Gly Tyr Val Ser Ala Val Gln Asn Val Asp Ala Ala  
35 40 45

Gly Val Glu Pro Met Ser His Pro His Ser Ile Ala Thr Thr Met Arg  
50 55 60

Glu Asp Val Val His Lys Thr Leu Asp Ala Ala Ala Leu Asp Gln  
65 70 75 80

Ala Pro Ala Val Glu Asp Gly Arg Phe Met Val Pro Gln Ile Leu Gly  
85 90 95

Glu Gly Asp

<210> 377

<211> 1260

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1237)

<223> RXA02686

<400> 377

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tgggttacaca gcttaaccg ccgaactaag gtgggtgtcc atg tct gtt gct caa 115  
Met Ser Val Ala Gln  
1 5

tta gcg aac cgc ttg gcc caa ctc tcc ccc gcc gag cat ggt ttt gca 163  
Leu Ala Asn Arg Leu Ala Gln Leu Ser Pro Ala Glu His Gly Phe Ala  
10 15 20

tgg ttc gac cct gaa atc acc gct ggc cat ggc gtt ggc ccg ttg cat 211  
Trp Phe Asp Pro Glu Ile Thr Ala Gly His Gly Val Gly Pro Leu His  
25 30 35

ggc atg gtg att cca gcc aag gac ctc aac gat gtc gca ggc atg ccc 259  
Gly Met Val Ile Pro Ala Lys Asp Leu Asn Asp Val Ala Gly Met Pro  
40 45 50

acc gcg ttc gga aat gca tct cgg cga aag gta gca aca gat acc gat	307
Thr Ala Phe Gly Asn Ala Ser Arg Arg Lys Val Ala Thr Asp Thr Asp	
55 60 65	
ccg ttc atc caa aat ctc atc gac cgc ggc gcg atc atc gct ggc aaa	355
Pro Phe Ile Gln Asn Leu Ile Asp Arg Gly Ala Ile Ile Ala Gly Lys	
70 75 80 85	
acc caa acc agc gag ctc ggc atg acg gcg tat tgc gaa ccc atc gac	403
Thr Gln Thr Ser Glu Leu Gly Met Thr Ala Tyr Cys Glu Pro Ile Asp	
90 95 100	
atg gac gca ccc agc aac ccg gtt ttg cct ggt cac acg ccc ggc ggt	451
Met Asp Ala Pro Ser Asn Pro Val Leu Pro Gly His Thr Pro Gly Gly	
105 110 115	
tcg tcg ggt ggt gcg gcg gtt gcc gtt gcc agg tcg ctt gtc gac gcc	499
Ser Ser Gly Gly Ala Ala Val Ala Val Ala Arg Ser Leu Val Asp Ala	
120 125 130	
gcc cac gcc tca gac gga ggc ggc tcg atc cgg gtt cca gcc gcc gcg	547
Ala His Ala Ser Asp Gly Gly Gly Ser Ile Arg Val Pro Ala Ala Ala	
135 140 145	
tgc ggg ctg gtc ggg ttt aaa ccc gcc cac gat tcc agc ggc gga aac	595
Cys Gly Leu Val Gly Phe Lys Pro Ala His Asp Ser Ser Gly Gly Asn	
150 155 160 165	
ccc tcc acg cag ggg ttt atc acc cgc gat gtg gcc acc caa gtg cgc	643
Pro Ser Thr Gln Gly Phe Ile Thr Arg Asp Val Ala Thr Gln Val Arg	
170 175 180	
ttg cac gca ctt caa cca cgc acc agg cgc ctg cgc atc ggc gtt ctc	691
Leu His Ala Leu Gln Pro Arg Thr Arg Arg Leu Arg Ile Gly Val Leu	
185 190 195	
gct gag ccc atc cat gct aat tcg ctt gtc gac gcc ccc ttc ctg agc	739
Ala Glu Pro Ile His Ala Asn Ser Leu Val Asp Ala Pro Phe Leu Ser	
200 205 210	
atc ctc gaa tcc acc gcc cac ctc ctg gag aaa gct ggc cac gaa ata	787
Ile Leu Glu Ser Thr Ala His Leu Leu Glu Lys Ala Gly His Glu Ile	
215 220 225	
gtg tcc gta ccc ctc cct tat ggc gct tgg gct ttt gac gct tat aca	835
Val Ser Val Pro Leu Pro Tyr Gly Ala Trp Ala Phe Asp Ala Tyr Thr	
230 235 240 245	
gaa gtt ttc atg atg aaa tcc gct gga cta acc aac ctg ggt agc ccc	883
Glu Val Phe Met Met Lys Ser Ala Gly Leu Thr Asn Leu Gly Ser Pro	
250 255 260	
att aca aga tgg ttg agt gaa caa ggc cgt agt ctt tct cct tct gat	931
Ile Thr Arg Trp Leu Ser Glu Gln Gly Arg Ser Leu Ser Pro Ser Asp	
265 270 275	
aga caa tca agt gtc aag gct ttt gat tcc gtg gct gag act gta cac	979
Arg Gln Ser Ser Val Lys Ala Phe Asp Ser Val Ala Glu Thr Val His	
280 285 290	
gga gca tgg gac atc gat gtt tta tta acc cct acc ttg gct tat gca	1027

Gly Ala Trp Asp Ile Asp Val Leu Leu Thr Pro Thr Leu Ala Tyr Ala  
 295 300 305  
 cct ccc aag att ggg tac ttt tca tcc atg cca cct gaa gaa gac ttc 1075  
 Pro Pro Lys Ile Gly Tyr Phe Ser Ser Met Pro Pro Glu Glu Asp Phe  
 310 315 320 325  
 ctt gca caa acc aaa tgg acg ccg tgg gca acg ctg ttc aac atg acc 1123  
 Leu Ala Gln Thr Lys Trp Thr Pro Trp Ala Thr Leu Phe Asn Met Thr  
 330 335 340  
 ggt ggt gca gcc atc agc gtg cct gtt gaa ggt gtc ggc att cat ctt 1171  
 Gly Gly Ala Ala Ile Ser Val Pro Val Glu Gly Val Gly Ile His Leu  
 345 350 355  
 ggt ggg ata cgc gta cga gat gaa gac ctc tta gga tta gca gca ttt 1219  
 Gly Gly Ile Arg Val Arg Asp Glu Asp Leu Leu Gly Leu Ala Ala Phe  
 360 365 370  
 gtg gaa aga gct gtg gca tgagtagttc agtaatgtca ccg 1260  
 Val Glu Arg Ala Val Ala  
 375

&lt;210&gt; 378

&lt;211&gt; 379

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 378

Met Ser Val Ala Gln Leu Ala Asn Arg Leu Ala Gln Leu Ser Pro Ala  
 1 5 10 15  
 Glu His Gly Phe Ala Trp Phe Asp Pro Glu Ile Thr Ala Gly His Gly  
 20 25 30  
 Val Gly Pro Leu His Gly Met Val Ile Pro Ala Lys Asp Leu Asn Asp  
 35 40 45  
 Val Ala Gly Met Pro Thr Ala Phe Gly Asn Ala Ser Arg Arg Lys Val  
 50 55 60  
 Ala Thr Asp Thr Asp Pro Phe Ile Gln Asn Leu Ile Asp Arg Gly Ala  
 65 70 75 80  
 Ile Ile Ala Gly Lys Thr Gln Thr Ser Glu Leu Gly Met Thr Ala Tyr  
 85 90 95  
 Cys Glu Pro Ile Asp Met Asp Ala Pro Ser Asn Pro Val Leu Pro Gly  
 100 105 110  
 His Thr Pro Gly Gly Ser Ser Gly Gly Ala Ala Val Ala Val Ala Arg  
 115 120 125  
 Ser Leu Val Asp Ala Ala His Ala Ser Asp Gly Gly Gly Ser Ile Arg  
 130 135 140  
 Val Pro Ala Ala Ala Cys Gly Leu Val Gly Phe Lys Pro Ala His Asp  
 145 150 155 160  
 Ser Ser Gly Gly Asn Pro Ser Thr Gln Gly Phe Ile Thr Arg Asp Val

165										170					175				
Ala	Thr	Gln	Val	Arg	Leu	His	Ala	Leu	Gln	Pro	Arg	Thr	Arg	Arg	Leu				
			180						185					190					
Arg	Ile	Gly	Val	Leu	Ala	Glu	Pro	Ile	His	Ala	Asn	Ser	Leu	Val	Asp				
		195					200					205							
Ala	Pro	Phe	Leu	Ser	Ile	Leu	Glu	Ser	Thr	Ala	His	Leu	Leu	Glu	Lys				
	210					215					220								
Ala	Gly	His	Glu	Ile	Val	Ser	Val	Pro	Leu	Pro	Tyr	Gly	Ala	Trp	Ala				
225					230					235					240				
Phe	Asp	Ala	Tyr	Thr	Glu	Val	Phe	Met	Met	Lys	Ser	Ala	Gly	Leu	Thr				
				245					250					255					
Asn	Leu	Gly	Ser	Pro	Ile	Thr	Arg	Trp	Leu	Ser	Glu	Gln	Gly	Arg	Ser				
			260					265					270						
Leu	Ser	Pro	Ser	Asp	Arg	Gln	Ser	Ser	Val	Lys	Ala	Phe	Asp	Ser	Val				
		275					280					285							
Ala	Glu	Thr	Val	His	Gly	Ala	Trp	Asp	Ile	Asp	Val	Leu	Leu	Thr	Pro				
	290					295					300								
Thr	Leu	Ala	Tyr	Ala	Pro	Pro	Lys	Ile	Gly	Tyr	Phe	Ser	Ser	Met	Pro				
305					310					315				320					
Pro	Glu	Glu	Asp	Phe	Leu	Ala	Gln	Thr	Lys	Trp	Thr	Pro	Trp	Ala	Thr				
			325						330					335					
Leu	Phe	Asn	Met	Thr	Gly	Gly	Ala	Ala	Ile	Ser	Val	Pro	Val	Glu	Gly				
		340						345					350						
Val	Gly	Ile	His	Leu	Gly	Gly	Ile	Arg	Val	Arg	Asp	Glu	Asp	Leu	Leu				
	355						360					365							
Gly	Leu	Ala	Ala	Phe	Val	Glu	Arg	Ala	Val	Ala									
	370					375													

&lt;210&gt; 379

&lt;211&gt; 886

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(886)

&lt;223&gt; RXA02625

&lt;400&gt; 379

ctcaattaag cagcaatccg agccggggga gcgctgtcag aaatggaccg tgccacccca 60

tgacaacatg	cttgacacaat	gatgactaga	ataatgaccc	atg	act	gca	gcc	ttt	115
				Met	Thr	Ala	Ala	Phe	
				1				5	

tat	gat	ctg	atg	gac	ttc	gat	gaa	gtt	cta	gag	aaa	tat	gac	ccg	gtg	163
Tyr	Asp	Leu	Met	Asp	Phe	Asp	Glu	Val	Leu	Glu	Lys	Tyr	Asp	Pro	Val	

10										15					20					
atg gga ctt gag gtc cac gtc gaa ctg ggc act gag acc aag atg ttc	211																			
Met Gly Leu Glu Val His Val Glu Leu Gly Thr Glu Thr Lys Met Phe																				
25 30 35																				
tct gca tct tct gca cac ttt ggc gct gaa ccc aat agc aat gtt gac	259																			
Ser Ala Ser Ser Ala His Phe Gly Ala Glu Pro Asn Ser Asn Val Asp																				
40 45 50																				
cca gtt tct ttg ggt ctc cca ggc gca ctt cct gtg gtt aac gcc aag	307																			
Pro Val Ser Leu Gly Leu Pro Gly Ala Leu Pro Val Val Asn Ala Lys																				
55 60 65																				
ggc gtg gag tgg gca att aag att gga ctg gcg ctg aac tgc agc atc	355																			
Gly Val Glu Trp Ala Ile Lys Ile Gly Leu Ala Leu Asn Cys Ser Ile																				
70 75 80 85																				
gct gag tcc tca cgc ttt gca cgt aag aac tac ttc tac ccg gat cag	403																			
Ala Glu Ser Ser Arg Phe Ala Arg Lys Asn Tyr Phe Tyr Pro Asp Gln																				
90 95 100																				
cct aag aac tac cag atc tcc cag tat gac gag cca atc gca tac gac	451																			
Pro Lys Asn Tyr Gln Ile Ser Gln Tyr Asp Glu Pro Ile Ala Tyr Asp																				
105 110 115																				
ggc tac ctg gat gtt gtt ctg gag gac ggc acc gag tgg cgt gtg gaa	499																			
Gly Tyr Leu Asp Val Val Leu Glu Asp Gly Thr Glu Trp Arg Val Glu																				
120 125 130																				
atc gaa cgc gct cac atg gag gaa gac acc gga aag ctc acc cac ctg	547																			
Ile Glu Arg Ala His Met Glu Glu Asp Thr Gly Lys Leu Thr His Leu																				
135 140 145																				
ggt ggt act tct ggt cgt att cac ggc gca acc gct tct ttg gtg gac	595																			
Gly Gly Thr Ser Gly Arg Ile His Gly Ala Thr Ala Ser Leu Val Asp																				
150 155 160 165																				
tgc aac cgt gca ggc gtc cct ttg att gag gtt gtc acc aag cca atc	643																			
Cys Asn Arg Ala Gly Val Pro Leu Ile Glu Val Val Thr Lys Pro Ile																				
170 175 180																				
gaa ggc gct ggc gct cgc gct cca gag atc gct aag gct tat gtc tcc	691																			
Glu Gly Ala Gly Ala Arg Ala Pro Glu Ile Ala Lys Ala Tyr Val Ser																				
185 190 195																				
gca ctg cgc gat ctg gtt aag gcg ctc ggt gtg tcc gac ggc cgc ttg	739																			
Ala Leu Arg Asp Leu Val Lys Ala Leu Gly Val Ser Asp Gly Arg Leu																				
200 205 210																				
gat cag ggt tct atg cgt gtc gac gcc aac ctg tcc ctg cgc ccg atc	787																			
Asp Gln Gly Ser Met Arg Val Asp Ala Asn Leu Ser Leu Arg Pro Ile																				
215 220 225																				
ggc cag gag gaa ttc ggc acc cgt acc gaa acc aag aac atc aac tcc	835																			
Gly Gln Glu Glu Phe Gly Thr Arg Thr Glu Thr Lys Asn Ile Asn Ser																				
230 235 240 245																				
ctg aag tcc gtt gag cag gcc agc acc ttt gag atg cag cgc cag gct	883																			
Leu Lys Ser Val Glu Gln Ala Ser Thr Phe Glu Met Gln Arg Gln Ala																				
250 255 260																				

cag  
Gln

886

<210> 380  
<211> 262  
<212> PRT  
<213> *Corynebacterium glutamicum*

<400> 380  
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Lys Tyr Asp Pro Val Met Gly Leu Glu Val His Val Glu Leu Gly Thr  
20 25 30  
Glu Thr Lys Met Phe Ser Ala Ser Ser Ala His Phe Gly Ala Glu Pro  
35 40 45  
Asn Ser Asn Val Asp Pro Val Ser Leu Gly Leu Pro Gly Ala Leu Pro  
50 55 60  
Val Val Asn Ala Lys Gly Val Glu Trp Ala Ile Lys Ile Gly Leu Ala  
65 70 75 80  
Leu Asn Cys Ser Ile Ala Glu Ser Ser Arg Phe Ala Arg Lys Asn Tyr  
85 90 95  
Phe Tyr Pro Asp Gln Pro Lys Asn Tyr Gln Ile Ser Gln Tyr Asp Glu  
100 105 110  
Pro Ile Ala Tyr Asp Gly Tyr Leu Asp Val Val Leu Glu Asp Gly Thr  
115 120 125  
Glu Trp Arg Val Glu Ile Glu Arg Ala His Met Glu Glu Asp Thr Gly  
130 135 140  
Lys Leu Thr His Leu Gly Gly Thr Ser Gly Arg Ile His Gly Ala Thr  
145 150 155 160  
Ala Ser Leu Val Asp Cys Asn Arg Ala Gly Val Pro Leu Ile Glu Val  
165 170 175  
Val Thr Lys Pro Ile Glu Gly Ala Gly Ala Arg Ala Pro Glu Ile Ala  
180 185 190  
Lys Ala Tyr Val Ser Ala Leu Arg Asp Leu Val Lys Ala Leu Gly Val  
195 200 205  
Ser Asp Gly Arg Leu Asp Gln Gly Ser Met Arg Val Asp Ala Asn Leu  
210 215 220  
Ser Leu Arg Pro Ile Gly Gln Glu Glu Phe Gly Thr Arg Thr Glu Thr  
225 230 235 240  
Lys Asn Ile Asn Ser Leu Lys Ser Val Glu Gln Ala Ser Thr Phe Glu  
245 250 255  
Met Gln Arg Gln Ala Gln

260

<210> 381  
 <211> 659  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(636)  
 <223> RXA01398

<400> 381  
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 Lys Glu Thr Ala Glu Asp Tyr Arg Tyr Phe Asn Asp Pro Asp Leu Pro  
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 cca gtg att gcg cct cgt gag tgg gtg gaa gaa atc cgc gca act ctt 96  
 Pro Val Ile Ala Pro Arg Glu Trp Val Glu Glu Ile Arg Ala Thr Leu  
 20 25 30  
 cca gag ctg cct tgg gtt cgc cgt gca cgt atc cag gaa gag tgg aag 144  
 Pro Glu Leu Pro Trp Val Arg Arg Ala Arg Ile Gln Glu Glu Trp Lys  
 35 40 45  
 ctt tcc gac gcc gag atg cgc gac ctc atc aac gcc aac gcg ctc gac 192  
 Leu Ser Asp Ala Glu Met Arg Asp Leu Ile Asn Ala Asn Ala Leu Asp  
 50 55 60  
 ctc atc atc gag acc gtg gaa gcg ggt acc act cct gat gaa gct cgt 240  
 Leu Ile Ile Glu Thr Val Glu Ala Gly Thr Thr Pro Asp Glu Ala Arg  
 65 70 75 80  
 gct tgg tgg gtt tct tac atc tct cag aag gct aac gag tct ggt gtc 288  
 Ala Trp Trp Val Ser Tyr Ile Ser Gln Lys Ala Asn Glu Ser Gly Val  
 85 90 95  
 gag ctc gat gct ctc ggt gtt gcg cca gct cac gtt gct cgc gtc gtt 336  
 Glu Leu Asp Ala Leu Gly Val Ala Pro Ala His Val Ala Arg Val Val  
 100 105 110  
 gcg ctt gtt tct gaa ggc aag ctg acc aat aag ctg gca cgt cag gct 384  
 Ala Leu Val Ser Glu Gly Lys Leu Thr Asn Lys Leu Ala Arg Gln Ala  
 115 120 125  
 atc gac ggc gtt att gct ggc gaa ggc gat gtg gac gcg gtt gtt gct 432  
 Ile Asp Gly Val Ile Ala Gly Glu Gly Asp Val Asp Ala Val Val Ala  
 130 135 140  
 gct cgt gga ctg gaa gtt gtt cgc gat gac ggc gca att gaa aag gct 480  
 Ala Arg Gly Leu Glu Val Val Arg Asp Asp Gly Ala Ile Glu Lys Ala  
 145 150 155 160  
 gtc gat gat gcc ttg gct gca aac cca gac atc gtg gag aag tac cgc 528  
 Val Asp Asp Ala Leu Ala Ala Asn Pro Asp Ile Val Glu Lys Tyr Arg  
 165 170 175  
 gct ggc aac acc aag gtc acc ggc gcc atc gtt ggt gct gtc atg aag 576  
 Ala Gly Asn Thr Lys Val Thr Gly Ala Ile Val Gly Ala Val Met Lys  
 180 185 190

gcg acc cgc ggt aag gct gac cca gct cag gtg aac cag ctg atc gca 624  
 Ala Thr Arg Gly Lys Ala Asp Pro Ala Gln Val Asn Gln Leu Ile Ala  
           195                          200                          205

aag aag ttg gct taagcttttt gccgttgagc tgc 659  
 Lys Lys Leu Ala  
           210

<210> 382

<211> 212

<212> PRT

<213> Corynebacterium glutamicum

<400> 382

Lys Glu Thr Ala Glu Asp Tyr Arg Tyr Phe Asn Asp Pro Asp Leu Pro  
       1                          5                          10                          15

Pro Val Ile Ala Pro Arg Glu Trp Val Glu Glu Ile Arg Ala Thr Leu  
                           20                          25                          30

Pro Glu Leu Pro Trp Val Arg Arg Ala Arg Ile Gln Glu Glu Trp Lys  
                           35                          40                          45

Leu Ser Asp Ala Glu Met Arg Asp Leu Ile Asn Ala Asn Ala Leu Asp  
       50                          55                          60

Leu Ile Ile Glu Thr Val Glu Ala Gly Thr Thr Pro Asp Glu Ala Arg  
       65                          70                          75                          80

Ala Trp Trp Val Ser Tyr Ile Ser Gln Lys Ala Asn Glu Ser Gly Val  
                           85                          90                          95

Glu Leu Asp Ala Leu Gly Val Ala Pro Ala His Val Ala Arg Val Val  
                           100                          105                          110

Ala Leu Val Ser Glu Gly Lys Leu Thr Asn Lys Leu Ala Arg Gln Ala  
                           115                          120                          125

Ile Asp Gly Val Ile Ala Gly Glu Gly Asp Val Asp Ala Val Val Ala  
       130                          135                          140

Ala Arg Gly Leu Glu Val Val Arg Asp Asp Gly Ala Ile Glu Lys Ala  
       145                          150                          155                          160

Val Asp Asp Ala Leu Ala Ala Asn Pro Asp Ile Val Glu Lys Tyr Arg  
                           165                          170                          175

Ala Gly Asn Thr Lys Val Thr Gly Ala Ile Val Gly Ala Val Met Lys  
                           180                          185                          190

Ala Thr Arg Gly Lys Ala Asp Pro Ala Gln Val Asn Gln Leu Ile Ala  
                           195                          200                          205

Lys Lys Leu Ala  
       210

<210> 383

<211> 1026

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1003)

&lt;223&gt; RXA02228

&lt;400&gt; 383

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acagaagcgt caactgctca acttctcgac agcgacgaca cacacggcgt gggacgctac 60

gttgctcgct ggacttttta acttaaggga gatctagatc gtg gta aca ccg atc 115
                Val Val Thr Pro Ile
                1 5

gca gtg gtt gga ccc act gca tct gga aaa tca gct ttg gga att gct 163
Ala Val Val Gly Pro Thr Ala Ser Gly Lys Ser Ala Leu Gly Ile Ala
                10 15 20

cta gcc cac aag ctt gac ggt gaa gta gtc aat gtg gat tcc atg cag 211
Leu Ala His Lys Leu Asp Gly Glu Val Val Asn Val Asp Ser Met Gln
                25 30 35

ctg tac aaa ggc atg gac atc ggc acg gca aag ctg act gtc gaa gaa 259
Leu Tyr Lys Gly Met Asp Ile Gly Thr Ala Lys Leu Thr Val Glu Glu
                40 45 50

cgc gaa ggc att gcg cat cat cag ctc gat gtc tgg gac gtt acc gaa 307
Arg Glu Gly Ile Ala His His Gln Leu Asp Val Trp Asp Val Thr Glu
                55 60 65

act gcg tca gtg gcg agg ttt caa tcc gac gcc gtt gcc gat gtg gaa 355
Thr Ala Ser Val Ala Arg Phe Gln Ser Asp Ala Val Ala Asp Val Glu
                70 75 80 85

gat att atg tcc cgt ggc aaa acc ccc atc ttg gtt ggc ggc tcc atg 403
Asp Ile Met Ser Arg Gly Lys Thr Pro Ile Leu Val Gly Gly Ser Met
                90 95 100

ttg tac gtc caa tct ttg gtc gat gat tgg caa ttc cca cct acc gac 451
Leu Tyr Val Gln Ser Leu Val Asp Asp Trp Gln Phe Pro Pro Thr Asp
                105 110 115

agc gct gtt cgc gca cgc ttt gag gcc cgc ttg gca gac atc ggt gtc 499
Ser Ala Val Arg Ala Arg Phe Glu Ala Arg Leu Ala Asp Ile Gly Val
                120 125 130

gaa gca cta cac gct gaa ctt act cag ctt gac cca gaa gca gca gcc 547
Glu Ala Leu His Ala Glu Leu Thr Gln Leu Asp Pro Glu Ala Ala Ala
                135 140 145

gtc atc gaa agc aat gat ccc cga cgc acc gtc cga gca tta gaa gtc 595
Val Ile Glu Ser Asn Asp Pro Arg Arg Thr Val Arg Ala Leu Glu Val
                150 155 160 165

att gaa cta acc ggc cag ccc ttc caa gca agc caa ccg ccc aaa gac 643
Ile Glu Leu Thr Gly Gln Pro Phe Gln Ala Ser Gln Pro Pro Lys Asp
                170 175 180

gcg cca cct cgc tgg gga act cga atc att ggc ctg aaa acc act cca 691
Ala Pro Pro Arg Trp Gly Thr Arg Ile Ile Gly Leu Lys Thr Thr Pro

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185	190	195	
gaa tgg cta aat cca cgc atc gag cag cgc acc gcc agg atg ttt gaa	739		
Glu Trp Leu Asn Pro Arg Ile Glu Gln Arg Thr Ala Arg Met Phe Glu			
200	205	210	
caa ggc ttt gtc gcc gaa gtg gaa cac ctt gtg cag caa gga ctc atc	787		
Gln Gly Phe Val Ala Glu Val Glu His Leu Val Gln Gln Gly Leu Ile			
215	220	225	
gct gac tcc acc gcg gga cga gca atc ggc tac tcc caa gta ctg gca	835		
Ala Asp Ser Thr Ala Gly Arg Ala Ile Gly Tyr Ser Gln Val Leu Ala			
230	235	240	245
gcc atg gca ggg gag atg acc tgg gaa gac gcc ttc gaa cgc acg gtc	883		
Ala Met Ala Gly Glu Met Thr Trp Glu Asp Ala Phe Glu Arg Thr Val			
250	255	260	
acc gga acc aga cgc tat gtc agg cgc caa cgc agc tgg ttc aac aga	931		
Thr Gly Thr Arg Arg Tyr Val Arg Arg Gln Arg Ser Trp Phe Asn Arg			
265	270	275	
gac cac cgc gtg tcc tgg gtc gac gcc tct ggc gat ccc acc gca caa	979		
Asp His Arg Val Ser Trp Val Asp Ala Ser Gly Asp Pro Thr Ala Gln			
280	285	290	
gcc ttg gag att ttg ggt cta caa tagcgagggt gaatttgacc atc	1026		
Ala Leu Glu Ile Leu Gly Leu Gln			
295	300		

&lt;210&gt; 384

&lt;211&gt; 301

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 384

Val Val Thr Pro Ile Ala Val Val Gly Pro Thr Ala Ser Gly Lys Ser	
1 5 10 15	
Ala Leu Gly Ile Ala Leu Ala His Lys Leu Asp Gly Glu Val Val Asn	
20 25 30	
Val Asp Ser Met Gln Leu Tyr Lys Gly Met Asp Ile Gly Thr Ala Lys	
35 40 45	
Leu Thr Val Glu Glu Arg Glu Gly Ile Ala His His Gln Leu Asp Val	
50 55 60	
Trp Asp Val Thr Glu Thr Ala Ser Val Ala Arg Phe Gln Ser Asp Ala	
65 70 75 80	
Val Ala Asp Val Glu Asp Ile Met Ser Arg Gly Lys Thr Pro Ile Leu	
85 90 95	
Val Gly Gly Ser Met Leu Tyr Val Gln Ser Leu Val Asp Asp Trp Gln	
100 105 110	
Phe Pro Pro Thr Asp Ser Ala Val Arg Ala Arg Phe Glu Ala Arg Leu	
115 120 125	

Ala Asp Ile Gly Val Glu Ala Leu His Ala Glu Leu Thr Gln Leu Asp  
 130 135 140

Pro Glu Ala Ala Ala Val Ile Glu Ser Asn Asp Pro Arg Arg Thr Val  
 145 150 155 160

Arg Ala Leu Glu Val Ile Glu Leu Thr Gly Gln Pro Phe Gln Ala Ser  
 165 170 175

Gln Pro Pro Lys Asp Ala Pro Pro Arg Trp Gly Thr Arg Ile Ile Gly  
 180 185 190

Leu Lys Thr Thr Pro Glu Trp Leu Asn Pro Arg Ile Glu Gln Arg Thr  
 195 200 205

Ala Arg Met Phe Glu Gln Gly Phe Val Ala Glu Val Glu His Leu Val  
 210 215 220

Gln Gln Gly Leu Ile Ala Asp Ser Thr Ala Gly Arg Ala Ile Gly Tyr  
 225 230 235 240

Ser Gln Val Leu Ala Ala Met Ala Gly Glu Met Thr Trp Glu Asp Ala  
 245 250 255

Phe Glu Arg Thr Val Thr Gly Thr Arg Arg Tyr Val Arg Arg Gln Arg  
 260 265 270

Ser Trp Phe Asn Arg Asp His Arg Val Ser Trp Val Asp Ala Ser Gly  
 275 280 285

Asp Pro Thr Ala Gln Ala Leu Glu Ile Leu Gly Leu Gln  
 290 295 300

&lt;210&gt; 385

&lt;211&gt; 1515

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1492)

&lt;223&gt; RXA02502

&lt;400&gt; 385

aatgctttgt tgtgatgtcc gcgaatgaaa gctaccgtat tttaatcaac taggattcat 60

tcttttggtg gatcaaaggc tccgttgaaa gtcgggtgga atg gtg agt gta ctc 115  
 Met Val Ser Val Leu  
 1 5

atc gta ggg atg tcg cac agg tct gcg cct gtg tcg ctt ctt gaa cgt 163  
 Ile Val Gly Met Ser His Arg Ser Ala Pro Val Ser Leu Leu Glu Arg  
 10 15 20

ctg agc atg gat gat tca gta cgt ggt gaa aca act caa gca ctc ctg 211  
 Leu Ser Met Asp Asp Ser Val Arg Gly Glu Thr Thr Gln Ala Leu Leu  
 25 30 35

ggt agg gcg tct tta agc gag gcc ctc att gtc tct acg tgt aac cgc 259  
 Gly Arg Ala Ser Leu Ser Glu Ala Leu Ile Val Ser Thr Cys Asn Arg

40					45					50						
ctg	gag	gtc	tac	acc	gtc	act	agc	agt	ttc	cat	act	ggg	gtt	aat	gat	307
Leu	Glu	Val	Tyr	Thr	Val	Thr	Ser	Ser	Phe	His	Thr	Gly	Val	Asn	Asp	
55					60					65						
gtg	gtg	gag	gtt	ctc	cat	gag	gca	agt	ggc	gta	gat	att	gaa	act	ttg	355
Val	Val	Glu	Val	Leu	His	Glu	Ala	Ser	Gly	Val	Asp	Ile	Glu	Thr	Leu	
70					75					80					85	
cgc	gga	tat	ctt	tat	gtc	cgt	tac	gcc	gat	gct	gct	gct	gaa	cac	atg	403
Arg	Gly	Tyr	Leu	Tyr	Val	Arg	Tyr	Ala	Asp	Ala	Ala	Ala	Glu	His	Met	
90					95					100						
ttg	gtg	gtg	act	tcc	ggg	ttg	gat	tcc	atg	gtg	ttg	ggg	gag	cag	cag	451
Leu	Val	Val	Thr	Ser	Gly	Leu	Asp	Ser	Met	Val	Leu	Gly	Glu	Gln	Gln	
105					110					115						
atc	att	ggg	cag	gtg	cgc	act	gcg	tac	caa	gca	gct	aat	gaa	tat	ggg	499
Ile	Ile	Gly	Gln	Val	Arg	Thr	Ala	Tyr	Gln	Ala	Ala	Asn	Glu	Tyr	Gly	
120					125					130						
tct	gtc	ggg	cct	gct	ttg	cat	tca	ctt	acc	cag	acc	gcg	ctg	cat	acc	547
Ser	Val	Gly	Pro	Ala	Leu	His	Ser	Leu	Thr	Gln	Thr	Ala	Leu	His	Thr	
135					140					145						
ggc	aag	cgc	gtg	cat	tcg	gag	act	gct	att	gat	gat	gct	ggg	gca	tcg	595
Gly	Lys	Arg	Val	His	Ser	Glu	Thr	Ala	Ile	Asp	Asp	Ala	Gly	Ala	Ser	
150					155					160					165	
atg	gtg	tct	ttc	gct	gtg	gat	cgc	gcg	ttg	gtg	cag	atg	ggg	ctt	gat	643
Met	Val	Ser	Phe	Ala	Val	Asp	Arg	Ala	Leu	Val	Gln	Met	Gly	Leu	Asp	
170					175					180						
tcg	gag	gca	gaa	gcc	cca	cta	tct	ggc	aag	aca	gcc	ttg	gtg	ttg	ggc	691
Ser	Glu	Ala	Glu	Ala	Pro	Leu	Ser	Gly	Lys	Thr	Ala	Leu	Val	Leu	Gly	
185					190					195						
gct	ggc	gcg	atg	agt	tct	ctt	gca	gcc	act	cac	ctt	ggg	cgc	gct	gga	739
Ala	Gly	Ala	Met	Ser	Ser	Leu	Ala	Ala	Thr	His	Leu	Gly	Arg	Ala	Gly	
200					205					210						
att	tcc	aac	ttg	atc	atg	gcc	aac	cgc	act	ctg	gaa	cgt	gcc	gaa	agg	787
Ile	Ser	Asn	Leu	Ile	Met	Ala	Asn	Arg	Thr	Leu	Glu	Arg	Ala	Glu	Arg	
215					220					225						
ctt	gcg	gag	cat	tcc	cta	gaa	gcc	gga	gtt	cct	gca	gag	gtt	gtg	gaa	835
Leu	Ala	Glu	His	Ser	Leu	Glu	Ala	Gly	Val	Pro	Ala	Glu	Val	Val	Glu	
230					235					240					245	
tac	gat	cag	cga	gct	tcc	gcc	tac	aat	cgc	gtt	gac	ctg	gta	gtt	tcc	883
Tyr	Asp	Gln	Arg	Ala	Ser	Ala	Tyr	Asn	Arg	Val	Asp	Leu	Val	Val	Ser	
250					255					260						
gcc	acg	gga	gcg	gat	gat	ttc	acc	gtg	aag	cct	gag	gat	att	cca	gaa	931
Ala	Thr	Gly	Ala	Asp	Asp	Phe	Thr	Val	Lys	Pro	Glu	Asp	Ile	Pro	Glu	
265					270					275						
ggg	gct	tcg	ttg	atg	ttg	gtg	gat	ttg	tcc	atg	cca	cga	gac	atc	gat	979
Gly	Ala	Ser	Leu	Met	Leu	Val	Asp	Leu	Ser	Met	Pro	Arg	Asp	Ile	Asp	
280					285					290						

gat gct tgt gcg gat ctg ccg ggc gtt gat ttg gtg aac atc gaa cgc 1027  
Asp Ala Cys Ala Asp Leu Pro Gly Val Asp Leu Val Asn Ile Glu Arg  
295 300 305

ctg cac aag gcc tcc cgt gag ggt gga tcg ggc atg gcg cca agc gag 1075  
Leu His Lys Ala Ser Arg Glu Gly Gly Ser Gly Met Ala Pro Ser Glu  
310 315 320 325

gaa gaa gct ttg gcg att gtt cgg gaa gag ttg gat tct ttc acc tct 1123  
Glu Glu Ala Leu Ala Ile Val Arg Glu Glu Leu Asp Ser Phe Thr Ser  
330 335 340

gag cag cgc att cgc gat atc gtt cca gct gtg tcc gcg ttg cgc agg 1171  
Glu Gln Arg Ile Arg Asp Ile Val Pro Ala Val Ser Ala Leu Arg Arg  
345 350 355

cag gcc gcg tcg gtg gga agc gat gaa ttg gat cga ctc cgc caa cgt 1219  
Gln Ala Ala Ser Val Gly Ser Asp Glu Leu Asp Arg Leu Arg Gln Arg  
360 365 370

gcc ccc ggg att tcc gag gtg gaa tgg ggg gaa gtg gag aaa aca ggg 1267  
Ala Pro Gly Ile Ser Glu Val Glu Trp Gly Glu Val Glu Lys Thr Gly  
375 380 385

aga cgg gtc gtc gat aag ctt ctt cat gaa ccc act gtg cgc gtc aag 1315  
Arg Arg Val Val Asp Lys Leu Leu His Glu Pro Thr Val Arg Val Lys  
390 395 400 405

gaa ctg gcg gcc cgg tcc ggc agc atc tct tat gat tca gct ctg caa 1363  
Glu Leu Ala Ala Arg Ser Gly Ser Ile Ser Tyr Asp Ser Ala Leu Gln  
410 415 420

gag ctg ttc ggt ttg gag tcg ctg gcg agc acc gca gca ccg gca acc 1411  
Glu Leu Phe Gly Leu Glu Ser Leu Ala Ser Thr Ala Ala Pro Ala Thr  
425 430 435

acg tcc gtc aac gcg tca gaa ctg ccg gat gcg ggt atc gtc gca ttc 1459  
Thr Ser Val Asn Ala Ser Glu Leu Pro Asp Ala Gly Ile Val Ala Phe  
440 445 450

gtg aac gca cct tct gcc aca caa acg agg gag taacatgacc ttaaaaattg 1512  
Val Asn Ala Pro Ser Ala Thr Gln Thr Arg Glu  
455 460

gta 1515

&lt;210&gt; 386

&lt;211&gt; 464

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 386

Met Val Ser Val Leu Ile Val Gly Met Ser His Arg Ser Ala Pro Val  
1 5 10 15

Ser Leu Leu Glu Arg Leu Ser Met Asp Asp Ser Val Arg Gly Glu Thr  
20 25 30

Thr Gln Ala Leu Leu Gly Arg Ala Ser Leu Ser Glu Ala Leu Ile Val

35					40					45						
Ser	Thr	Cys	Asn	Arg	Leu	Glu	Val	Tyr	Thr	Val	Thr	Ser	Ser	Phe	His	
50					55					60						
Thr	Gly	Val	Asn	Asp	Val	Val	Glu	Val	Leu	His	Glu	Ala	Ser	Gly	Val	
65					70					75					80	
Asp	Ile	Glu	Thr	Leu	Arg	Gly	Tyr	Leu	Tyr	Val	Arg	Tyr	Ala	Asp	Ala	
85					90					95						
Ala	Ala	Glu	His	Met	Leu	Val	Val	Thr	Ser	Gly	Leu	Asp	Ser	Met	Val	
100					105					110						
Leu	Gly	Glu	Gln	Gln	Ile	Ile	Gly	Gln	Val	Arg	Thr	Ala	Tyr	Gln	Ala	
115					120					125						
Ala	Asn	Glu	Tyr	Gly	Ser	Val	Gly	Pro	Ala	Leu	His	Ser	Leu	Thr	Gln	
130					135					140						
Thr	Ala	Leu	His	Thr	Gly	Lys	Arg	Val	His	Ser	Glu	Thr	Ala	Ile	Asp	
145					150					155					160	
Asp	Ala	Gly	Ala	Ser	Met	Val	Ser	Phe	Ala	Val	Asp	Arg	Ala	Leu	Val	
165					170					175						
Gln	Met	Gly	Leu	Asp	Ser	Glu	Ala	Glu	Ala	Pro	Leu	Ser	Gly	Lys	Thr	
180					185					190						
Ala	Leu	Val	Leu	Gly	Ala	Gly	Ala	Met	Ser	Ser	Leu	Ala	Ala	Thr	His	
195					200					205						
Leu	Gly	Arg	Ala	Gly	Ile	Ser	Asn	Leu	Ile	Met	Ala	Asn	Arg	Thr	Leu	
210					215					220						
Glu	Arg	Ala	Glu	Arg	Leu	Ala	Glu	His	Ser	Leu	Glu	Ala	Gly	Val	Pro	
225					230					235					240	
Ala	Glu	Val	Val	Glu	Tyr	Asp	Gln	Arg	Ala	Ser	Ala	Tyr	Asn	Arg	Val	
245					250					255						
Asp	Leu	Val	Val	Ser	Ala	Thr	Gly	Ala	Asp	Asp	Phe	Thr	Val	Lys	Pro	
260					265					270						
Glu	Asp	Ile	Pro	Glu	Gly	Ala	Ser	Leu	Met	Leu	Val	Asp	Leu	Ser	Met	
275					280					285						
Pro	Arg	Asp	Ile	Asp	Asp	Ala	Cys	Ala	Asp	Leu	Pro	Gly	Val	Asp	Leu	
290					295					300						
Val	Asn	Ile	Glu	Arg	Leu	His	Lys	Ala	Ser	Arg	Glu	Gly	Gly	Ser	Gly	
305					310					315					320	
Met	Ala	Pro	Ser	Glu	Glu	Glu	Ala	Leu	Ala	Ile	Val	Arg	Glu	Glu	Leu	
325					330					335						
Asp	Ser	Phe	Thr	Ser	Glu	Gln	Arg	Ile	Arg	Asp	Ile	Val	Pro	Ala	Val	
340					345					350						
Ser	Ala	Leu	Arg	Arg	Gln	Ala	Ala	Ser	Val	Gly	Ser	Asp	Glu	Leu	Asp	
355					360					365						

Arg Leu Arg Gln Arg Ala Pro Gly Ile Ser Glu Val Glu Trp Gly Glu  
 370 375 380

Val Glu Lys Thr Gly Arg Arg Val Val Asp Lys Leu Leu His Glu Pro  
 385 390 395 400

Thr Val Arg Val Lys Glu Leu Ala Ala Arg Ser Gly Ser Ile Ser Tyr  
 405 410 415

Asp Ser Ala Leu Gln Glu Leu Phe Gly Leu Glu Ser Leu Ala Ser Thr  
 420 425 430

Ala Ala Pro Ala Thr Thr Ser Val Asn Ala Ser Glu Leu Pro Asp Ala  
 435 440 445

Gly Ile Val Ala Phe Val Asn Ala Pro Ser Ala Thr Gln Thr Arg Glu  
 450 455 460

&lt;210&gt; 387

&lt;211&gt; 897

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(874)

&lt;223&gt; RXA02182

&lt;400&gt; 387

gacctgtggc agctttcgtg cgcacgtttt ctgaagtcaa tgactaccta tggagcactg 60

cacagcaagt gtaggtcgct cgactgttat tctcggggct gtg aaa aag ctt gca 115  
 Val Lys Lys Leu Ala  
 1 5

tcc ata gcg atc ctc tcc agc ctc cct ttg gct tcg tgt tcc act cct 163  
 Ser Ile Ala Ile Leu Ser Ser Leu Pro Leu Ala Ser Cys Ser Thr Pro  
 10 15 20

cca aca gat tca gag gct gtc gtt gag cat ctg gtt cca gaa att atc 211  
 Pro Thr Asp Ser Glu Ala Val Val Glu His Leu Val Pro Glu Ile Ile  
 25 30 35

tcc acc cac tct ttt gat tcc acc tcg ttt act cag ggg ttg gaa tta 259  
 Ser Thr His Ser Phe Asp Ser Thr Ser Phe Thr Gln Gly Leu Glu Leu  
 40 45 50

gat ggc gac gag ctg att gtg gga act ggc caa tac ggt ggt tcc cga 307  
 Asp Gly Asp Glu Leu Ile Val Gly Thr Gly Gln Tyr Gly Gly Ser Arg  
 55 60 65

atc tat cgc agc tcc gtt gat ggc cag gaa tct gtt tcc caa tcg ctt 355  
 Ile Tyr Arg Ser Ser Val Asp Gly Gln Glu Ser Val Ser Gln Ser Leu  
 70 75 80 85

gat cca gaa ttc ttc ggt gaa ggc atc acc aag tct ggt gat gcc atc 403  
 Asp Pro Glu Phe Phe Gly Glu Gly Ile Thr Lys Ser Gly Asp Ala Ile  
 90 95 100

Gln Gly Leu Glu Leu Asp Gly Asp Glu Leu Ile Val Gly Thr Gly Gln  
50 55 60

Tyr Gly Gly Ser Arg Ile Tyr Arg Ser Ser Val Asp Gly Gln Glu Ser  
 65 70 75 80  
 Val Ser Gln Ser Leu Asp Pro Glu Phe Phe Gly Glu Gly Ile Thr Lys  
 85 90 95  
 Ser Gly Asp Ala Ile Trp Gln Leu Thr Trp Asn Glu Gly Val Ala Phe  
 100 105 110  
 Lys Arg Asp Ala Asp Thr Leu Glu Glu Leu Asp Arg Val Ser Tyr Asn  
 115 120 125  
 Gly Gln Gly Trp Gly Ile Cys Ser Thr Asp Asp Ala Leu Ile Thr Ser  
 130 135 140  
 Asp Gly Ser Ser Thr Leu Thr Phe Arg Asp Pro Glu Thr Phe Ala Glu  
 145 150 155 160  
 Asn Ser Thr Val Asp Val Thr Leu Asp Gly Ser Pro Val Gly Asn Leu  
 165 170 175  
 Asn Glu Leu Glu Cys Val Asp Gly Glu Val Tyr Ala Asn Ile Phe Leu  
 180 185 190  
 Asp Thr Asp Ile Met Arg Ile Asp Pro Asn Ser Gly Glu Val Thr Ala  
 195 200 205  
 Val Ile Asp Ala Ser Asn Ile Pro Asn Asn Ala Thr Pro Asp Thr Asn  
 210 215 220  
 Asn Val Leu Asn Gly Ile Ala His Ile Pro Asp Ser Asp Arg Phe Tyr  
 225 230 235 240  
 Ile Thr Gly Lys Arg Trp Pro Asp Leu Tyr Glu Val Arg Phe Val Pro  
 245 250 255  
 Ala Asp

&lt;210&gt; 389

&lt;211&gt; 786

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(763)

&lt;223&gt; RXN00211

&lt;400&gt; 389

tgagccaaaa tcaataaggt gtttttcagc ctgaggtaaa aatacggtgg tactgtcgaa 60  
 accaatcatc ccctagtttt gaaaagaagg aagcgagcca atg tca ttc ctg atc 115  
 Met Ser Phe Leu Ile  
 1 5

cgc gtc ctg ttg tcc gac acc cca ggc agc ctc gcg tta ctc gct gaa 163  
 Arg Val Leu Leu Ser Asp Thr Pro Gly Ser Leu Ala Leu Leu Ala Glu  
 10 15 20

gcc ctt ggg att gta gag gcc aat att caa tcc gtg gac gtg gtg gaa 211  
 Ala Leu Gly Ile Val Glu Ala Asn Ile Gln Ser Val Asp Val Val Glu  
                   25                                  30                                  35

cgc ttc ccc aat ggc acg gtc atg gac gat ctg gtg atc tcc atc cct 259  
 Arg Phe Pro Asn Gly Thr Val Met Asp Asp Leu Val Ile Ser Ile Pro  
                   40                                  45                                  50

cgc gat gtc atg gca gac acc atc atc acc gca gct gaa gaa gtc gac 307  
 Arg Asp Val Met Ala Asp Thr Ile Ile Thr Ala Ala Glu Glu Val Asp  
                   55                                  60                                  65

ggc gtg gag att gat tcc atc cgc cca ttc tcc ggg act gtt gac cgc 355  
 Gly Val Glu Ile Asp Ser Ile Arg Pro Phe Ser Gly Thr Val Asp Arg  
                   70                                  75                                  80                                  85

cgc gga cag atc caa atg ctg gct gct gtt gct cac caa cgc cgc gat 403  
 Arg Gly Gln Ile Gln Met Leu Ala Ala Val Ala His Gln Arg Arg Asp  
                                   90                                  95                                  100

atc acc gca gcg atg gaa gaa atg gtc gat gtc atc ccc cgc acc atg 451  
 Ile Thr Ala Ala Met Glu Glu Met Val Asp Val Ile Pro Arg Thr Met  
                   105                                  110                                  115

acc tct ggt tgg gct ttg gtc att gat cta aaa gga ccc atc act cgc 499  
 Thr Ser Gly Trp Ala Leu Val Ile Asp Leu Lys Gly Pro Ile Thr Arg  
                   120                                  125                                  130

atc gct ggt tcc cta gca gcg ccc gaa gat gac ggc acc gtt ccg gag 547  
 Ile Ala Gly Ser Leu Ala Ala Pro Glu Asp Asp Gly Thr Val Pro Glu  
                   135                                  140                                  145

aac atc gtt ctc aaa gaa gct cgc atg ctc aac ccg gaa aac gat ccg 595  
 Asn Ile Val Leu Lys Glu Ala Arg Met Leu Asn Pro Glu Asn Asp Pro  
                   150                                  155                                  160                                  165

tgg att cca gag tcc tgg aca ctg ctt gat tct tcc ctt gcc atc gct 643  
 Trp Ile Pro Glu Ser Trp Thr Leu Leu Asp Ser Ser Leu Ala Ile Ala  
                                   170                                  175                                  180

ccg atc ggc aag cac ggc ctg gct ctg att atc ggt cgc cct ggt ggc 691  
 Pro Ile Gly Lys His Gly Leu Ala Leu Ile Ile Gly Arg Pro Gly Gly  
                   185                                  190                                  195

cct gat ttc ttg gcc agc gaa gtg gag cac tta ggc caa gtc ggt gac 739  
 Pro Asp Phe Leu Ala Ser Glu Val Glu His Leu Gly Gln Val Gly Asp  
                   200                                  205                                  210

att atc gga gca atg ctt caa aaa taatctgagc tgtttaaaaa atg 786  
 Ile Ile Gly Ala Met Leu Gln Lys  
                   215                                  220

&lt;210&gt; 390

&lt;211&gt; 221

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 390

Met Ser Phe Leu Ile Arg Val Leu Leu Ser Asp Thr Pro Gly Ser Leu  
           1                                  5                                  10                                  15

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<210> 391
<211> 1005
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(982)
<223> RXN00669
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<400> 391
tttactgcgg gcattttacg tatctgcacc ccgcccggct gcgctgagca gccgtaaagc 60

gtggggcgctg acgtcgaaaa gcaaaaaatg aaaggcagac atg gac aat tca acg 115
                                         Met Asp Asn Ser Thr
                                         1                               5

gtg cga atc cgg ctg gat cta gcg tat gac ggc acg gat ttt cat ggc 163
Val Arg Ile Arg Leu Asp Leu Ala Tyr Asp Gly Thr Asp Phe His Gly
          10                      15                      20

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tgg gcg aag cag ggg acc agc gat cta cgc acc gtg caa aaa gtg ttg	211
Trp Ala Lys Gln Gly Thr Ser Asp Leu Arg Thr Val Gln Lys Val Leu	
25 30 35	
gaa gac aat ttg agc atg gtg ctg cgt gag act gtt gaa ttg act gtg	259
Glu Asp Asn Leu Ser Met Val Leu Arg Glu Thr Val Glu Leu Thr Val	
40 45 50	
gcc ggg cga acc gat gcg ggg gtg cat gcg gcg ggc cag gtg gcg cac	307
Ala Gly Arg Thr Asp Ala Gly Val His Ala Ala Gly Gln Val Ala His	
55 60 65	
ttt gat att ccg gca cac gct tta gag cag cgc agt att gat ggc gat	355
Phe Asp Ile Pro Ala His Ala Leu Glu Gln Arg Ser Ile Asp Gly Asp	
70 75 80 85	
cca agc aag ttg gtt cgg cgc ttg ggt cgg ttg ctg ccc gat gat att	403
Pro Ser Lys Leu Val Arg Arg Leu Gly Arg Leu Leu Pro Asp Asp Ile	
90 95 100	
cgg gtg cat ggc gta cgt ttt gcc gag ccc ggg ttt gat gcg cga ttt	451
Arg Val His Gly Val Arg Phe Ala Glu Pro Gly Phe Asp Ala Arg Phe	
105 110 115	
tcc gcg atg cgc agg cac tac gtt tat cgc att acg acg cat ccc gcc	499
Ser Ala Met Arg Arg His Tyr Val Tyr Arg Ile Thr Thr His Pro Ala	
120 125 130	
ggc gcg ctg cct acg cgc cgc cac gac acg gcg cag tgg cca aaa cct	547
Gly Ala Leu Pro Thr Arg Arg His Asp Thr Ala Gln Trp Pro Lys Pro	
135 140 145	
gtc gaa cta gag cgg atg caa tta gcc gcc gat gca ctg ctg ggg ctg	595
Val Glu Leu Glu Arg Met Gln Leu Ala Ala Asp Ala Leu Leu Gly Leu	
150 155 160 165	
cat gat ttt gtg gcg ttt tgc aaa gct aag cca cat gcg acg acg gtg	643
His Asp Phe Val Ala Phe Cys Lys Ala Lys Pro His Ala Thr Thr Val	
170 175 180	
cgt gaa cta caa aaa ttt gcg tgg aaa gac gtc tcc act gac atc gaa	691
Arg Glu Leu Gln Lys Phe Ala Trp Lys Asp Val Ser Thr Asp Ile Glu	
185 190 195	
ccg cag gtg tat gaa gca cac gtg gtg gcc gat gct ttt tgc tgg tcg	739
Pro Gln Val Tyr Glu Ala His Val Val Ala Asp Ala Phe Cys Trp Ser	
200 205 210	
atg gtg cgc tcg ctg gtc ggc tcc tgc atg gcc gtg ggc gaa gga cgc	787
Met Val Arg Ser Leu Val Gly Ser Cys Met Ala Val Gly Glu Gly Arg	
215 220 225	
cgc gga tca ggg ttt act gca gaa ttg ctt gat gca agc gaa cgc agc	835
Arg Gly Ser Gly Phe Thr Ala Glu Leu Leu Asp Ala Ser Glu Arg Ser	
230 235 240 245	
ccc atg gtt cca gta gca cct gcg aaa ggt ttg agc ttg gtt ggc gtg	883
Pro Met Val Pro Val Ala Pro Ala Lys Gly Leu Ser Leu Val Gly Val	
250 255 260	

gat tat cct tcc gct gat aag tta cag gaa aga gcg ctg gaa acc cga 931  
 Asp Tyr Pro Ser Ala Asp Lys Leu Gln Glu Arg Ala Leu Glu Thr Arg  
                   265                                  270                                  275

gct gtt cgc gag ttt ccg gac gcg tcc gcg agc cta aaa cta gat gat 979  
 Ala Val Arg Glu Phe Pro Asp Ala Ser Ala Ser Leu Lys Leu Asp Asp  
                   280                                  285                                  290

gag taaaagggac taaactcgtc tct 1005  
 Glu

<210> 392

<211> 294

<212> PRT

<213> Corynebacterium glutamicum

<400> 392

Met Asp Asn Ser Thr Val Arg Ile Arg Leu Asp Leu Ala Tyr Asp Gly  
   1                                  5                                  10                                  15

Thr Asp Phe His Gly Trp Ala Lys Gln Gly Thr Ser Asp Leu Arg Thr  
                   20                                  25                                  30

Val Gln Lys Val Leu Glu Asp Asn Leu Ser Met Val Leu Arg Glu Thr  
                   35                                  40                                  45

Val Glu Leu Thr Val Ala Gly Arg Thr Asp Ala Gly Val His Ala Ala  
                   50                                  55                                  60

Gly Gln Val Ala His Phe Asp Ile Pro Ala His Ala Leu Glu Gln Arg  
   65                                  70                                  75                                  80

Ser Ile Asp Gly Asp Pro Ser Lys Leu Val Arg Arg Leu Gly Arg Leu  
                                   85                                  90                                  95

Leu Pro Asp Asp Ile Arg Val His Gly Val Arg Phe Ala Glu Pro Gly  
                   100                                  105                                  110

Phe Asp Ala Arg Phe Ser Ala Met Arg Arg His Tyr Val Tyr Arg Ile  
                   115                                  120                                  125

Thr Thr His Pro Ala Gly Ala Leu Pro Thr Arg Arg His Asp Thr Ala  
   130                                  135                                  140

Gln Trp Pro Lys Pro Val Glu Leu Glu Arg Met Gln Leu Ala Ala Asp  
  145                                  150                                  155                                  160

Ala Leu Leu Gly Leu His Asp Phe Val Ala Phe Cys Lys Ala Lys Pro  
                                   165                                  170                                  175

His Ala Thr Thr Val Arg Glu Leu Gln Lys Phe Ala Trp Lys Asp Val  
                   180                                  185                                  190

Ser Thr Asp Ile Glu Pro Gln Val Tyr Glu Ala His Val Val Ala Asp  
                   195                                  200                                  205

Ala Phe Cys Trp Ser Met Val Arg Ser Leu Val Gly Ser Cys Met Ala  
                   210                                  215                                  220

Val Gly Glu Gly Arg Arg Gly Ser Gly Phe Thr Ala Glu Leu Leu Asp  
 225 230 235 240

Ala Ser Glu Arg Ser Pro Met Val Pro Val Ala Pro Ala Lys Gly Leu  
 245 250 255

Ser Leu Val Gly Val Asp Tyr Pro Ser Ala Asp Lys Leu Gln Glu Arg  
 260 265 270

Ala Leu Glu Thr Arg Ala Val Arg Glu Phe Pro Asp Ala Ser Ala Ser  
 275 280 285

Leu Lys Leu Asp Asp Glu  
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<210> 393  
 <211> 1053  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1030)  
 <223> RXN02651

<400> 393  
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cccagcatgc caaagcaact gacgagaagg atgaggcctg atg aac aac cga caa 115  
 Met Asn Asn Arg Gln  
 1 5

agc aga acc ctt ccc gta cca gaa gga ctg gca ggc atg cgt gtg gac 163  
 Ser Arg Thr Leu Pro Val Pro Glu Gly Leu Ala Gly Met Arg Val Asp  
 10 15 20

gca gca ctg tcc aag ttg ctg gga att tca cgc acc gta gct gca gaa 211  
 Ala Ala Leu Ser Lys Leu Leu Gly Ile Ser Arg Thr Val Ala Ala Glu  
 25 30 35

ctc gcc acc gcc ggc gat gtc agc gtt gat ggg gct gtg gta ggt aaa 259  
 Leu Ala Thr Ala Gly Asp Val Ser Val Asp Gly Ala Val Val Gly Lys  
 40 45 50

agc gag cgg ctc gtt gcc gat tcc atg ctg gat gtc ttg ctg cct gaa 307  
 Ser Glu Arg Leu Val Ala Asp Ser Met Leu Asp Val Leu Leu Pro Glu  
 55 60 65

cca gca gct ccg ttg atg ccc aag gaa gaa atc gtt ccc ggc ctg gat 355  
 Pro Ala Ala Pro Leu Met Pro Lys Glu Glu Ile Val Pro Gly Leu Asp  
 70 75 80 85

att ttg tac tct gat gac gat gtc atc gca gtc aac aaa ccc gtc ggc 403  
 Ile Leu Tyr Ser Asp Asp Asp Val Ile Ala Val Asn Lys Pro Val Gly  
 90 95 100

gtg gcg gca cat ccc acc gtg ggt tgg gaa ggc cca act gtg gtg ggc 451  
 Val Ala Ala His Pro Thr Val Gly Trp Glu Gly Pro Thr Val Val Gly  
 105 110 115

gga ctt gca gct gca ggt ttc cgc att tcc acc tcc ggc cca cca gag 499  
 Gly Leu Ala Ala Ala Gly Phe Arg Ile Ser Thr Ser Gly Pro Pro Glu  
 120 125 130

cgc aag ggt att gtg cag cgc ctt gac gtt ggc acg tct ggc gtg atg 547  
 Arg Lys Gly Ile Val Gln Arg Leu Asp Val Gly Thr Ser Gly Val Met  
 135 140 145

gtg gtt gct gcc tct gaa cgt gga tac acc gtg ctc aag cgc gct ttc 595  
 Val Val Ala Ala Ser Glu Arg Gly Tyr Thr Val Leu Lys Arg Ala Phe  
 150 155 160 165

cgg gac cgc acc gtg gac aag acc tac cac gcg ttg gtg caa ggc cac 643  
 Arg Asp Arg Thr Val Asp Lys Thr Tyr His Ala Leu Val Gln Gly His  
 170 175 180

cct gat ccg ctg acc gga acc atc gaa gca ccg atc ggc cgc cac ccc 691  
 Pro Asp Pro Leu Thr Gly Thr Ile Glu Ala Pro Ile Gly Arg His Pro  
 185 190 195

tca gca ggt tgg cgt ttc gca gta aca act gaa ggc aaa cac gcc gtc 739  
 Ser Ala Gly Trp Arg Phe Ala Val Thr Thr Glu Gly Lys His Ala Val  
 200 205 210

aca cac tac gaa acc ctg gag gcc ttc caa gag gca acc ctg ctg aaa 787  
 Thr His Tyr Glu Thr Leu Glu Ala Phe Gln Glu Ala Thr Leu Leu Lys  
 215 220 225

atc cac ctg gaa act ggc cgc acc cac cag atc cgc gtg cat ttc tcc 835  
 Ile His Leu Glu Thr Gly Arg Thr His Gln Ile Arg Val His Phe Ser  
 230 235 240 245

gcg ctg cac cac cca tgc tgt ggc gac ccc atg tac ggc tct gat cct 883  
 Ala Leu His His Pro Cys Cys Gly Asp Pro Met Tyr Gly Ser Asp Pro  
 250 255 260

gcg ttg tcc gag cgc ctt ggc ctt aac cgt cag tgg ctg cac gcc gtc 931  
 Ala Leu Ser Glu Arg Leu Gly Leu Asn Arg Gln Trp Leu His Ala Val  
 265 270 275

tcg ctt gga ttc aac cac cca gca gat ggc cga tgg atg gaa atc gtc 979  
 Ser Leu Gly Phe Asn His Pro Ala Asp Gly Arg Trp Met Glu Ile Val  
 280 285 290

tcc cca tat cca act gat ctc caa cac gct tta gac gtt ctc cgc gag 1027  
 Ser Pro Tyr Pro Thr Asp Leu Gln His Ala Leu Asp Val Leu Arg Glu  
 295 300 305

caa taatggatgg tgtcgataaa ggg 1053  
 Gln  
 310

&lt;210&gt; 394

&lt;211&gt; 310

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 394

Met Asn Asn Arg Gln Ser Arg Thr Leu Pro Val Pro Glu Gly Leu Ala  
 1 5 10 15

Gly Met Arg Val Asp Ala Ala Leu Ser Lys Leu Leu Gly Ile Ser Arg  
 20 25 30  
 Thr Val Ala Ala Glu Leu Ala Thr Ala Gly Asp Val Ser Val Asp Gly  
 35 40 45  
 Ala Val Val Gly Lys Ser Glu Arg Leu Val Ala Asp Ser Met Leu Asp  
 50 55 60  
 Val Leu Leu Pro Glu Pro Ala Ala Pro Leu Met Pro Lys Glu Glu Ile  
 65 70 75 80  
 Val Pro Gly Leu Asp Ile Leu Tyr Ser Asp Asp Asp Val Ile Ala Val  
 85 90 95  
 Asn Lys Pro Val Gly Val Ala Ala His Pro Thr Val Gly Trp Glu Gly  
 100 105 110  
 Pro Thr Val Val Gly Gly Leu Ala Ala Ala Gly Phe Arg Ile Ser Thr  
 115 120 125  
 Ser Gly Pro Pro Glu Arg Lys Gly Ile Val Gln Arg Leu Asp Val Gly  
 130 135 140  
 Thr Ser Gly Val Met Val Val Ala Ala Ser Glu Arg Gly Tyr Thr Val  
 145 150 155 160  
 Leu Lys Arg Ala Phe Arg Asp Arg Thr Val Asp Lys Thr Tyr His Ala  
 165 170 175  
 Leu Val Gln Gly His Pro Asp Pro Leu Thr Gly Thr Ile Glu Ala Pro  
 180 185 190  
 Ile Gly Arg His Pro Ser Ala Gly Trp Arg Phe Ala Val Thr Thr Glu  
 195 200 205  
 Gly Lys His Ala Val Thr His Tyr Glu Thr Leu Glu Ala Phe Gln Glu  
 210 215 220  
 Ala Thr Leu Leu Lys Ile His Leu Glu Thr Gly Arg Thr His Gln Ile  
 225 230 235 240  
 Arg Val His Phe Ser Ala Leu His His Pro Cys Cys Gly Asp Pro Met  
 245 250 255  
 Tyr Gly Ser Asp Pro Ala Leu Ser Glu Arg Leu Gly Leu Asn Arg Gln  
 260 265 270  
 Trp Leu His Ala Val Ser Leu Gly Phe Asn His Pro Ala Asp Gly Arg  
 275 280 285  
 Trp Met Glu Ile Val Ser Pro Tyr Pro Thr Asp Leu Gln His Ala Leu  
 290 295 300  
 Asp Val Leu Arg Glu Gln  
 305 310

&lt;210&gt; 395

&lt;211&gt; 2647

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2647)

&lt;223&gt; RXA01344

&lt;400&gt; 395

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gggggatcgg gttcctcagc agaccaattg ctcaaaaata ccagcgggtgt tgatctgcac 60

ttaatggcct tgaccagcca ggtgcaatta cccgcgtgag gtg ctg gaa gga ccc 115
                                   Val Leu Glu Gly Pro
                                   1 5

atc ttg gca gtc tcc cgc cag acc aag tca gtc gtc gat att ccc ggt 163
Ile Leu Ala Val Ser Arg Gln Thr Lys Ser Val Val Val Asp Ile Pro Gly
                                   10 15 20

gca ccg cag cgt tat tct ttc gcg aag gtg tcc gca ccc att gag gtg 211
Ala Pro Gln Arg Tyr Ser Phe Ala Lys Val Ser Ala Pro Ile Glu Val
                                   25 30 35

ccc ggg cta cta gat ctt caa ctg gat tct tac tcc tgg ctg att ggt 259
Pro Gly Leu Leu Asp Leu Gln Leu Asp Ser Tyr Ser Trp Leu Ile Gly
                                   40 45 50

acg cct gag tgg cgt gct cgt cag aag gaa gaa ttc ggc gag gga gcc 307
Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu Phe Gly Glu Gly Ala
                                   55 60 65

cgc gta acc agc ggc ctt gag aac att ctc gag gag ctc tcc cca atc 355
Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu Glu Leu Ser Pro Ile
                                   70 75 80 85

cag gat tac tct gga aac atg tcc ctg agc ctt tcg gag cca cgc ttc 403
Gln Asp Tyr Ser Gly Asn Met Ser Leu Ser Leu Ser Glu Pro Arg Phe
                                   90 95 100

gaa gac gtc aag aac acc att gac gag gcg aaa gaa aag gac atc aac 451
Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys Glu Lys Asp Ile Asn
                                   105 110 115

tac gcg gcg cca ctg tat gtg acc gcg gag ttc gtc aac aac acc acc 499
Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe Val Asn Asn Thr Thr
                                   120 125 130

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Gly Glu Ile Lys Ser Gln Thr Val Phe Ile Gly Asp Phe Pro Met Met
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Thr Asp Lys Gly Thr Phe Ile Ile Asn Gly Thr Glu Arg Val Val Val
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Ser Gln Leu Val Arg Ser Pro Gly Val Tyr Phe Asp Gln Thr Ile Asp
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Lys Ser Thr Glu Arg Pro Leu His Ala Val Lys Val Ile Pro Ser Arg

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gtc	atg	act	tct	cca	aat	ggt	gaa	gag	atc	cca	gtc	gag	acc	gat	gac	1171														
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Gly	Ser	Leu	Ala	Ser	Tyr	Ala	Arg	Val	Asn	Pro	Phe	Gly	Phe	Ile	Glu	
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Thr	Pro	Tyr	Arg	Arg	Ile	Ile	Asp	Gly	Lys	Leu	Thr	Asp	Gln	Ile	Asp	
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Tyr	Leu	Thr	Ala	Asp	Glu	Glu	Asp	Arg	Phe	Val	Val	Ala	Gln	Ala	Asn	
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Thr	His	Tyr	Asp	Glu	Glu	Gly	Asn	Ile	Thr	Asp	Glu	Thr	Val	Thr	Val	
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Ile	Pro	Phe	Leu	Glu	His	Asp	Asp	Ala	Asn	Arg	Ala	Leu	Met	Gly	Ala	
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Val	Gly	Thr	Gly	Met	Glu	Gln	Arg	Ala	Ala	Tyr	Asp	Ala	Gly	Asp	Leu	
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Ile	Thr	Ile	Met	Ala	Asp	Asp	Gly	Lys	Arg	Glu	Thr	Tyr	Leu	Leu	Arg	
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Lys	Phe	Gln	Arg	Thr	Asn	Gln	Gly	Thr	Ser	Tyr	Asn	Gln	Lys	Pro	Leu	
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&lt;211&gt; 849

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 396

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Val Asp Ile Pro Gly Ala Pro Gln Arg Tyr Ser Phe Ala Lys Val Ser  
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Ala Pro Ile Glu Val Pro Gly Leu Leu Asp Leu Gln Leu Asp Ser Tyr  
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Ser Trp Leu Ile Gly Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu

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Val	Ile	Pro 195	Ser	Arg	Gly	Ala	Trp 200	Leu	Glu	Phe	Asp	Val	Asp	Lys	Arg 205
Asp 210	Ser	Val	Gly	Val	Arg	Ile 215	Asp	Arg	Lys	Arg	Arg	Gln	Pro	Val	Thr 220
Val 225	Leu	Leu	Lys	Ala	Leu	Gly 230	Trp	Thr	Thr	Glu	Gln	Ile	Thr	Glu	Arg 240
Phe	Gly	Phe	Ser	Glu 245	Ile	Met	Met	Ser	Thr 250	Leu	Glu	Ser	Asp	Gly	Val 255
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Phe 290	Phe	Arg	Ala	Lys	Arg	Tyr 295	Asp	Leu	Ala	Arg	Val	Gly	Arg	Tyr	Lys 300
Ile 305	Asn	Arg	Lys	Leu	Gly 310	Leu	Gly	Gly	Asp	His 315	Asp	Gly	Leu	Met	Thr 320
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Val 370	Gly	Glu	Leu	Ile	Gln	Asn	Gln	Val	Arg	Val	Gly 380	Leu	Ser	Arg	Met

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 Thr Pro Thr Ser Leu Ile Asn Val Arg Pro Val Ser Ala Ala Ile Arg  
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 Gly Gly Leu Ser Arg Glu Arg Ala Gly Ile Glu Val Arg Asp Val His  
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 Pro Ser His Tyr Gly Arg Met Cys Pro Ile Glu Thr Pro Glu Gly Pro  
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 Phe Gly Phe Ile Glu Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu  
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 Thr Tyr Leu Leu Arg Lys Phe Gln Arg Thr Asn Gln Gly Thr Ser Tyr  
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Arg Asn Leu Leu Val Ala Phe Met Pro Trp Glu Gly His Asn Tyr Glu  
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 Leu Lys Asp Leu Asp Asp Arg Gly Ile Val Arg Ile Gly Ala Asp Val  
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 Val Leu Asp Val Asn 1 5  
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 Val Phe Asp Glu Leu Arg Ile Gly Leu Ala Thr Ala Asp Asp Ile Arg 10 15 20  
 cgt tgg tcc aag ggt gag gtc aag aag ccg gag acc atc aac tac cga 211  
 Arg Trp Ser Lys Gly Glu Val Lys Lys Pro Glu Thr Ile Asn Tyr Arg 25 30 35  
 acc ctc aag cct gag aag gac ggt ctg ttc tgc gag cgt atc ttc ggt 259  
 Thr Leu Lys Pro Glu Lys Asp Gly Leu Phe Cys Glu Arg Ile Phe Gly 40 45 50  
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Pro Thr Arg Asp Trp Glu Cys Ala Cys Gly Lys Tyr Lys Arg Val Arg  
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tac aag ggc atc atc tgt gaa cgc tgt ggc gtt gag gtc acc aag tcc 355  
 Tyr Lys Gly Ile Ile Cys Glu Arg Cys Gly Val Glu Val Thr Lys Ser  
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 Lys Val Arg Arg Glu Arg Met Gly His Ile Glu Leu Ala Ala Pro Val  
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Glu Arg Ile Phe Gly Pro Thr Arg Asp Trp Glu Cys Ala Cys Gly Lys  
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Tyr Lys Arg Val Arg Tyr Lys Gly Ile Ile Cys Glu Arg Cys Gly Val  
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Glu Val Thr Lys Ser Lys Val Arg Arg Glu Arg Met Gly His Ile Glu  
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Asn	Ala	Gly	Ala	Phe	Ile	Glu	Arg	Thr	Leu	Thr	Glu	Gly	Asp	Arg	Val	
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acc	gtt	ggg	cag	cgt	ctg	ctc	cgt	ggg	gca	gct	gat	cca	cac	gac	gtg	720
Thr	Val	Gly	Gln	Arg	Leu	Leu	Arg	Gly	Ala	Ala	Asp	Pro	His	Asp	Val	
225					230				235						240	
ctc	gag	atc	ctc	ggg	cgc	cgc	ggg	gtg	gag	cag	cac	ctc	atc	tat	gag	768
Leu	Glu	Ile	Leu	Gly	Arg	Arg	Gly	Val	Glu	Gln	His	Leu	Ile	Tyr	Glu	
				245				250						255		
gtg	cag	gct	gtt	tac	cgt	gca	cag	ggg	gtg	gcc	atc	cac	gac	aag	cac	816
Val	Gln	Ala	Val	Tyr	Arg	Ala	Gln	Gly	Val	Ala	Ile	His	Asp	Lys	His	
			260					265					270			
atc	gaa	atc	atc	att	cgt	cag	atg	ctg	cgt	cgc	ggg	acc	gtc	att	gag	864
Ile	Glu	Ile	Ile	Ile	Arg	Gln	Met	Leu	Arg	Arg	Gly	Thr	Val	Ile	Glu	
		275					280					285				

tcc ggt tcc acc gag ttc ctt cct ggt tct ttg gtt gac ctc tct gag 912  
 Ser Gly Ser Thr Glu Phe Leu Pro Gly Ser Leu Val Asp Leu Ser Glu  
 290 295 300

gcg aag ctg gct aac tct gag gca atc ggt gcg ggc ggt cag cct gca 960  
 Ala Lys Leu Ala Asn Ser Glu Ala Ile Gly Ala Gly Gly Gln Pro Ala  
 305 310 315 320

gag ctg cgt tct gag atc atg ggt atc acc aag gcc tct ctc gca act 1008  
 Glu Leu Arg Ser Glu Ile Met Gly Ile Thr Lys Ala Ser Leu Ala Thr  
 325 330 335

gag tct tgg ctg tct gca gcg tcc ttc cag gag acc act cgt gtc ctg 1056  
 Glu Ser Trp Leu Ser Ala Ala Ser Phe Gln Glu Thr Thr Arg Val Leu  
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act gat gct gct atc aac aag cgc tcc gat aag ctc atc ggc ctg aag 1104  
 Thr Asp Ala Ala Ile Asn Lys Arg Ser Asp Lys Leu Ile Gly Leu Lys  
 355 360 365

gag aac gtg atc atc ggt aag ctg atc cca gct ggt act ggt att tcc 1152  
 Glu Asn Val Ile Ile Gly Lys Leu Ile Pro Ala Gly Thr Gly Ile Ser  
 370 375 380

cgt tac cgc aac atc tcc atc aag cca acc gag gct gct cgc aac gcc 1200  
 Arg Tyr Arg Asn Ile Ser Ile Lys Pro Thr Glu Ala Ala Arg Asn Ala  
 385 390 395 400

gca tac tcg atc cca act tat ggt gag tcg att tac ggt gac gat gga 1248  
 Ala Tyr Ser Ile Pro Thr Tyr Gly Glu Ser Ile Tyr Gly Asp Asp Gly  
 405 410 415

ttc ggt gag ttc acc ggc gca tcc gtc cca ttg gat gag gct ttc 1293  
 Phe Gly Glu Phe Thr Gly Ala Ser Val Pro Leu Asp Glu Ala Phe  
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tagagcaagg aaaccttaaa tcc 1316

&lt;210&gt; 402

&lt;211&gt; 431

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 402

Thr Arg Gln Gly Val Arg Val Pro Val Ala Ala Glu Val Leu Asp Ala  
 1 5 10 15

Thr Gly Ala Val Thr Gly Tyr Thr Arg His Asp Leu Ile Glu Thr Ser  
 20 25 30

Val Ser Gly Arg Val Leu Ala Gly Asp Ala Thr Asn Ala Ala Gly Glu  
 35 40 45

Val Val Leu Ala Ala Gly Thr Asp Leu Thr Glu Leu Asn Ile Asp Leu  
 50 55 60

Leu Val Glu Ala Gly Ile Lys Asp Val Lys Val Arg Ser Val Leu Thr  
 65 70 75 80

Cys Gln Thr Pro Thr Gly Val Cys Ala Lys Cys Tyr Gly Lys Ser Met

85					90					95					
Ala	Ser	Gly	Gln	Gln	Val	Asp	Ile	Gly	Glu	Ala	Val	Gly	Ile	Val	Ala
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Ala	Gln	Ser	Ile	Gly	Glu	Pro	Gly	Thr	Gln	Leu	Thr	Met	Arg	Thr	Phe
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His	Gln	Gly	Gly	Val	Gly	Gly	Asp	Ile	Thr	Gly	Gly	Leu	Pro	Arg	Val
	130					135					140				
Gln	Glu	Leu	Phe	Glu	Ala	Arg	Val	Pro	Lys	Asn	Cys	Ala	Pro	Ile	Ala
145					150					155					160
Ser	Val	Glu	Gly	Val	Ile	His	Leu	Glu	Asp	Glu	Gly	Asn	Phe	Tyr	Thr
				165					170					175	
Leu	Thr	Ile	Val	Pro	Asp	Asp	Gly	Ser	Asp	Asn	Val	Val	Tyr	Glu	Lys
			180					185					190		
Leu	Ser	Lys	Arg	Gln	Gly	Leu	Ala	Ser	Thr	Arg	Val	Ala	Met	Glu	Ser
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Asn	Ala	Gly	Ala	Phe	Ile	Glu	Arg	Thr	Leu	Thr	Glu	Gly	Asp	Arg	Val
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Thr	Val	Gly	Gln	Arg	Leu	Leu	Arg	Gly	Ala	Ala	Asp	Pro	His	Asp	Val
225					230					235					240
Leu	Glu	Ile	Leu	Gly	Arg	Arg	Gly	Val	Glu	Gln	His	Leu	Ile	Tyr	Glu
				245					250					255	
Val	Gln	Ala	Val	Tyr	Arg	Ala	Gln	Gly	Val	Ala	Ile	His	Asp	Lys	His
			260					265					270		
Ile	Glu	Ile	Ile	Ile	Arg	Gln	Met	Leu	Arg	Arg	Gly	Thr	Val	Ile	Glu
		275					280					285			
Ser	Gly	Ser	Thr	Glu	Phe	Leu	Pro	Gly	Ser	Leu	Val	Asp	Leu	Ser	Glu
	290					295					300				
Ala	Lys	Leu	Ala	Asn	Ser	Glu	Ala	Ile	Gly	Ala	Gly	Gly	Gln	Pro	Ala
305					310					315					320
Glu	Leu	Arg	Ser	Glu	Ile	Met	Gly	Ile	Thr	Lys	Ala	Ser	Leu	Ala	Thr
				325					330					335	
Glu	Ser	Trp	Leu	Ser	Ala	Ala	Ser	Phe	Gln	Glu	Thr	Thr	Arg	Val	Leu
			340					345					350		
Thr	Asp	Ala	Ala	Ile	Asn	Lys	Arg	Ser	Asp	Lys	Leu	Ile	Gly	Leu	Lys
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Glu	Asn	Val	Ile	Ile	Gly	Lys	Leu	Ile	Pro	Ala	Gly	Thr	Gly	Ile	Ser
	370					375					380				
Arg	Tyr	Arg	Asn	Ile	Ser	Ile	Lys	Pro	Thr	Glu	Ala	Ala	Arg	Asn	Ala
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Ala	Tyr	Ser	Ile	Pro	Thr	Tyr	Gly	Glu	Ser	Ile	Tyr	Gly	Asp	Asp	Gly
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Met Thr Val Leu Pro 5															
aaa aac cat gac cta agc gat acc caa ctc gtc aaa cag ttt ata tct 163															
Lys Asn His Asp Leu Ser Asp Thr Gln Leu Val Lys Gln Phe Ile Ser 20															
ggc gac tcc agg gca ttt tcc acc atc att cac cgc cac gaa cga cat 211															
Gly Asp Ser Arg Ala Phe Ser Thr Ile Ile His Arg His Glu Arg His 35															
atg atg cag gca gcc aga aaa tac ggg cgg aaa cca gaa gac gcc caa 259															
Met Met Gln Ala Ala Arg Lys Tyr Gly Arg Lys Pro Glu Asp Ala Gln 50															
gac att ctg caa gaa gct ctg ttt cgc gcc agc cga aac atg cac ctt 307															
Asp Ile Leu Gln Glu Ala Leu Phe Arg Ala Ser Arg Asn Met His Leu 65															
tat aga gca gaa gca gct ctg ggc acg tgg ctg cac aaa ctt gtc ctg 355															
Tyr Arg Ala Glu Ala Ala Leu Gly Thr Trp Leu His Lys Leu Val Leu 85															
aat agc ggc ttc gat tgg gct acc cac cgc tcc caa gta gaa ttc ccc 403															
Asn Ser Gly Phe Asp Trp Ala Thr His Arg Ser Gln Val Glu Phe Pro 100															
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Ile Leu Asn Glu Pro Thr Ile Asp Leu Glu Lys Asp Pro Arg Leu Ala 115															
acc gac ccc ttg ggc tac ctg gat gtc gcc atg aca att cga tcc gcc 499															
Thr Asp Pro Leu Gly Tyr Leu Asp Val Ala Met Thr Ile Arg Ser Ala 130															
atc gac caa tta cac ccc gat caa cgc atc gcc tta ata ctt gtc gac 547															
Ile Asp Gln Leu His Pro Asp Gln Arg Ile Ala Leu Ile Leu Val Asp 145															
ctc ggc ggc tac acc gta gaa gat gtg gcc gaa atc gaa gga atc aaa 595															
Leu Gly Gly Tyr Thr Val Glu Asp Val Ala Glu Ile Glu Gly Ile Lys 165															

gta ggt acc gtt aaa tca cgc cga ggg cgc gca cgc aaa gcg ttg cgc 643  
 Val Gly Thr Val Lys Ser Arg Arg Gly Arg Ala Arg Lys Ala Leu Arg  
                   170                                  175                                  180

gcc ctt tta cat gca gat ttc ttc ggg ccc gaa gat ggc tcc ata cag 691  
 Ala Leu Leu His Ala Asp Phe Phe Gly Pro Glu Asp Gly Ser Ile Gln  
                   185                                  190                                  195

tgc gaa agc aac tgatggaagt ttttcaaagt gtc 726  
 Cys Glu Ser Asn  
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<212> PRT

<213> Corynebacterium glutamicum

<400> 404

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Lys Gln Phe Ile Ser Gly Asp Ser Arg Ala Phe Ser Thr Ile Ile His  
                   20                                  25                                  30

Arg His Glu Arg His Met Met Gln Ala Ala Arg Lys Tyr Gly Arg Lys  
                   35                                  40                                  45

Pro Glu Asp Ala Gln Asp Ile Leu Gln Glu Ala Leu Phe Arg Ala Ser  
           50                                  55                                  60

Arg Asn Met His Leu Tyr Arg Ala Glu Ala Ala Leu Gly Thr Trp Leu  
           65                                  70                                  75                                  80

His Lys Leu Val Leu Asn Ser Gly Phe Asp Trp Ala Thr His Arg Ser  
                   85                                  90                                  95

Gln Val Glu Phe Pro Ile Leu Asn Glu Pro Thr Ile Asp Leu Glu Lys  
                   100                                  105                                  110

Asp Pro Arg Leu Ala Thr Asp Pro Leu Gly Tyr Leu Asp Val Ala Met  
           115                                  120                                  125

Thr Ile Arg Ser Ala Ile Asp Gln Leu His Pro Asp Gln Arg Ile Ala  
           130                                  135                                  140

Leu Ile Leu Val Asp Leu Gly Gly Tyr Thr Val Glu Asp Val Ala Glu  
           145                                  150                                  155                                  160

Ile Glu Gly Ile Lys Val Gly Thr Val Lys Ser Arg Arg Gly Arg Ala  
                   165                                  170                                  175

Arg Lys Ala Leu Arg Ala Leu Leu His Ala Asp Phe Phe Gly Pro Glu  
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Asp Gly Ser Ile Gln Cys Glu Ser Asn  
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                                         Met Ala Glu Asn Arg
                                         1           5

acc ggc aca gtc gat gga gac gcg ttg gct gcc cgc ttt gaa gag gag 163
Thr Gly Thr Val Asp Gly Asp Ala Leu Ala Ala Arg Phe Glu Glu Glu
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gca ctg cca ctc ctt gac cag ctc tat ggc ggt gct ctg cgc atg act 211
Ala Leu Pro Leu Leu Asp Gln Leu Tyr Gly Gly Ala Leu Arg Met Thr
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aga aat ccc gca gat gcg gaa gat ctc gtg caa gac acc tat atc aag 259
Arg Asn Pro Ala Asp Ala Glu Asp Leu Val Gln Asp Thr Tyr Ile Lys
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gcg tac cag gcg ttc gcg agc ttc aaa cca ggc acc aac ctg aag gct 307
Ala Tyr Gln Ala Phe Ala Ser Phe Lys Pro Gly Thr Asn Leu Lys Ala
                        55                        60                        65

tgg ctc tat cgg atc atg acg aat acc tac atc aac atg tac cga aag 355
Trp Leu Tyr Arg Ile Met Thr Asn Thr Tyr Ile Asn Met Tyr Arg Lys
                        70                        75                        80                        85

aaa cag agg cag cca tcg caa acc tct gcc gat gag atc act gac tac 403
Lys Gln Arg Gln Pro Ser Gln Thr Ser Ala Asp Glu Ile Thr Asp Tyr
                        90                        95                        100

cag ctc gtt gaa tct caa tcg cat acc tca aca ggg ctg gaa tcc gcc 451
Gln Leu Val Glu Ser Gln Ser His Thr Ser Thr Gly Leu Glu Ser Ala
                        105                        110                        115

gag gtt gag gct ctg aaa aat ctg cca gac gga aaa att ggc gat gca 499
Glu Val Glu Ala Leu Lys Asn Leu Pro Asp Gly Lys Ile Gly Asp Ala
                        120                        125                        130

atg aat caa ctc agc ccg gaa tac cgg atg gtg gtt tat tat gcc gat 547
Met Asn Gln Leu Ser Pro Glu Tyr Arg Met Val Val Tyr Tyr Ala Asp
                        135                        140                        145

gta gaa gat ctc gca tac aaa gaa atc gcc gag atc atg gac gtt cca 595
Val Glu Asp Leu Ala Tyr Lys Glu Ile Ala Glu Ile Met Asp Val Pro
                        150                        155                        160                        165

ctc gga act gtg atg tcc cga ctc cat cgt gga aga aaa cag ctc cga 643
Leu Gly Thr Val Met Ser Arg Leu His Arg Gly Arg Lys Gln Leu Arg
                        170                        175                        180

gga atg tta aag gaa gta gcg aag gaa caa ggc att ggt ctt gaa cat 691

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Gly Met Leu Lys Glu Val Ala Lys Glu Gln Gly Ile Gly Leu Glu His  
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ccc gac atg aag aaa aat tcg gag gca taacgatgac gaatctcaac cgc 741  
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 35 40 45

Asp Thr Tyr Ile Lys Ala Tyr Gln Ala Phe Ala Ser Phe Lys Pro Gly  
 50 55 60

Thr Asn Leu Lys Ala Trp Leu Tyr Arg Ile Met Thr Asn Thr Tyr Ile  
 65 70 75 80

Asn Met Tyr Arg Lys Lys Gln Arg Gln Pro Ser Gln Thr Ser Ala Asp  
 85 90 95

Glu Ile Thr Asp Tyr Gln Leu Val Glu Ser Gln Ser His Thr Ser Thr  
 100 105 110

Gly Leu Glu Ser Ala Glu Val Glu Ala Leu Lys Asn Leu Pro Asp Gly  
 115 120 125

Lys Ile Gly Asp Ala Met Asn Gln Leu Ser Pro Glu Tyr Arg Met Val  
 130 135 140

Val Tyr Tyr Ala Asp Val Glu Asp Leu Ala Tyr Lys Glu Ile Ala Glu  
 145 150 155 160

Ile Met Asp Val Pro Leu Gly Thr Val Met Ser Arg Leu His Arg Gly  
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Arg Lys Gln Leu Arg Gly Met Leu Lys Glu Val Ala Lys Glu Gln Gly  
 180 185 190

Ile Gly Leu Glu His Pro Asp Met Lys Lys Asn Ser Glu Ala  
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&lt;222&gt; (101)..(793)

&lt;223&gt; RXA00304

&lt;400&gt; 407

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tccgttgaac ctcttgaacc gcgaatttag gaggccagtt atg aca gca ccg tcc 115
                                         Met Thr Ala Pro Ser
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acg cag gat ctc gca acg act gaa cgt gag gta gat ccc ggc agc aga 163
Thr Gln Asp Leu Ala Thr Thr Glu Arg Glu Val Asp Pro Gly Ser Arg
                        10                               15                               20

agg ggc caa acc aac gac aat ccc tcg cag gac ctt gtt cgc gtt tac 211
Arg Gly Gln Thr Asn Asp Asn Pro Ser Gln Asp Leu Val Arg Val Tyr
                        25                               30                               35

ctc aac ggc atc ggc aaa act gcc ttg ctt acc gcg gag gat gaa gtt 259
Leu Asn Gly Ile Gly Lys Thr Ala Leu Leu Thr Ala Glu Asp Glu Val
                        40                               45                               50

gag ctc gca cag acc att gag gtt ggc ctt tat gca gag cac ctt ctg 307
Glu Leu Ala Gln Thr Ile Glu Val Gly Leu Tyr Ala Glu His Leu Leu
                        55                               60                               65

aaa aac tct gaa gag cca ctc acc cgc gcc atg aag cgc gat cta aag 355
Lys Asn Ser Glu Glu Pro Leu Thr Arg Ala Met Lys Arg Asp Leu Lys
                        70                               75                               80                               85

gtt ctt gcc aag gac ggc aag aag gct cgt tcc cac ctc ctc gag gca 403
Val Leu Ala Lys Asp Gly Lys Lys Ala Arg Ser His Leu Leu Glu Ala
                        90                               95                               100

aac ctg cgc ctg gtg gtg tcc ctt gct aag cgc tac acc ggc cgc ggc 451
Asn Leu Arg Leu Val Val Ser Leu Ala Lys Arg Tyr Thr Gly Arg Gly
                        105                               110                               115

atg cca ctg ctg gat ctt atc cag gag ggc aac ctc gga ctg atc cgc 499
Met Pro Leu Leu Asp Leu Ile Gln Glu Gly Asn Leu Gly Leu Ile Arg
                        120                               125                               130

gcg atg gaa aag ttt gat tac tcc aag ggc ttt aag ttc tcc acc tac 547
Ala Met Glu Lys Phe Asp Tyr Ser Lys Gly Phe Lys Phe Ser Thr Tyr
                        135                               140                               145

gca acc tgg tgg atc cgc cag gca atc acc cgc ggc atg gca gat cag 595
Ala Thr Trp Trp Ile Arg Gln Ala Ile Thr Arg Gly Met Ala Asp Gln
                        150                               155                               160                               165

tcc cgc acc atc cgc ctc cca gtc cac ctt gtg gag cag gtg aac aag 643
Ser Arg Thr Ile Arg Leu Pro Val His Leu Val Glu Gln Val Asn Lys
                        170                               175                               180

ctt tcc cgc atc aag cgc gag ttg tac cag cac ttg ggc cgt gaa gcc 691
Leu Ser Arg Ile Lys Arg Glu Leu Tyr Gln His Leu Gly Arg Glu Ala
                        185                               190                               195

acc aat gag gaa ctc gca gaa gag tcc ggc att gaa gag tcc aag att 739
Thr Asn Glu Glu Leu Ala Glu Glu Ser Gly Ile Glu Glu Ser Lys Ile
                        200                               205                               210

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gaa atg ctg ctt cgt cag tct cgc gat cca gtg agc ttg gac atg cca 787  
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gtc ggc 793  
 Val Gly  
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<210> 408

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<212> PRT

<213> Corynebacterium glutamicum

<400> 408

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 20 25 30

Leu Val Arg Val Tyr Leu Asn Gly Ile Gly Lys Thr Ala Leu Leu Thr  
 35 40 45

Ala Glu Asp Glu Val Glu Leu Ala Gln Thr Ile Glu Val Gly Leu Tyr  
 50 55 60

Ala Glu His Leu Leu Lys Asn Ser Glu Glu Pro Leu Thr Arg Ala Met  
 65 70 75 80

Lys Arg Asp Leu Lys Val Leu Ala Lys Asp Gly Lys Lys Ala Arg Ser  
 85 90 95

His Leu Leu Glu Ala Asn Leu Arg Leu Val Val Ser Leu Ala Lys Arg  
 100 105 110

Tyr Thr Gly Arg Gly Met Pro Leu Leu Asp Leu Ile Gln Glu Gly Asn  
 115 120 125

Leu Gly Leu Ile Arg Ala Met Glu Lys Phe Asp Tyr Ser Lys Gly Phe  
 130 135 140

Lys Phe Ser Thr Tyr Ala Thr Trp Trp Ile Arg Gln Ala Ile Thr Arg  
 145 150 155 160

Gly Met Ala Asp Gln Ser Arg Thr Ile Arg Leu Pro Val His Leu Val  
 165 170 175

Glu Gln Val Asn Lys Leu Ser Arg Ile Lys Arg Glu Leu Tyr Gln His  
 180 185 190

Leu Gly Arg Glu Ala Thr Asn Glu Glu Leu Ala Glu Glu Ser Gly Ile  
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Glu Glu Ser Lys Ile Glu Met Leu Leu Arg Gln Ser Arg Asp Pro Val  
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Ser Leu Asp Met Pro Val Gly  
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Arg Glu Leu Ala Asp Leu Val Pro Gln Ala Thr Ala Gly Asp Arg Arg

10                          15                          20

gca ttg caa aga ata atg gag att att cac ccc att gtt ttg cgt tat 211  
Ala Leu Gln Arg Ile Met Glu Ile Ile His Pro Ile Val Leu Arg Tyr  
25 30 35

gct cgc gct cgt att gga ggt gga cgc cag cca acg gca gaa gac gtt 259  
Ala Arg Ala Arg Ile Gly Gly Gly Arg Gln Pro Thr Ala Glu Asp Val  
40 45 50

gct caa gaa atc tgc ctg gcg gta gcc acc tcc att agg aac ttt gtc 307  
Ala Gln Glu Ile Cys Leu Ala Val Ala Thr Ser Ile Arg Asn Phe Val  
55 60 65

gac cag ggt agg ccg ttc atg gcg ttt gtc tac ggc att gca tct aac 355  
Asp Gln Gly Arg Pro Phe Met Ala Phe Val Tyr Gly Ile Ala Ser Asn  
70 75 80 85

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Lys Val Ala Asp Ala His Arg Ala Met Ser Arg Asp Lys Ser Thr Pro
          90                      95                      100
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att gag gaa gtc cca gaa act tca cca gat act ttt acc ccc gaa gac 451  
Ile Glu Glu Val Pro Glu Thr Ser Pro Asp Thr Phe Thr Pro Glu Asp  
105 110 115

ttt gcg ctg gtc agc gat gga agt aac aga gtt agg gaa ctt ctc gat 499  
Phe Ala Leu Val Ser Asp Gly Ser Asn Arg Val Arg Glu Leu Leu Asp  
120 125 130

cta ctg agt gaa aag gca cgc gac att ctt atc ttg aga gtt atc gtt 547  
Leu Leu Ser Glu Lys Ala Arg Asp Ile Leu Ile Leu Arg Val Ile Val  
135 140 145

ggt ctt tcc gca gaa gaa act gca gag atg gtg ggc agc acc cca ggt 595  
Gly Leu Ser Ala Glu Glu Thr Ala Glu Met Val Gly Ser Thr Pro Gly  
150 155 160 165

gct gta cga gtt gcc caa cac agg gca ctc acg aca ctt cga agc aca 643  
Ala Val Arg Val Ala Gln His Arg Ala Leu Thr Thr Leu Arg Ser Thr  
170 175 180

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687

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 Ile Val Leu Arg Tyr Ala Arg Ala Arg Ile Gly Gly Gly Arg Gln Pro  
 35 40 45  
 Thr Ala Glu Asp Val Ala Gln Glu Ile Cys Leu Ala Val Ala Thr Ser  
 50 55 60  
 Ile Arg Asn Phe Val Asp Gln Gly Arg Pro Phe Met Ala Phe Val Tyr  
 65 70 75 80  
 Gly Ile Ala Ser Asn Lys Val Ala Asp Ala His Arg Ala Met Ser Arg  
 85 90 95  
 Asp Lys Ser Thr Pro Ile Glu Glu Val Pro Glu Thr Ser Pro Asp Thr  
 100 105 110  
 Phe Thr Pro Glu Asp Phe Ala Leu Val Ser Asp Gly Ser Asn Arg Val  
 115 120 125  
 Arg Glu Leu Leu Asp Leu Leu Ser Glu Lys Ala Arg Asp Ile Leu Ile  
 130 135 140  
 Leu Arg Val Ile Val Gly Leu Ser Ala Glu Glu Thr Ala Glu Met Val  
 145 150 155 160  
 Gly Ser Thr Pro Gly Ala Val Arg Val Ala Gln His Arg Ala Leu Thr  
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 Thr Leu Arg Ser Thr Leu Glu Gln Gln Glu Asn Lys  
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Ala	Leu	Ala	Ala	Gly	Arg	Gly	Asp	Arg	Ala	Ala	Leu	Thr	Asp	Phe	Ile	
			20					25					30			
cgg	gaa	acc	caa	gac	gat	gtc	tgg	cgt	ctc	ctc	gcc	cac	ctt	ggc	ggc	144
Arg	Glu	Thr	Gln	Asp	Asp	Val	Trp	Arg	Leu	Leu	Ala	His	Leu	Gly	Gly	
		35					40					45				
cac	gaa	atc	gcc	gac	gat	cta	acc	caa	gaa	act	tat	ctg	cgg	gtc	atg	192
His	Glu	Ile	Ala	Asp	Asp	Leu	Thr	Gln	Glu	Thr	Tyr	Leu	Arg	Val	Met	
	50					55					60					
agc	gcc	ctc	ccc	cgc	ttc	gca	gcg	cgc	tcc	tcg	gcg	cgc	acc	tgg	cta	240
Ser	Ala	Leu	Pro	Arg	Phe	Ala	Ala	Arg	Ser	Ser	Ala	Arg	Thr	Trp	Leu	
65					70				75					80		
cta	tcg	cta	gcc	cgg	cgc	gtc	tgg	gtc	gac	aac	atc	cga	cac	gac	atg	288
Leu	Ser	Leu	Ala	Arg	Arg	Val	Trp	Val	Asp	Asn	Ile	Arg	His	Asp	Met	
				85					90					95		
gca	cgc	ccc	cgc	aaa	tcc	atc	gtc	gaa	tac	gaa	gac	acc	ggg	gcc	acc	336
Ala	Arg	Pro	Arg	Lys	Ser	Ile	Val	Glu	Tyr	Glu	Asp	Thr	Gly	Ala	Thr	
			100					105					110			
gac	gcg	agc	aac	gca	ggc	atc	tgg	tcc	gag	tgg	atc	gac	gtg	cgc	acg	384
Asp	Ala	Ser	Asn	Ala	Gly	Ile	Trp	Ser	Glu	Trp	Ile	Asp	Val	Arg	Thr	
		115				120						125				
ctt	atc	gac	gcc	ctc	cca	ccc	gaa	cgc	cgc	gaa	gcc	ctc	atc	ctc	acc	432
Leu	Ile	Asp	Ala	Leu	Pro	Pro	Glu	Arg	Arg	Glu	Ala	Leu	Ile	Leu	Thr	
	130					135					140					
caa	gtg	ttg	ggc	tac	acc	tac	gaa	gaa	gcc	gca	aaa	atc	gcc	gac	gtc	480
Gln	Val	Leu	Gly	Tyr	Thr	Tyr	Glu	Glu	Ala	Ala	Lys	Ile	Ala	Asp	Val	
145					150				155						160	
cga	gtc	gga	aca	atc	cgt	tcc	cgc	gta	gcc	cgc	gcc	aga	gcg	gac	ctc	528
Arg	Val	Gly	Thr	Ile	Arg	Ser	Arg	Val	Ala	Arg	Ala	Arg	Ala	Asp	Leu	
				165					170					175		
att	gct	gca	aca	gct	acc	ggg	gat	tcc	tca	gcc	gaa	gat	ggc	aaa	tcc	576
Ile	Ala	Ala	Thr	Ala	Thr	Gly	Asp	Ser	Ser	Ala	Glu	Asp	Gly	Lys	Ser	
			180				185						190			
gcc	caa	ggg	tagcagatga	gctacgtcaa	cgg											608
Ala	Gln	Gly														
		195														

&lt;210&gt; 412

&lt;211&gt; 195

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 412

Ala	Ile	Val	Lys	Ser	Lys	Glu	Arg	Asn	Asp	Ala	His	Val	Thr	Glu	Leu
1				5					10					15	

Ala Leu Ala Ala Gly Arg Gly Asp Arg Ala Ala Leu Thr Asp Phe Ile  
                   20                  25                  30

Arg Glu Thr Gln Asp Asp Val Trp Arg Leu Leu Ala His Leu Gly Gly  
                   35                  40                  45

His Glu Ile Ala Asp Asp Leu Thr Gln Glu Thr Tyr Leu Arg Val Met  
           50                  55                  60

Ser Ala Leu Pro Arg Phe Ala Ala Arg Ser Ser Ala Arg Thr Trp Leu  
       65                  70                  75                  80

Leu Ser Leu Ala Arg Arg Val Trp Val Asp Asn Ile Arg His Asp Met  
                   85                  90                  95

Ala Arg Pro Arg Lys Ser Ile Val Glu Tyr Glu Asp Thr Gly Ala Thr  
                   100                  105                  110

Asp Ala Ser Asn Ala Gly Ile Trp Ser Glu Trp Ile Asp Val Arg Thr  
           115                  120                  125

Leu Ile Asp Ala Leu Pro Pro Glu Arg Arg Glu Ala Leu Ile Leu Thr  
       130                  135                  140

Gln Val Leu Gly Tyr Thr Tyr Glu Glu Ala Ala Lys Ile Ala Asp Val  
   145                  150                  155                  160

Arg Val Gly Thr Ile Arg Ser Arg Val Ala Arg Ala Arg Ala Asp Leu  
                   165                  170                  175

Ile Ala Ala Thr Ala Thr Gly Asp Ser Ser Ala Glu Asp Gly Lys Ser  
           180                  185                  190

Ala Gln Gly  
       195

<210> 413  
 <211> 765  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(742)  
 <223> RXA01530

<400> 413  
 cgcgccatcg ctcgtgacgg cgcgaaggcg aaaaaccacc tcctggaagc caaccttcgt 60

ctggttgtct ccctggcaaa gacgctacac cggccgtggc atg gca ttc ctg gac 115  
   Met Ala Phe Leu Asp  
   1                  5

ctc atc cag gaa ggc aac ctc ggt ctg att cgt gcc gta gag aag ttc 163  
 Leu Ile Gln Glu Gly Asn Leu Gly Leu Ile Arg Ala Val Glu Lys Phe  
                   10                  15                  20

gac tac tcc aag ggc tac aag ttc tcc acc tac gca acc tgg tgg atc 211  
 Asp Tyr Ser Lys Gly Tyr Lys Phe Ser Thr Tyr Ala Thr Trp Trp Ile  
           25                  30                  35

cgt cag gca atc acc cgc gcc atg gcc gac caa gca cga acc atc cgt 259  
 Arg Gln Ala Ile Thr Arg Ala Met Ala Asp Gln Ala Arg Thr Ile Arg  
 40 45 50  
  
 atc cca gtc cac atg gtt gaa gtg atc aac aaa ctt ggt cgc atc caa 307  
 Ile Pro Val His Met Val Glu Val Ile Asn Lys Leu Gly Arg Ile Gln  
 55 60 65  
  
 cgt gaa ctc ctt cag gaa ctc ggc cgc gaa cca acc cca cag gaa ctg 355  
 Arg Glu Leu Leu Gln Glu Leu Gly Arg Glu Pro Thr Pro Gln Glu Leu  
 70 75 80 85  
  
 tcc aaa gaa atg gac atc tcc gag gaa aag gta ctg gaa atc cag cag 403  
 Ser Lys Glu Met Asp Ile Ser Glu Glu Lys Val Leu Glu Ile Gln Gln  
 90 95 100  
  
 tac gcc cgc gaa cca atc tcc ctg gac caa acc atc ggc gac gaa ggc 451  
 Tyr Ala Arg Glu Pro Ile Ser Leu Asp Gln Thr Ile Gly Asp Glu Gly  
 105 110 115  
  
 gac agc cag ctc ggc gac ttc atc gaa gac tcc gaa gcc gtc gtc gca 499  
 Asp Ser Gln Leu Gly Asp Phe Ile Glu Asp Ser Glu Ala Val Val Ala  
 120 125 130  
  
 gtc gac gcc gtc tca ttc acc ctg ctg caa gac cag cta cag gac gtc 547  
 Val Asp Ala Val Ser Phe Thr Leu Leu Gln Asp Gln Leu Gln Asp Val  
 135 140 145  
  
 cta gag acc ctc tcc gaa cgt gaa gcc ggc gtg gtt aaa ctc cgc ttc 595  
 Leu Glu Thr Leu Ser Glu Arg Glu Ala Gly Val Val Lys Leu Arg Phe  
 150 155 160 165  
  
 gga ctc acc gac gga atg cca cgc act tta gac gaa atc ggc caa gtt 643  
 Gly Leu Thr Asp Gly Met Pro Arg Thr Leu Asp Glu Ile Gly Gln Val  
 170 175 180  
  
 tac ggt gtc acc cgt gag cgc atc cgc cag att gag tcc aag acc atg 691  
 Tyr Gly Val Thr Arg Glu Arg Ile Arg Gln Ile Glu Ser Lys Thr Met  
 185 190 195  
  
 tct aag ctg cgc cac cca tca cgc tcc cag gtc ctt cgc gac tac ctg 739  
 Ser Lys Leu Arg His Pro Ser Arg Ser Gln Val Leu Arg Asp Tyr Leu  
 200 205 210  
  
 gac taaaacccca gtcgggctca aga 765  
 Asp

&lt;210&gt; 414

&lt;211&gt; 214

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 414

Met Ala Phe Leu Asp Leu Ile Gln Glu Gly Asn Leu Gly Leu Ile Arg  
 1 5 10 15

Ala Val Glu Lys Phe Asp Tyr Ser Lys Gly Tyr Lys Phe Ser Thr Tyr  
 20 25 30

Ala Thr Trp Trp Ile Arg Gln Ala Ile Thr Arg Ala Met Ala Asp Gln  
                   35                                  40                                  45

Ala Arg Thr Ile Arg Ile Pro Val His Met Val Glu Val Ile Asn Lys  
           50                                  55                                  60

Leu Gly Arg Ile Gln Arg Glu Leu Leu Gln Glu Leu Gly Arg Glu Pro  
       65                                  70                                  75                                  80

Thr Pro Gln Glu Leu Ser Lys Glu Met Asp Ile Ser Glu Glu Lys Val  
                                   85                                  90                                  95

Leu Glu Ile Gln Gln Tyr Ala Arg Glu Pro Ile Ser Leu Asp Gln Thr  
                                   100                                  105                                  110

Ile Gly Asp Glu Gly Asp Ser Gln Leu Gly Asp Phe Ile Glu Asp Ser  
           115                                  120                                  125

Glu Ala Val Val Ala Val Asp Ala Val Ser Phe Thr Leu Leu Gln Asp  
       130                                  135                                  140

Gln Leu Gln Asp Val Leu Glu Thr Leu Ser Glu Arg Glu Ala Gly Val  
       145                                  150                                  155                                  160

Val Lys Leu Arg Phe Gly Leu Thr Asp Gly Met Pro Arg Thr Leu Asp  
                                   165                                  170                                  175

Glu Ile Gly Gln Val Tyr Gly Val Thr Arg Glu Arg Ile Arg Gln Ile  
                                   180                                  185                                  190

Glu Ser Lys Thr Met Ser Lys Leu Arg His Pro Ser Arg Ser Gln Val  
           195                                  200                                  205

Leu Arg Asp Tyr Leu Asp  
       210

&lt;210&gt; 415

&lt;211&gt; 1140

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1117)

&lt;223&gt; RXA01531

&lt;400&gt; 415

taggcggaag gggcggttaag tacttgccat ttaatcctca gcatcactcg gatcagtcgg 60

agatgtcgat gaaaatgcac caggagccgt ggagagcagc atg gta gaa aac aac 115  
   Met Val Glu Asn Asn  
   1                                  5

gta gca aaa aag acg gtc gct aaa aag acc gca cgc aag acc gca cgc 163  
   Val Ala Lys Lys Thr Val Ala Lys Lys Thr Ala Arg Lys Thr Ala Arg  
                                   10                                  15                                  20

aaa gca gcc ccg cgc gtg gca acc cca ttg gga gtc gca tct gag tct 211  
   Lys Ala Ala Pro Arg Val Ala Thr Pro Leu Gly Val Ala Ser Glu Ser

25					30					35						
ccc	att	tcg	gcc	acc	cct	gcg	cgc	agc	atc	gat	gga	acc	tca	acc	cct	259
Pro	Ile	Ser	Ala	Thr	Pro	Ala	Arg	Ser	Ile	Asp	Gly	Thr	Ser	Thr	Pro	
		40					45					50				
ggt	gaa	gct	gct	gac	acc	ata	gag	acc	acc	gcc	cct	gca	gcg	aag	gct	307
Val	Glu	Ala	Ala	Asp	Thr	Ile	Glu	Thr	Thr	Ala	Pro	Ala	Ala	Lys	Ala	
	55					60					65					
cct	gcg	gcc	aag	gct	ccc	gct	aaa	aag	gtt	gcc	aag	aag	aca	gct	cgc	355
Pro	Ala	Ala	Lys	Ala	Pro	Ala	Lys	Lys	Val	Ala	Lys	Lys	Thr	Ala	Arg	
	70				75					80					85	
aag	gca	cct	gcg	aaa	aag	act	gtc	gcc	aag	aaa	gcc	aca	acc	gcc	aag	403
Lys	Ala	Pro	Ala	Lys	Lys	Thr	Val	Ala	Lys	Lys	Ala	Thr	Thr	Ala	Lys	
				90					95					100		
gct	gca	cct	gca	act	gcc	aag	gac	gaa	aac	gca	cct	gtt	gat	gac	gac	451
Ala	Ala	Pro	Ala	Thr	Ala	Lys	Asp	Glu	Asn	Ala	Pro	Val	Asp	Asp	Asp	
			105					110					115			
gag	gag	aac	ctc	gct	cag	gat	gaa	cag	gac	ttc	gac	ggc	gat	gac	ttc	499
Glu	Glu	Asn	Leu	Ala	Gln	Asp	Glu	Gln	Asp	Phe	Asp	Gly	Asp	Asp	Phe	
		120					125					130				
gta	gac	ggc	atc	gaa	gac	gaa	gaa	gat	gaa	gac	ggc	gtc	gaa	gcc	ctc	547
Val	Asp	Gly	Ile	Glu	Asp	Glu	Glu	Asp	Glu	Asp	Gly	Val	Glu	Ala	Leu	
	135					140					145					
ggt	gaa	gaa	agc	gaa	gac	gac	gaa	gag	gac	ggc	tca	tcc	gtt	tgg	gat	595
Gly	Glu	Glu	Ser	Glu	Asp	Asp	Glu	Glu	Asp	Gly	Ser	Ser	Val	Trp	Asp	
	150				155					160					165	
gaa	gac	gaa	tcc	gca	acc	ctg	cgt	cag	gca	cgt	aaa	gat	gcc	gag	ctc	643
Glu	Asp	Glu	Ser	Ala	Thr	Leu	Arg	Gln	Ala	Arg	Lys	Asp	Ala	Glu	Leu	
				170					175					180		
acc	gct	tcc	gcc	gac	tct	gtt	cgc	gct	tac	ctg	aag	caa	atc	ggg	aaa	691
Thr	Ala	Ser	Ala	Asp	Ser	Val	Arg	Ala	Tyr	Leu	Lys	Gln	Ile	Gly	Lys	
			185					190					195			
gtt	gcc	ctg	ctg	aac	gct	gaa	cag	gaa	gtc	tcc	ctg	gca	aag	cgc	atc	739
Val	Ala	Leu	Leu	Asn	Ala	Glu	Gln	Glu	Val	Ser	Leu	Ala	Lys	Arg	Ile	
		200					205					210				
gaa	gca	ggc	ctt	tac	gcc	acc	cac	cgc	atg	gag	gaa	atg	gaa	gaa	gct	787
Glu	Ala	Gly	Leu	Tyr	Ala	Thr	His	Arg	Met	Glu	Glu	Met	Glu	Glu	Ala	
	215					220					225					
ttc	gca	gcc	ggt	gac	aag	gac	gcg	aaa	ctc	acc	cca	gcc	gtc	aag	cgt	835
Phe	Ala	Ala	Gly	Asp	Lys	Asp	Ala	Lys	Leu	Thr	Pro	Ala	Val	Lys	Arg	
	230				235					240					245	
gac	ctc	cgc	gcc	atc	gct	cgt	gac	ggc	cgc	aag	gcg	aaa	aac	cac	ctc	883
Asp	Leu	Arg	Ala	Ile	Ala	Arg	Asp	Gly	Arg	Lys	Ala	Lys	Asn	His	Leu	
			250					255						260		
ctg	gaa	gcc	aac	ctt	cgt	ctg	gtt	gtc	tcc	ctg	gca	aag	acg	cta	cac	931
Leu	Glu	Ala	Asn	Leu	Arg	Leu	Val	Val	Ser	Leu	Ala	Lys	Thr	Leu	His	
			265					270					275			

cgg ccg tgg cat ggc att cct gga cct cat cca gga agg caa cct cgg 979  
 Arg Pro Trp His Gly Ile Pro Gly Pro His Pro Gly Arg Gln Pro Arg  
 280 285 290  
 tct gat tcg tgc cgt aga gaa gtt cga cta ctc caa ggg cta caa gtt 1027  
 Ser Asp Ser Cys Arg Arg Glu Val Arg Leu Leu Gln Gly Leu Gln Val  
 295 300 305  
 ctc cac cta cgc aac ctg gtg gat ccg tca ggc aat cac ccg cgc cat 1075  
 Leu His Leu Arg Asn Leu Val Asp Pro Ser Gly Asn His Pro Arg His  
 310 315 320 325  
 ggc cga cca agc acg aac cat ccg tat ccc agt cca cat ggt 1117  
 Gly Arg Pro Ser Thr Asn His Pro Tyr Pro Ser Pro His Gly  
 330 335  
 tgaagtgatc aacaaacttg gtc 1140

&lt;210&gt; 416

&lt;211&gt; 339

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 416

Met Val Glu Asn Asn Val Ala Lys Lys Thr Val Ala Lys Lys Thr Ala  
 1 5 10 15  
 Arg Lys Thr Ala Arg Lys Ala Ala Pro Arg Val Ala Thr Pro Leu Gly  
 20 25 30  
 Val Ala Ser Glu Ser Pro Ile Ser Ala Thr Pro Ala Arg Ser Ile Asp  
 35 40 45  
 Gly Thr Ser Thr Pro Val Glu Ala Ala Asp Thr Ile Glu Thr Thr Ala  
 50 55 60  
 Pro Ala Ala Lys Ala Pro Ala Ala Lys Ala Pro Ala Lys Lys Val Ala  
 65 70 75 80  
 Lys Lys Thr Ala Arg Lys Ala Pro Ala Lys Lys Thr Val Ala Lys Lys  
 85 90 95  
 Ala Thr Thr Ala Lys Ala Ala Pro Ala Thr Ala Lys Asp Glu Asn Ala  
 100 105 110  
 Pro Val Asp Asp Asp Glu Glu Asn Leu Ala Gln Asp Glu Gln Asp Phe  
 115 120 125  
 Asp Gly Asp Asp Phe Val Asp Gly Ile Glu Asp Glu Glu Asp Glu Asp  
 130 135 140  
 Gly Val Glu Ala Leu Gly Glu Glu Ser Glu Asp Asp Glu Glu Asp Gly  
 145 150 155 160  
 Ser Ser Val Trp Asp Glu Asp Glu Ser Ala Thr Leu Arg Gln Ala Arg  
 165 170 175  
 Lys Asp Ala Glu Leu Thr Ala Ser Ala Asp Ser Val Arg Ala Tyr Leu  
 180 185 190

Lys Gln Ile Gly Lys Val Ala Leu Leu Asn Ala Glu Gln Glu Val Ser  
 195 200 205  
 Leu Ala Lys Arg Ile Glu Ala Gly Leu Tyr Ala Thr His Arg Met Glu  
 210 215 220  
 Glu Met Glu Glu Ala Phe Ala Ala Gly Asp Lys Asp Ala Lys Leu Thr  
 225 230 235 240  
 Pro Ala Val Lys Arg Asp Leu Arg Ala Ile Ala Arg Asp Gly Arg Lys  
 245 250 255  
 Ala Lys Asn His Leu Leu Glu Ala Asn Leu Arg Leu Val Val Ser Leu  
 260 265 270  
 Ala Lys Thr Leu His Arg Pro Trp His Gly Ile Pro Gly Pro His Pro  
 275 280 285  
 Gly Arg Gln Pro Arg Ser Asp Ser Cys Arg Arg Glu Val Arg Leu Leu  
 290 295 300  
 Gln Gly Leu Gln Val Leu His Leu Arg Asn Leu Val Asp Pro Ser Gly  
 305 310 315 320  
 Asn His Pro Arg His Gly Arg Pro Ser Thr Asn His Pro Tyr Pro Ser  
 325 330 335  
 Pro His Gly

<210> 417

<211> 771

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(748)

<223> RXA02065

<400> 417

cgagatgtga agtacctaca cgcattaagt gcaaatgaat tcacaattgc cagaagatgc 60

acaggatgta atctagattt cccaagttca gtggggcaaa atg act tat atg aaa 115  
 Met Thr Tyr Met Lys  
 1 5

aag aag tcc cga gat gac gca ccc gtc gta atc gaa acc gtt caa gca 163  
 Lys Lys Ser Arg Asp Ala Pro Val Val Ile Glu Thr Val Gln Ala  
 10 15 20

gaa cat gct gaa gaa ctc acg ggc act gca gca ttc gat gct gga cag 211  
 Glu His Ala Glu Glu Leu Thr Gly Thr Ala Ala Phe Asp Ala Gly Gln  
 25 30 35

gca gac atg cca aca tgg ggc gag cta gtc gca gaa cat gca gat agc 259  
 Ala Asp Met Pro Thr Trp Gly Glu Leu Val Ala Glu His Ala Asp Ser  
 40 45 50

gtt tac cgc ctc gcg tac cgt ctt tcc ggc aac cag cac gat gct gaa 307  
 Val Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn Gln His Asp Ala Glu  
 55 60 65  
 gac ctg acc caa gaa aca ttc atg cgt gtc ttc cgc tcg ttg aag agc 355  
 Asp Leu Thr Gln Glu Thr Phe Met Arg Val Phe Arg Ser Leu Lys Ser  
 70 75 80 85  
 tac cag cca ggc acc ttt gag ggc tgg ctg cac cgc atc acc acc aac 403  
 Tyr Gln Pro Gly Thr Phe Glu Gly Trp Leu His Arg Ile Thr Thr Asn  
 90 95 100  
 ttg ttc ctt gat atg gtt cgc cac cgc ggc aag atc cgc atg gag gcg 451  
 Leu Phe Leu Asp Met Val Arg His Arg Gly Lys Ile Arg Met Glu Ala  
 105 110 115  
 ctg cct gaa gat tat gag cgc gtt ccg ggc aat gac atc acc cca gag 499  
 Leu Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn Asp Ile Thr Pro Glu  
 120 125 130  
 cag gca tac acc gaa gct aac ctt gac cca gct ctg cag gca gcc ctc 547  
 Gln Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala Leu Gln Ala Ala Leu  
 135 140 145  
 gat gag ttg agc cca gac ttc cgc gtg gca gtg atc ctc tgt gat gtt 595  
 Asp Glu Leu Ser Pro Asp Phe Arg Val Ala Val Ile Leu Cys Asp Val  
 150 155 160 165  
 gtt ggt atg agc tat gac gaa atc gca gag acc ctc gga gtg aaa atg 643  
 Val Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr Leu Gly Val Lys Met  
 170 175 180  
 ggt acc gtg cgt tcc cgt att cac cgt gga cgc agc cag ctt cgt gca 691  
 Gly Thr Val Arg Ser Arg Ile His Arg Gly Arg Ser Gln Leu Arg Ala  
 185 190 195  
 agt ttg gaa gct gca gca atg acc agc gag gaa gtt tct ttg ttg gtt 739  
 Ser Leu Glu Ala Ala Ala Met Thr Ser Glu Glu Val Ser Leu Leu Val  
 200 205 210  
 cca acc cac taaagttggt gtgttttctg aca 771  
 Pro Thr His  
 215

&lt;210&gt; 418

&lt;211&gt; 216

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 418

Met Thr Tyr Met Lys Lys Lys Ser Arg Asp Asp Ala Pro Val Val Ile  
 1 5 10 15

Glu Thr Val Gln Ala Glu His Ala Glu Glu Leu Thr Gly Thr Ala Ala  
 20 25 30

Phe Asp Ala Gly Gln Ala Asp Met Pro Thr Trp Gly Glu Leu Val Ala  
 35 40 45

Glu His Ala Asp Ser Val Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn

50	55	60
Gln His Asp Ala Glu Asp Leu Thr Gln Glu Thr Phe Met Arg Val Phe 65 70 75 80		
Arg Ser Leu Lys Ser Tyr Gln Pro Gly Thr Phe Glu Gly Trp Leu His 85 90 95		
Arg Ile Thr Thr Asn Leu Phe Leu Asp Met Val Arg His Arg Gly Lys 100 105 110		
Ile Arg Met Glu Ala Leu Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn 115 120 125		
Asp Ile Thr Pro Glu Gln Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala 130 135 140		
Leu Gln Ala Ala Leu Asp Glu Leu Ser Pro Asp Phe Arg Val Ala Val 145 150 155 160		
Ile Leu Cys Asp Val Val Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr 165 170 175		
Leu Gly Val Lys Met Gly Thr Val Arg Ser Arg Ile His Arg Gly Arg 180 185 190		
Ser Gln Leu Arg Ala Ser Leu Glu Ala Ala Ala Met Thr Ser Glu Glu 195 200 205		
Val Ser Leu Leu Val Pro Thr His 210 215		

&lt;210&gt; 419

&lt;211&gt; 645

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(622)

&lt;223&gt; RXA00588

&lt;400&gt; 419

tcatacatct tggccccgga aaaccggggc caatcttatg gctcaagtcg ctagtttagcc 60

gatgatccac ctctactggt cccaggagg gtaagtaatt atg gca agt gta gat	115
Met Ala Ser Val Asp	
1 5	

aag caa tac atc acc cca gaa acc aag gcc aag ctg gag gaa gag ctc	163
Lys Gln Tyr Ile Thr Pro Glu Thr Lys Ala Lys Leu Glu Glu Glu Leu	
10 15 20	

aac gcc ctc atc gca cac cgc cct gca gtt gct gcg gaa atc aat gag	211
Asn Ala Leu Ile Ala His Arg Pro Ala Val Ala Ala Glu Ile Asn Glu	
25 30 35	

cgc cgt gaa gaa ggc gac ctc aag gaa aac gct ggc tat gac gcc gct	259
Arg Arg Glu Glu Gly Asp Leu Lys Glu Asn Ala Gly Tyr Asp Ala Ala	
40 45 50	

cgt gaa atg cag gac cag gaa gag gcc cgc atc aag cag atc tat gag 307  
 Arg Glu Met Gln Asp Gln Glu Glu Ala Arg Ile Lys Gln Ile Tyr Glu  
 55 60 65  
  
 ctg ctg gcc aac tcc acc act gag cgc gaa ggc atc atc gaa ggt gtc 355  
 Leu Leu Ala Asn Ser Thr Glu Arg Glu Gly Ile Ile Glu Gly Val  
 70 75 80 85  
  
 gca aac gtt ggc tcc gtt gtt cac gtc tac tac gac ggc gac gag aac 403  
 Ala Asn Val Gly Ser Val Val His Val Tyr Tyr Asp Gly Asp Glu Asn  
 90 95 100  
  
 gac aag gaa acc ttc ctc atc ggt acc cgt gct ggc gct tcc gag aac 451  
 Asp Lys Glu Thr Phe Leu Ile Gly Thr Arg Ala Gly Ala Ser Glu Asn  
 105 110 115  
  
 cca gat ctt gag acc tac tct gag cag tcc cca ctc ggc gct gca att 499  
 Pro Asp Leu Glu Thr Tyr Ser Glu Gln Ser Pro Leu Gly Ala Ala Ile  
 120 125 130  
  
 ctc gga gct cag gaa ggc gac acc cgt cag tac acc gct cca aat ggt 547  
 Leu Gly Ala Gln Glu Gly Asp Thr Arg Gln Tyr Thr Ala Pro Asn Gly  
 135 140 145  
  
 tcc gtt atc tcc gta act gtt gtt tct gca gaa cca tac aac tca gca 595  
 Ser Val Ile Ser Val Thr Val Val Ser Ala Glu Pro Tyr Asn Ser Ala  
 150 155 160 165  
  
 aaa gcc gcg aca ctc cgc ggc aaa aac taaccaagga tttaaaagtc ttc 645  
 Lys Ala Ala Thr Leu Arg Gly Lys Asn  
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<210> 420

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 420

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 Leu Glu Glu Glu Leu Asn Ala Leu Ile Ala His Arg Pro Ala Val Ala  
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 Ala Glu Ile Asn Glu Arg Arg Glu Glu Gly Asp Leu Lys Glu Asn Ala  
 35 40 45  
  
 Gly Tyr Asp Ala Ala Arg Glu Met Gln Asp Gln Glu Glu Ala Arg Ile  
 50 55 60  
  
 Lys Gln Ile Tyr Glu Leu Leu Ala Asn Ser Thr Thr Glu Arg Glu Gly  
 65 70 75 80  
  
 Ile Ile Glu Gly Val Ala Asn Val Gly Ser Val Val His Val Tyr Tyr  
 85 90 95  
  
 Asp Gly Asp Glu Asn Asp Lys Glu Thr Phe Leu Ile Gly Thr Arg Ala  
 100 105 110

Gly Ala Ser Glu Asn Pro Asp Leu Glu Thr Tyr Ser Glu Gln Ser Pro  
 115 120 125

Leu Gly Ala Ala Ile Leu Gly Ala Gln Glu Gly Asp Thr Arg Gln Tyr  
 130 135 140

Thr Ala Pro Asn Gly Ser Val Ile Ser Val Thr Val Val Ser Ala Glu  
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Pro Tyr Asn Ser Ala Lys Ala Ala Thr Leu Arg Gly Lys Asn  
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 <223> RXN01724

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 Arg Ala Thr Gln Pro Ser Ala Pro Val Glu Gln Ala Gln Glu Ala Pro  
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gcg caa act tca act gca cct gct tca gca cca tct gaa gag act ccc 96  
 Ala Gln Thr Ser Thr Ala Pro Ala Ser Ala Pro Ser Glu Glu Thr Pro  
 20 25 30

gca gct ccc gct cgt cgt gga cgt cgc cgt gta acc acc acc gcg acc 144  
 Ala Ala Pro Ala Arg Arg Gly Arg Arg Val Thr Thr Thr Ala Thr  
 35 40 45

acc cca gag cca gca gcg cct gca caa tcc cag cct gca gaa gct caa 192  
 Thr Pro Glu Pro Ala Ala Pro Ala Gln Ser Gln Pro Ala Glu Ala Gln  
 50 55 60

cca gca cag act cag gct gca cag caa gaa gaa ctt cct gtt gca gcg 240  
 Pro Ala Gln Thr Gln Ala Ala Gln Gln Glu Glu Leu Pro Val Ala Ala  
 65 70 75 80

aag gag tcc gca cca gct aca gaa aac act cag ggc caa gct cag ggc 288  
 Lys Glu Ser Ala Pro Ala Thr Glu Asn Thr Gln Gly Gln Ala Gln Gly  
 85 90 95

caa gct cag ggc caa gct cag ggc gat gag cac gat gat cgt ttt gag 336  
 Gln Ala Gln Gly Gln Ala Gln Gly Asp Glu His Asp Asp Arg Phe Glu  
 100 105 110

tcc cgt tct gct gca cgc cga gca cgc cgc aac cgt cag cgc cag atc 384  
 Ser Arg Ser Ala Ala Arg Arg Ala Arg Arg Asn Arg Gln Arg Gln Ile  
 115 120 125

cac cgc gat ggc gat gac aat gcg aat gca aac aca gag tct gag cag 432  
 His Arg Asp Gly Asp Asp Asn Ala Asn Ala Asn Thr Glu Ser Glu Gln  
 130 135 140

aac acc cct gcc cag aac gca acc gca cag gct gag tct gag cag act 480

Asn 145	Thr	Pro	Ala	Gln	Asn 150	Ala	Thr	Ala	Gln	Ala 155	Glu	Ser	Glu	Gln	Thr 160	
gca	gct	cct	gca	cag	gct	gaa	gca	gct	gag	cag	aac	cag	aac	gat	aac	528
Ala	Ala	Pro	Ala	Gln 165	Ala	Glu	Ala	Ala	Glu 170	Gln	Asn	Gln	Asn	Asp 175	Asn	
agc	gag	tcc	tcc	gag	aac	cgc	agc	gat	aac	tac	cgc	aac	aac	aat	cgt	576
Ser	Glu	Ser	Ser 180	Glu	Asn	Arg	Ser	Asp 185	Asn	Tyr	Arg	Asn	Asn	Asn	Arg	
cgt	tcc	cgc	aac	aac	cgg	aac	aat	cgc	aat	tac	cgc	gat	aac	aac	gag	624
Arg	Ser	Arg	Asn 195	Asn	Arg	Asn	Asn	Arg	Asn	Tyr	Arg	Asp 205	Asn	Asn	Glu	
tcc	tct	gat	aat	gca	gga	cag	tcc	agc	aat	gat	gat	gcc	gac	aac	aat	672
Ser	Ser	Asp	Asn	Ala	Gly	Gln 215	Ser	Ser	Asn	Asp 220	Asp	Ala	Asp	Asn	Asn	
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Gln	Ala	Arg	Ser	Glu	Asp 230	Asn	Asn	Asp	Asp	Arg 235	Arg	Ser	Arg	Asn	Asn 240	
cgt	aac	aac	gac	cgc	aat	gat	cgt	aac	gat	cgc	aat	gac	cgc	gac	aac	768
Arg	Asn	Asn	Asp 245	Arg	Asn	Asp	Arg	Asn	Asp 250	Arg	Asn	Asp	Arg	Asp 255	Asn	
gac	gac	aac	gat	gat	cgc	cgc	aac	cgt	cgc	gga	cgc	cgc	aat	cgc	cgt	816
Asp	Asp	Asn	Asp 260	Asp	Arg	Arg	Asn	Arg 265	Arg	Gly	Arg	Arg	Asn	Arg	Arg	
gga	cgc	aac	gac	cgt	aac	gat	cgc	gac	aac	cga	gat	aac	cgg	gat	aac	864
Gly	Arg	Asn 275	Asp	Arg	Asn	Asp 280	Arg	Asp	Asn	Arg	Asp 285	Asn	Arg	Asp	Asn	
cgc	gac	aac	agc	aac	gat	ggc	gac	aac	aac	cag	caa	gat	gag	ctg	cag	912
Arg	Asp 290	Asn	Ser	Asn	Asp	Gly 295	Asp	Asn	Asn	Gln	Gln 300	Asp	Glu	Leu	Gln	
cag	gta	gca	ggc	atc	ctg	gac	atc	gtg	gac	cat	aac	gtc	gca	ttc	gtg	960
Gln	Val	Ala	Gly	Ile	Leu 310	Asp	Ile	Val	Asp 315	His	Asn	Val	Ala	Phe	Val 320	
cgc	acc	acc	ggt	tac	cac	gct	gca	cct	tct	gac	gtg	ttt	gtc	agc	aac	1008
Arg	Thr	Thr	Gly 325	Tyr	His	Ala	Ala	Pro	Ser 330	Asp	Val	Phe	Val	Ser	Asn 335	
cag	ctg	atc	cgc	cgt	atg	ggt	ctt	cgt	tcc	ggt	gac	gcc	att	gaa	ggt	1056
Gln	Leu	Ile	Arg 340	Arg	Met	Gly	Leu	Arg 345	Ser	Gly	Asp	Ala	Ile	Glu	Gly	
cag	gtt	cgt	atg	aac	cag	ggt	ggt	ggc	aac	cac	aac	aac	cat	ggt	cgc	1104
Gln	Val 355	Arg	Met	Asn	Gln	Gly 360	Gly	Gly	Asn	His	Asn	Asn	His	Gly	Arg	
aac	cgt	cag	aag	tac	aac	aac	ttg	gtg	cgc	gtg	gag	atg	gtt	aac	ggt	1152
Asn	Arg	Gln	Lys	Tyr	Asn	Asn 375	Leu	Val	Arg	Val	Glu 380	Met	Val	Asn	Gly	
ctt	cct	gct	gaa	gag	act	cgc	aac	cgt	cct	gag	ttc	ggc	aag	ctg	act	1200
Leu	Pro	Ala	Glu	Glu	Thr	Arg	Asn	Arg	Pro	Glu	Phe	Gly	Lys	Leu	Thr	

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Ala	Gln	Thr	Ser 20	Thr	Ala	Pro	Ala	Ser 25	Ala	Pro	Ser	Glu	Glu 30	Thr	Pro
Ala	Ala	Pro 35	Ala	Arg	Arg	Gly	Arg 40	Arg	Arg	Val	Thr	Thr 45	Thr	Ala	Thr
Thr	Pro 50	Glu	Pro	Ala	Ala	Pro 55	Ala	Gln	Ser	Gln	Pro 60	Ala	Glu	Ala	Gln
Pro 65	Ala	Gln	Thr	Gln	Ala 70	Ala	Gln	Gln	Glu	Glu 75	Leu	Pro	Val	Ala	Ala 80
Lys	Glu	Ser	Ala	Pro 85	Ala	Thr	Glu	Asn	Thr 90	Gln	Gly	Gln	Ala	Gln 95	Gly
Gln	Ala	Gln	Gly 100	Gln	Ala	Gln	Gly	Asp 105	Glu	His	Asp	Asp	Arg 110	Phe	Glu
Ser	Arg	Ser 115	Ala	Ala	Arg	Arg	Ala 120	Arg	Arg	Asn	Arg	Gln 125	Arg	Gln	Ile
His	Arg 130	Asp	Gly	Asp	Asp	Asn 135	Ala	Asn	Ala	Asn	Thr 140	Glu	Ser	Glu	Gln
Asn 145	Thr	Pro	Ala	Gln	Asn 150	Ala	Thr	Ala	Gln	Ala 155	Glu	Ser	Glu	Gln	Thr 160
Ala	Ala	Pro	Ala	Gln 165	Ala	Glu	Ala	Ala	Glu 170	Gln	Asn	Gln	Asn	Asp 175	Asn
Ser	Glu	Ser	Ser 180	Glu	Asn	Arg	Ser	Asp 185	Asn	Tyr	Arg	Asn	Asn 190	Asn	Arg
Arg	Ser	Arg 195	Asn	Asn	Arg	Asn	Asn 200	Arg	Asn	Tyr	Arg	Asp 205	Asn	Asn	Glu
Ser	Ser	Asp	Asn	Ala	Gly	Gln	Ser	Ser	Asn	Asp	Asp	Ala	Asp	Asn	Asn

210	215	220
Gln Ala Arg Ser Glu Asp Asn Asn Asp Asp Arg Arg Ser Arg Asn Asn		
225	230	235 240
Arg Asn Asn Asp Arg Asn Asp Arg Asn Asp Arg Asn Asp Arg Asp Asn		
	245	250 255
Asp Asp Asn Asp Asp Arg Arg Asn Arg Arg Gly Arg Arg Asn Arg Arg		
	260	265 270
Gly Arg Asn Asp Arg Asn Asp Arg Asp Asn Arg Asp Asn Arg Asp Asn		
	275	280 285
Arg Asp Asn Ser Asn Asp Gly Asp Asn Asn Gln Gln Asp Glu Leu Gln		
	290	295 300
Gln Val Ala Gly Ile Leu Asp Ile Val Asp His Asn Val Ala Phe Val		
305	310	315 320
Arg Thr Thr Gly Tyr His Ala Ala Pro Ser Asp Val Phe Val Ser Asn		
	325	330 335
Gln Leu Ile Arg Arg Met Gly Leu Arg Ser Gly Asp Ala Ile Glu Gly		
	340	345 350
Gln Val Arg Met Asn Gln Gly Gly Gly Asn His Asn Asn His Gly Arg		
	355	360 365
Asn Arg Gln Lys Tyr Asn Asn Leu Val Arg Val Glu Met Val Asn Gly		
	370	375 380
Leu Pro Ala Glu Glu Thr Arg Asn Arg Pro Glu Phe Gly Lys Leu Thr		
385	390	395 400
Pro Leu Tyr Pro Asn Gln Arg Leu Arg Leu Glu Thr Glu Gln Lys Ile		
	405	410 415
Leu Thr Thr Arg Val Ile Asp Leu Ile Met Pro Ile Gly Lys Gly Gln		
	420	425 430
Leu Cys Phe Asp Cys Val Ala Thr		
	435	440

&lt;210&gt; 423

&lt;211&gt; 960

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(937)

&lt;223&gt; FRXA01723

&lt;220&gt;

&lt;223&gt; All occurrences of Xaa = any amino acid

&lt;220&gt;

&lt;223&gt; All occurrences of n = any nucleotide

&lt;400&gt; 423

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ccttccgcac  cggttgagca  agcacaagaa  gctcccgcgc  aaacttcaac  tgcacctgct  60

tcagcaccat  ctgaagagac  tcccgcagct  cccgctcgtc  gtg  gac  ktc  agc  cgt      115
                        Val Asp Xaa Ser Arg
                        1                      5

gta  acc  acc  acc  gcg  acc  acc  cca  gag  cca  gca  gcg  cct  gca  caa  tcc      163
Val  Thr  Thr  Thr  Ala  Thr  Thr  Pro  Glu  Pro  Ala  Ala  Pro  Ala  Gln  Ser
                        10                      15                      20

cag  cct  gca  gaa  gct  caa  cca  gca  cag  act  cag  gct  gca  cag  caa  gaa      211
Gln  Pro  Ala  Glu  Ala  Gln  Pro  Ala  Gln  Thr  Gln  Ala  Ala  Gln  Gln  Glu
                        25                      30                      35

gaa  ctt  cct  gtt  gca  gcg  aag  gag  tcc  gca  cca  gct  aca  gaa  aac  act      259
Glu  Leu  Pro  Val  Ala  Ala  Lys  Glu  Ser  Ala  Pro  Ala  Thr  Glu  Asn  Thr
                        40                      45                      50

cag  ggc  caa  kcy  cag  ggc  caa  gct  cag  ggc  saa  gct  cag  ggc  gat  gag      307
Gln  Gly  Gln  Xaa  Gln  Gly  Gln  Ala  Gln  Gly  Xaa  Ala  Gln  Gly  Asp  Glu
                        55                      60                      65

cac  gat  gat  cgy  ttt  gag  tcc  cgt  tct  gct  gca  cgc  cga  gca  cgc  cgc      355
His  Asp  Asp  Xaa  Phe  Glu  Ser  Arg  Ser  Ala  Ala  Arg  Arg  Ala  Arg  Arg
                        70                      75                      80                      85

aac  cgt  cag  cgc  cag  atc  cac  cgc  gat  ggc  gat  gac  aat  gcg  aat  gca      403
Asn  Arg  Gln  Arg  Gln  Ile  His  Arg  Asp  Gly  Asp  Asp  Asn  Ala  Asn  Ala
                        90                      95                      100

aac  aca  gag  tct  gag  cag  aac  acc  cct  gcc  cag  aac  gca  acc  gca  cag      451
Asn  Thr  Glu  Ser  Glu  Gln  Asn  Thr  Pro  Ala  Gln  Asn  Ala  Thr  Ala  Gln
                        105                      110                      115

gct  gag  tct  gag  cag  act  gca  gct  cct  gca  cag  gct  gaa  gca  gct  gag      499
Ala  Glu  Ser  Glu  Gln  Thr  Ala  Ala  Pro  Ala  Gln  Ala  Glu  Ala  Ala  Glu
                        120                      125                      130

cag  aac  cag  aac  gat  aac  agc  gag  tcc  tcc  gag  aac  cgc  agc  gat  aac      547
Gln  Asn  Gln  Asn  Asp  Asn  Ser  Glu  Ser  Ser  Glu  Asn  Arg  Ser  Asp  Asn
                        135                      140                      145

tac  cgc  aac  aac  aat  cgt  cgt  tcc  cgc  aac  aac  cgg  aac  aat  cgc  aat      595
Tyr  Arg  Asn  Asn  Asn  Arg  Arg  Ser  Arg  Asn  Asn  Arg  Asn  Asn  Arg  Asn
                        150                      155                      160                      165

tac  cgc  gat  aac  aac  gag  tcc  tct  gat  aat  gca  gga  cag  tcc  agc  aat      643
Tyr  Arg  Asp  Asn  Asn  Glu  Ser  Ser  Asp  Asn  Ala  Gly  Gln  Ser  Ser  Asn
                        170                      175                      180

gat  gat  gcc  gac  aac  aat  cag  gca  cgg  tct  gag  gac  aat  aac  gac  gat      691
Asp  Asp  Ala  Asp  Asn  Asn  Gln  Ala  Arg  Ser  Glu  Asp  Asn  Asn  Asp  Asp
                        185                      190                      195

cgc  cgt  tct  cgt  aat  aac  cgt  aac  aac  gac  cgc  aat  gat  cgt  aac  gat      739
Arg  Arg  Ser  Arg  Asn  Asn  Arg  Asn  Asn  Asp  Arg  Asn  Asp  Arg  Asn  Asp
                        200                      205                      210

cgc  aat  gac  cgc  gac  aac  gac  gac  aac  gat  gat  cgc  cgc  aac  cgt  cgc      787
Arg  Asn  Asp  Arg  Asp  Asn  Asp  Asp  Asn  Asp  Asp  Arg  Arg  Asn  Arg  Arg

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215	220	225	
gga cgc cgc aat cgc cgt	gga ncn gca acg acc	gta acg atc gcg aca	835
Gly Arg Arg Asn Arg Arg	Gly Xaa Ala Thr Thr	Val Thr Ile Ala Thr	
230	235	240	245
acc gag ata acc ggg ata acc gcg aca aca gca acg atg gcg aca aca			883
Thr Glu Ile Thr Gly Ile Thr Ala Thr Thr Ala Thr Met Ala Thr Thr			
250	255		260
acc agc aag atn gag nct gca gca ggt agc agg cat cct gga cat cgt			931
Thr Ser Lys Xaa Glu Xaa Ala Ala Gly Ser Arg His Pro Gly His Arg			
265	270		275
gga cca taacgtcgca ttcgtgcgca cca			960
Gly Pro			

&lt;210&gt; 424

&lt;211&gt; 279

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;223&gt; All occurrences of Xaa = any amino acid

&lt;400&gt; 424

Val Asp Xaa Ser Arg Val Thr Thr Thr Ala Thr Thr Pro Glu Pro Ala
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Ala Pro Ala Gln Ser Gln Pro Ala Glu Ala Gln Pro Ala Gln Thr Gln
20 25 30

Ala Ala Gln Gln Glu Glu Leu Pro Val Ala Ala Lys Glu Ser Ala Pro
35 40 45

Ala Thr Glu Asn Thr Gln Gly Gln Xaa Gln Gly Gln Ala Gln Gly Xaa
50 55 60

Ala Gln Gly Asp Glu His Asp Asp Xaa Phe Glu Ser Arg Ser Ala Ala
65 70 75 80

Arg Arg Ala Arg Arg Asn Arg Gln Arg Gln Ile His Arg Asp Gly Asp
85 90 95

Asp Asn Ala Asn Ala Asn Thr Glu Ser Glu Gln Asn Thr Pro Ala Gln
100 105 110

Asn Ala Thr Ala Gln Ala Glu Ser Glu Gln Thr Ala Ala Pro Ala Gln
115 120 125

Ala Glu Ala Ala Glu Gln Asn Gln Asn Asp Asn Ser Glu Ser Ser Glu
130 135 140

Asn Arg Ser Asp Asn Tyr Arg Asn Asn Asn Arg Arg Ser Arg Asn Asn
145 150 155 160

Arg Asn Asn Arg Asn Tyr Arg Asp Asn Asn Glu Ser Ser Asp Asn Ala
165 170 175

Gly Gln Ser Ser Asn Asp Asp Ala Asp Asn Asn Gln Ala Arg Ser Glu  
 180 185 190  
 Asp Asn Asn Asp Asp Arg Arg Ser Arg Asn Asn Arg Asn Asn Asp Arg  
 195 200 205  
 Asn Asp Arg Asn Asp Arg Asn Asp Arg Asp Asn Asp Asp Asn Asp Asp  
 210 215 220  
 Arg Arg Asn Arg Arg Gly Arg Arg Asn Arg Arg Gly Xaa Ala Thr Thr  
 225 230 235 240  
 Val Thr Ile Ala Thr Thr Glu Ile Thr Gly Ile Thr Ala Thr Thr Ala  
 245 250 255  
 Thr Met Ala Thr Thr Thr Ser Lys Xaa Glu Xaa Ala Ala Gly Ser Arg  
 260 265 270  
 His Pro Gly His Arg Gly Pro  
 275

<210> 425  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(484)  
 <223> FRXA01724

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 aagatngagn ctgcagcagg tagcaggcat cctggacatc gtg gac cat aac gtc 115  
 Val Asp His Asn Val  
 1 5  
 gca ttc gtg cgc acc acc ggt tac cac gct gca cct tct gac gtg ttt 163  
 Ala Phe Val Arg Thr Thr Gly Tyr His Ala Ala Pro Ser Asp Val Phe  
 10 15 20  
 gtc agc aac cag ctg atc cgc cgt atg ggt ctt cgt tcc ggt gac gcc 211  
 Val Ser Asn Gln Leu Ile Arg Arg Met Gly Leu Arg Ser Gly Asp Ala  
 25 30 35  
 att gaa ggt cag gtt cgt atg aac cag ggt ggt ggc aac cac aac aac 259  
 Ile Glu Gly Gln Val Arg Met Asn Gln Gly Gly Gly Asn His Asn Asn  
 40 45 50  
 cat ggt cgc aac cgt cag aag tac aac aac ttg gtg cgc gtg gag atg 307  
 His Gly Arg Asn Arg Gln Lys Tyr Asn Asn Leu Val Arg Val Glu Met  
 55 60 65  
 gtt aac ggt ctt cct gct gaa gag act cgc aac cgt cct gag ttc ggc 355  
 Val Asn Gly Leu Pro Ala Glu Glu Thr Arg Asn Arg Pro Glu Phe Gly  
 70 75 80 85  
 aag ctg act cct ctg tac ccg aac cag cgt ctg cgt ttg gaa act gag 403  
 Lys Leu Thr Pro Leu Tyr Pro Asn Gln Arg Leu Arg Leu Glu Thr Glu

90 95 100  
 cag aag att ctt acc act cgt gtg atc gac ttg atc atg cct att ggt 451  
 Gln Lys Ile Leu Thr Thr Arg Val Ile Asp Leu Ile Met Pro Ile Gly  
 105 110 115  
 aag gga cag ctg tgc ttt gat tgt gtc gcc acc taaggctggt aagaccacga 504  
 Lys Gly Gln Leu Cys Phe Asp Cys Val Ala Thr  
 120 125  
 tcc 507

<210> 426  
 <211> 128  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 426  
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 Pro Ser Asp Val Phe Val Ser Asn Gln Leu Ile Arg Arg Met Gly Leu  
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 Arg Ser Gly Asp Ala Ile Glu Gly Gln Val Arg Met Asn Gln Gly Gly  
 35 40 45  
 Gly Asn His Asn Asn His Gly Arg Asn Arg Gln Lys Tyr Asn Asn Leu  
 50 55 60  
 Val Arg Val Glu Met Val Asn Gly Leu Pro Ala Glu Glu Thr Arg Asn  
 65 70 75 80  
 Arg Pro Glu Phe Gly Lys Leu Thr Pro Leu Tyr Pro Asn Gln Arg Leu  
 85 90 95  
 Arg Leu Glu Thr Glu Gln Lys Ile Leu Thr Thr Arg Val Ile Asp Leu  
 100 105 110  
 Ile Met Pro Ile Gly Lys Gly Gln Leu Cys Phe Asp Cys Val Ala Thr  
 115 120 125

<210> 427  
 <211> 330  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXN01725

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 Leu Ile Val Ser Pro  
 1 5

cct aag gct ggt aag acc acg atc ctg cag aac att gcg aac gct att 163  
 Pro Lys Ala Gly Lys Thr Thr Ile Leu Gln Asn Ile Ala Asn Ala Ile  
                   10                  15                  20

tcc acc aac aac cca gag tgc tac ctc atg gtt gtt ttg gtt gat gag 211  
 Ser Thr Asn Asn Pro Glu Cys Tyr Leu Met Val Val Leu Val Asp Glu  
                   25                  30                  35

cgt ccg aaa gaa gtt act gat atg cag cgc tcc gtc aac ggc gaa gtg 259  
 Arg Pro Lys Glu Val Thr Asp Met Gln Arg Ser Val Asn Gly Glu Val  
                   40                  45                  50

att tct tct act ttc gat cgt cca cca tca gag cac act gcg gtt gct 307  
 Ile Ser Ser Thr Phe Asp Arg Pro Pro Ser Glu His Thr Ala Val Ala  
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tgagctggcg attgagcgtg cga 330

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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 428  
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Ile Ala Asn Ala Ile Ser Thr Asn Asn Pro Glu Cys Tyr Leu Met Val  
                   20                  25                  30

Val Leu Val Asp Glu Arg Pro Lys Glu Val Thr Asp Met Gln Arg Ser  
           35                  40                  45

Val Asn Gly Glu Val Ile Ser Ser Thr Phe Asp Arg Pro Pro Ser Glu  
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His Thr Ala Val Ala  
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<210> 429  
 <211> 231  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(208)  
 <223> FRXA01725

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atttccacca acaaccaga gtgctacctc atggcttgtt ttg gtt gat gag cgt 115  
   Leu Val Asp Glu Arg  
   1                  5

ccg aaa gaa gtt act gat atg cag cgc tcc gtc aac ggc gaa gtg att 163  
 Pro Lys Glu Val Thr Asp Met Gln Arg Ser Val Asn Gly Glu Val Ile  
                   10                  15                  20

tgagctggcg attgagcgtg cga 231

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<400> 430
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Asn Gly Glu Val Ile Ser Ser Thr Phe Asp Arg Pro Pro Ser Glu His
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Thr Ala Val Ala
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<223> RXA01726
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Leu Leu Glu Leu Ala																5
1																
att gag cgt gcg aag cgc ctg gtg gag cag ggc cag gac gtc gtt gtt																163
Ile Glu Arg Ala Lys Arg Leu Val Glu Gln Gly Gln Asp Val Val Val																20
10 15																
ctg ctt gac tcc att act cgt ttg ggc cgt gcg tac aac aac agc tca																211
Leu Leu Asp Ser Ile Thr Arg Leu Gly Arg Ala Tyr Asn Asn Ser Ser																35
25 30																
cct gca tcg gga cgt att ttg tcc ggt ggt gtg gat tcc aat gca ctg																259
Pro Ala Ser Gly Arg Ile Leu Ser Gly Gly Val Asp Ser Asn Ala Leu																50
40 45																
tac ccg ccg aag cgt ttc ttg ggt gct gct cga aac atc gaa aat ggt																307
Tyr Pro Pro Lys Arg Phe Leu Gly Ala Ala Arg Asn Ile Glu Asn Gly																65
55 60																
gga tct ttg acc atc atc gca act gcc atg gtg gaa acc ggc tct gct																355
Gly Ser Leu Thr Ile Ile Ala Thr Ala Met Val Glu Thr Gly Ser Ala																85
70 75 80																

ggt gac acc gtg atc ttc gag gag ttc aag ggc act ggt aac gct gag 403  
 Gly Asp Thr Val Ile Phe Glu Glu Phe Lys Gly Thr Gly Asn Ala Glu  
                     90                    95                    100

ctg aag ctg gat cgt aag atc tct gag cgc cgc gtt ttc cca gct gtg 451  
 Leu Lys Leu Asp Arg Lys Ile Ser Glu Arg Arg Val Phe Pro Ala Val  
                     105                    110                    115

gat gtt aat cct tct ggt act cgt aag gac gag ctg ttg ctc aac ccg 499  
 Asp Val Asn Pro Ser Gly Thr Arg Lys Asp Glu Leu Leu Leu Asn Pro  
                     120                    125                    130

gac gag gct cgc att atg cac aag ctg cgt cgt att ctg tct gca ctt 547  
 Asp Glu Ala Arg Ile Met His Lys Leu Arg Arg Ile Leu Ser Ala Leu  
                     135                    140                    145

gat aat cag caa gcc att gat ctg ttg atc aag cag ctg aag aag acc 595  
 Asp Asn Gln Gln Ala Ile Asp Leu Leu Ile Lys Gln Leu Lys Lys Thr  
                     150                    155                    160                    165

aag tcc aat gcg gaa ttc ctc atg cag gtt gct tcc agc gct cca atg 643  
 Lys Ser Asn Ala Glu Phe Leu Met Gln Val Ala Ser Ser Ala Pro Met  
                     170                    175                    180

gca ggc aca gaa aaa gag gag gat tac tcc taatggcatc gcagggtttct gca 696  
 Ala Gly Thr Glu Lys Glu Glu Asp Tyr Ser  
                     185                    190

<210> 432

<211> 191

<212> PRT

<213> Corynebacterium glutamicum

<400> 432

Leu Leu Glu Leu Ala Ile Glu Arg Ala Lys Arg Leu Val Glu Gln Gly  
   1                    5                    10                    15

Gln Asp Val Val Val Leu Leu Asp Ser Ile Thr Arg Leu Gly Arg Ala  
                     20                    25                    30

Tyr Asn Asn Ser Ser Pro Ala Ser Gly Arg Ile Leu Ser Gly Gly Val  
                     35                    40                    45

Asp Ser Asn Ala Leu Tyr Pro Pro Lys Arg Phe Leu Gly Ala Ala Arg  
                     50                    55                    60

Asn Ile Glu Asn Gly Gly Ser Leu Thr Ile Ile Ala Thr Ala Met Val  
   65                    70                    75                    80

Glu Thr Gly Ser Ala Gly Asp Thr Val Ile Phe Glu Glu Phe Lys Gly  
                     85                    90                    95

Thr Gly Asn Ala Glu Leu Lys Leu Asp Arg Lys Ile Ser Glu Arg Arg  
                     100                    105                    110

Val Phe Pro Ala Val Asp Val Asn Pro Ser Gly Thr Arg Lys Asp Glu  
                     115                    120                    125

Leu Leu Leu Asn Pro Asp Glu Ala Arg Ile Met His Lys Leu Arg Arg  
   130                    135                    140

Ile Leu Ser Ala Leu Asp Asn Gln Gln Ala Ile Asp Leu Leu Ile Lys  
145 150 155 160

Gln Leu Lys Lys Thr Lys Ser Asn Ala Glu Phe Leu Met Gln Val Ala  
165 170 175

Ser Ser Ala Pro Met Ala Gly Thr Glu Lys Glu Glu Asp Tyr Ser  
180 185 190

<210> 433

<211> 1887

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1887)

<223> RXA00736

<400> 433

gct ggc ctg gtg ttt ccg aag gtg cgt aaa cac cgc gat ggc gct gca 48  
Ala Gly Leu Val Phe Pro Lys Val Arg Lys His Arg Asp Gly Ala Ala  
1 5 10 15

atg ccg ttg gtg gtt att aca gaa acc gat ctg act ggt aac cgt gtt 96  
Met Pro Leu Val Val Ile Thr Glu Thr Asp Leu Thr Gly Asn Arg Val  
20 25 30

ggc gat att gca ggg gcg aaa cgt cga cct gca aaa cgc cgc aac aag 144  
Gly Asp Ile Ala Gly Ala Lys Arg Arg Pro Ala Lys Arg Arg Asn Lys  
35 40 45

gtg gat cct ttg gcg ctg gag cca ggg gat ttg gtg gtt cat gaa acc 192  
Val Asp Pro Leu Ala Leu Glu Pro Gly Asp Leu Val Val His Glu Thr  
50 55 60

cac ggc att ggt cgt ttt gtg aag atg act gaa cga acc att tct gcg 240  
His Gly Ile Gly Arg Phe Val Lys Met Thr Glu Arg Thr Ile Ser Ala  
65 70 75 80

ggt gat gag acc tcg cgc cgt gaa tac att gtg ctg gag tac gcg cca 288  
Gly Asp Glu Thr Ser Arg Arg Glu Tyr Ile Val Leu Glu Tyr Ala Pro  
85 90 95

tct aag cgc gga cag ccc ggc gat cag ctg tat gtg ccg atg gat gcg 336  
Ser Lys Arg Gly Gln Pro Gly Asp Gln Leu Tyr Val Pro Met Asp Ala  
100 105 110

ctg gat atg ctc agc cgc tac gtc ggt ggc gag aag ccg acg ctg tcc 384  
Leu Asp Met Leu Ser Arg Tyr Val Gly Gly Glu Lys Pro Thr Leu Ser  
115 120 125

aaa atg ggt ggt tct gac tgg aag aac gcc aag aag aag gct cgc gct 432  
Lys Met Gly Gly Ser Asp Trp Lys Asn Ala Lys Lys Lys Ala Arg Ala  
130 135 140

gcc gtg cgt gaa atc gcc ggt gag ctg gta gaa ctc tac gct aag cgc 480  
Ala Val Arg Glu Ile Ala Gly Glu Leu Val Glu Leu Tyr Ala Lys Arg  
145 150 155 160

caa tcc gcg ccg ggt cac ccg ttt gcg ccg gat acg ccg tgg caa aaa	528
Gln Ser Ala Pro Gly His Pro Phe Ala Pro Asp Thr Pro Trp Gln Lys	
165 170 175	
gag atg gaa gat aac ttc ccc tac gtt gag acc gaa gac cag atg ttg	576
Glu Met Glu Asp Asn Phe Pro Tyr Val Glu Thr Glu Asp Gln Met Leu	
180 185 190	
gcg atc gat gcg gtc aag gag gac atg gag aaa agt gtc ccc atg gac	624
Ala Ile Asp Ala Val Lys Glu Asp Met Glu Lys Ser Val Pro Met Asp	
195 200 205	
cgc gtc atc atc ggc gat gtg ggt tat ggc aag acg gaa gtg gcg gtg	672
Arg Val Ile Ile Gly Asp Val Gly Tyr Gly Lys Thr Glu Val Ala Val	
210 215 220	
cgc gcg gcg ttc aag gct gtg caa gac ggc aag cag gta gcc gtt ctg	720
Arg Ala Ala Phe Lys Ala Val Gln Asp Gly Lys Gln Val Ala Val Leu	
225 230 235 240	
gtg ccc acc acg ttg ctt gcg cag cag cac cag tcc acg ttt gaa gag	768
Val Pro Thr Thr Leu Leu Ala Gln Gln His Gln Ser Thr Phe Glu Glu	
245 250 255	
cgt atg act ggt ttc cct gtc acc atc aag gga ttg tca cgc ttt act	816
Arg Met Thr Gly Phe Pro Val Thr Ile Lys Gly Leu Ser Arg Phe Thr	
260 265 270	
tcg cct gcg gaa tcg cgg gag att ctc tcc ggt ttg gct gca gga tcg	864
Ser Pro Ala Glu Ser Arg Glu Ile Leu Ser Gly Leu Ala Ala Gly Ser	
275 280 285	
gtg gat atc gtc atc ggt act cac cgt ttg ctg cag act ggc gtg cag	912
Val Asp Ile Val Ile Gly Thr His Arg Leu Leu Gln Thr Gly Val Gln	
290 295 300	
tgg aaa aac cta ggg ctt gtc att gtg gat gag gag cag cgt ttc ggc	960
Trp Lys Asn Leu Gly Leu Val Ile Val Asp Glu Glu Gln Arg Phe Gly	
305 310 315 320	
gtg gaa cat aag gag cac atc aag gct ctg cgt act cac gtg gat gtg	1008
Val Glu His Lys Glu His Ile Lys Ala Leu Arg Thr His Val Asp Val	
325 330 335	
ctg acc atg tcc gcg acc ccg att ccg cgc acc ctg gaa atg tcc atg	1056
Leu Thr Met Ser Ala Thr Pro Ile Pro Arg Thr Leu Glu Met Ser Met	
340 345 350	
gcc ggt atc cgt gag atg acc acc atg ctc acc ccg ccg gaa gat cgc	1104
Ala Gly Ile Arg Glu Met Thr Thr Met Leu Thr Pro Pro Glu Asp Arg	
355 360 365	
cac cca att ctt acc tat gtg gga ccg tat gaa gac aag cag gtc gcg	1152
His Pro Ile Leu Thr Tyr Val Gly Pro Tyr Glu Asp Lys Gln Val Ala	
370 375 380	
gca tca att cgc cgt gag ctg ctg cgc gat ggc cag gtc ttt ttc atc	1200
Ala Ser Ile Arg Arg Glu Leu Leu Arg Asp Gly Gln Val Phe Phe Ile	
385 390 395 400	

cac aac aag gtg gca gat att gag aag aag gcc cgc gag atc cgc gat His Asn Lys Val Ala Asp Ile Glu Lys Lys Ala Arg Glu Ile Arg Asp 405 410 415	1248
cta gtt ccc gaa gcc cga gtg gtc gtt gcc cac ggc cag atg agt gaa Leu Val Pro Glu Ala Arg Val Val Val Ala His Gly Gln Met Ser Glu 420 425 430	1296
gag ctg ctg gaa caa acc gtt caa ggt ttc tgg gac cgc gaa tac gat Glu Leu Leu Glu Gln Thr Val Gln Gly Phe Trp Asp Arg Glu Tyr Asp 435 440 445	1344
gtg ctg gtg tgt acc acc atc gtg gaa act ggt ctg gat att tcc aac Val Leu Val Cys Thr Thr Ile Val Glu Thr Gly Leu Asp Ile Ser Asn 450 455 460	1392
gcc aac acg ctt atc gtg gaa aat gcc cac cac atg ggc ttg tct cag Ala Asn Thr Leu Ile Val Glu Asn Ala His His Met Gly Leu Ser Gln 465 470 475 480	1440
ctg cac cag ctg cgt ggc cgc gtg ggt cgt tcc cgt gag cgc ggt tac Leu His Gln Leu Arg Gly Arg Val Gly Arg Ser Arg Glu Arg Gly Tyr 485 490 495	1488
gcc tac ttc ctg tat cca aag ggc gcg aca ctg act gaa atg tcc tac Ala Tyr Phe Leu Tyr Pro Lys Gly Ala Thr Leu Thr Glu Met Ser Tyr 500 505 510	1536
gac cgc ctg gca acg att gcc caa aac aat gat ttg ggt gcc ggt atg Asp Arg Leu Ala Thr Ile Ala Gln Asn Asn Asp Leu Gly Ala Gly Met 515 520 525	1584
gcg gtt gcc atg aag gat ttg gaa atg cgt ggc gcc gcc aac gtg ctg Ala Val Ala Met Lys Asp Leu Glu Met Arg Gly Ala Gly Asn Val Leu 530 535 540	1632
ggt gca gaa caa tca ggc cat atc gct ggc gtg ggc ttt gac ctg tac Gly Ala Glu Gln Ser Gly His Ile Ala Gly Val Gly Phe Asp Leu Tyr 545 550 555 560	1680
gtt cgc ctc gtc ggc gaa gca gtg gaa gcc tac cgc gcg ctg gct gat Val Arg Leu Val Gly Glu Ala Val Glu Ala Tyr Arg Ala Leu Ala Asp 565 570 575	1728
ggc aaa gtt gtt gat ggc acc gtc aag gga cca aag gaa atc cgc gtg Gly Lys Val Val Asp Gly Thr Val Lys Gly Pro Lys Glu Ile Arg Val 580 585 590	1776
gac ctt ccc gtg gat gcc cac att ccc gaa aag tac atc aac gcc gag Asp Leu Pro Val Asp Ala His Ile Pro Glu Lys Tyr Ile Asn Ala Glu 595 600 605	1824
cgt ctg cgt ctg gaa atc tac cgc aag ctc gcg cag tcc gaa tcg gaa Arg Leu Arg Leu Glu Ile Tyr Arg Lys Leu Ala Gln Ser Glu Ser Glu 610 615 620	1872
gtg gat ctg cgc ctt Val Asp Leu Arg Leu 625	1887

<210> 434  
 <211> 629  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 434

Ala	Gly	Leu	Val	Phe	Pro	Lys	Val	Arg	Lys	His	Arg	Asp	Gly	Ala	Ala	1	5	10	15
Met	Pro	Leu	Val	Val	Ile	Thr	Glu	Thr	Asp	Leu	Thr	Gly	Asn	Arg	Val	20	25	30	
Gly	Asp	Ile	Ala	Gly	Ala	Lys	Arg	Arg	Pro	Ala	Lys	Arg	Arg	Asn	Lys	35	40	45	
Val	Asp	Pro	Leu	Ala	Leu	Glu	Pro	Gly	Asp	Leu	Val	Val	His	Glu	Thr	50	55	60	
His	Gly	Ile	Gly	Arg	Phe	Val	Lys	Met	Thr	Glu	Arg	Thr	Ile	Ser	Ala	65	70	75	
Gly	Asp	Glu	Thr	Ser	Arg	Arg	Glu	Tyr	Ile	Val	Leu	Glu	Tyr	Ala	Pro	85	90	95	
Ser	Lys	Arg	Gly	Gln	Pro	Gly	Asp	Gln	Leu	Tyr	Val	Pro	Met	Asp	Ala	100	105	110	
Leu	Asp	Met	Leu	Ser	Arg	Tyr	Val	Gly	Gly	Glu	Lys	Pro	Thr	Leu	Ser	115	120	125	
Lys	Met	Gly	Gly	Ser	Asp	Trp	Lys	Asn	Ala	Lys	Lys	Lys	Ala	Arg	Ala	130	135	140	
Ala	Val	Arg	Glu	Ile	Ala	Gly	Glu	Leu	Val	Glu	Leu	Tyr	Ala	Lys	Arg	145	150	155	
Gln	Ser	Ala	Pro	Gly	His	Pro	Phe	Ala	Pro	Asp	Thr	Pro	Trp	Gln	Lys	165	170	175	
Glu	Met	Glu	Asp	Asn	Phe	Pro	Tyr	Val	Glu	Thr	Glu	Asp	Gln	Met	Leu	180	185	190	
Ala	Ile	Asp	Ala	Val	Lys	Glu	Asp	Met	Glu	Lys	Ser	Val	Pro	Met	Asp	195	200	205	
Arg	Val	Ile	Ile	Gly	Asp	Val	Gly	Tyr	Gly	Lys	Thr	Glu	Val	Ala	Val	210	215	220	
Arg	Ala	Ala	Phe	Lys	Ala	Val	Gln	Asp	Gly	Lys	Gln	Val	Ala	Val	Leu	225	230	235	
Val	Pro	Thr	Thr	Leu	Leu	Ala	Gln	Gln	His	Gln	Ser	Thr	Phe	Glu	Glu	245	250	255	
Arg	Met	Thr	Gly	Phe	Pro	Val	Thr	Ile	Lys	Gly	Leu	Ser	Arg	Phe	Thr	260	265	270	
Ser	Pro	Ala	Glu	Ser	Arg	Glu	Ile	Leu	Ser	Gly	Leu	Ala	Ala	Gly	Ser	275	280	285	
Val	Asp	Ile	Val	Ile	Gly	Thr	His	Arg	Leu	Leu	Gln	Thr	Gly	Val	Gln				

290	295	300
Trp Lys Asn Leu Gly Leu Val Ile Val Asp Glu Glu Gln Arg Phe Gly 305 310 315 320		
Val Glu His Lys Glu His Ile Lys Ala Leu Arg Thr His Val Asp Val 325 330 335		
Leu Thr Met Ser Ala Thr Pro Ile Pro Arg Thr Leu Glu Met Ser Met 340 345 350		
Ala Gly Ile Arg Glu Met Thr Thr Met Leu Thr Pro Pro Glu Asp Arg 355 360 365		
His Pro Ile Leu Thr Tyr Val Gly Pro Tyr Glu Asp Lys Gln Val Ala 370 375 380		
Ala Ser Ile Arg Arg Glu Leu Leu Arg Asp Gly Gln Val Phe Phe Ile 385 390 395 400		
His Asn Lys Val Ala Asp Ile Glu Lys Lys Ala Arg Glu Ile Arg Asp 405 410 415		
Leu Val Pro Glu Ala Arg Val Val Val Ala His Gly Gln Met Ser Glu 420 425 430		
Glu Leu Leu Glu Gln Thr Val Gln Gly Phe Trp Asp Arg Glu Tyr Asp 435 440 445		
Val Leu Val Cys Thr Thr Ile Val Glu Thr Gly Leu Asp Ile Ser Asn 450 455 460		
Ala Asn Thr Leu Ile Val Glu Asn Ala His His Met Gly Leu Ser Gln 465 470 475 480		
Leu His Gln Leu Arg Gly Arg Val Gly Arg Ser Arg Glu Arg Gly Tyr 485 490 495		
Ala Tyr Phe Leu Tyr Pro Lys Gly Ala Thr Leu Thr Glu Met Ser Tyr 500 505 510		
Asp Arg Leu Ala Thr Ile Ala Gln Asn Asn Asp Leu Gly Ala Gly Met 515 520 525		
Ala Val Ala Met Lys Asp Leu Glu Met Arg Gly Ala Gly Asn Val Leu 530 535 540		
Gly Ala Glu Gln Ser Gly His Ile Ala Gly Val Gly Phe Asp Leu Tyr 545 550 555 560		
Val Arg Leu Val Gly Glu Ala Val Glu Ala Tyr Arg Ala Leu Ala Asp 565 570 575		
Gly Lys Val Val Asp Gly Thr Val Lys Gly Pro Lys Glu Ile Arg Val 580 585 590		
Asp Leu Pro Val Asp Ala His Ile Pro Glu Lys Tyr Ile Asn Ala Glu 595 600 605		
Arg Leu Arg Leu Glu Ile Tyr Arg Lys Leu Ala Gln Ser Glu Ser Glu 610 615 620		

Val Asp Leu Arg Leu  
625

<210> 435  
<211> 1116  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(1093)  
<223> RXN00737

<400> 435  
tcgatatggg ggccaagcgc ggtgatttgc ctaccgcgcg tgcattttga tattttcccc 60  
accacattgg attatccggt gcgtgtggag ttctggggcg atg aag gtc tct gac 115  
Met Lys Val Ser Asp  
1 5  
att agg cag ttc tct gtc gcc gat cag cgc acc att cca gaa atc acc 163  
Ile Arg Gln Phe Ser Val Ala Asp Gln Arg Thr Ile Pro Glu Ile Thr  
10 15 20  
atc aag agc att gag att ttc ccg gca cgg gaa ttg ctc att act gaa 211  
Ile Lys Ser Ile Glu Ile Phe Pro Ala Arg Glu Leu Leu Ile Thr Glu  
25 30 35  
gaa gtg gca tcg cgt gcg gag tct ctt att tct aag cac ccg ggc aac 259  
Glu Val Ala Ser Arg Ala Glu Ser Leu Ile Ser Lys His Pro Gly Asn  
40 45 50  
ccg acg ctt gtg gag atg ctg tcg agg att gcg gat tcc caa gat gtt 307  
Pro Thr Leu Val Glu Met Leu Ser Arg Ile Ala Asp Ser Gln Asp Val  
55 60 65  
gat ggc atg gag gcg ttg att ccg gcg ctg acg gat acg ccg atg gtt 355  
Asp Gly Met Glu Ala Leu Ile Pro Ala Leu Thr Asp Thr Pro Met Val  
70 75 80 85  
ccg atg ctg gag ctc atg ccg gaa aac acc cat gtg ttg gtg att gct 403  
Pro Met Leu Glu Leu Met Pro Glu Asn Thr His Val Leu Val Ile Ala  
90 95 100  
ccg gag aag gtg cgc cga cgc att gcg gat ctg gaa gca acc gat gct 451  
Pro Glu Lys Val Arg Arg Arg Ile Ala Asp Leu Glu Ala Thr Asp Ala  
105 110 115  
gag ttt ttg atg gct ggt tgg gaa gca gct gcg atg ggt gct gat ggt 499  
Glu Phe Leu Met Ala Gly Trp Glu Ala Ala Ala Met Gly Ala Asp Gly  
120 125 130  
cca gtg gct gcg gaa ggc ctg gac ttg gaa gct tct agc tat cgc agt 547  
Pro Val Ala Ala Glu Gly Leu Asp Leu Glu Ala Ser Ser Tyr Arg Ser  
135 140 145  
tat gaa agt ttg gag gtt tct gcg tcg aaa agc gat gtg cgt tgg tgg 595  
Tyr Glu Ser Leu Glu Val Ser Ala Ser Lys Ser Asp Val Arg Trp Trp  
150 155 160 165

act ttc gcg ccg ccg ggc atg ttt gag gcc tcg gag gag gcg acg ctg 643  
 Thr Phe Ala Pro Pro Gly Met Phe Glu Ala Ser Glu Glu Ala Thr Leu  
 170 175 180

ccg ctt gat ttt gaa gcc ggg ccg gcg ccg cgc ggt gag ctg ccg aag 691  
 Pro Leu Asp Phe Glu Ala Gly Pro Ala Pro Arg Gly Glu Leu Pro Lys  
 185 190 195

atc gat gcg atg atg gcg cag ctg ctt gcg cac aca acc ggc ggt ggg 739  
 Ile Asp Ala Met Met Ala Gln Leu Leu Ala His Thr Thr Gly Gly Gly  
 200 205 210

cgg gct gcg ttt atc gcg ccg acc caa ggt gcg att aag cgc atg gtc 787  
 Arg Ala Ala Phe Ile Ala Pro Thr Gln Gly Ala Ile Lys Arg Met Val  
 215 220 225

gat cgt ttc gcg gaa aag ggc att ccc acc cat gtg gcg acc ccg ggt 835  
 Asp Arg Phe Ala Glu Lys Gly Ile Pro Thr His Val Ala Thr Pro Gly  
 230 235 240 245

tgg gag cca acg cct ggt caa gtg act ctt tat cat gcg ctg agc cat 883  
 Trp Glu Pro Thr Pro Gly Gln Val Thr Leu Tyr His Ala Leu Ser His  
 250 255 260

gct ggc ctg gtg ttt ccg aag gtg cgt aaa cac cgc gat ggc gct gca 931  
 Ala Gly Leu Val Phe Pro Lys Val Arg Lys His Arg Asp Gly Ala Ala  
 265 270 275

atg ccg ttg gtg gtt att aca gaa acc gat ctg act ggt aac cgt gtt 979  
 Met Pro Leu Val Val Ile Thr Glu Thr Asp Leu Thr Gly Asn Arg Val  
 280 285 290

ggc gat att gca ggg cga aac gtc gac ctg caa aac gcc gca aca agg 1027  
 Gly Asp Ile Ala Gly Arg Asn Val Asp Leu Gln Asn Ala Ala Thr Arg  
 295 300 305

tgg atc ctt tgg cgc tgg agc cag ggg att tgg tgg ttc atg aaa ccc 1075  
 Trp Ile Leu Trp Arg Trp Ser Gln Gly Ile Trp Trp Phe Met Lys Pro  
 310 315 320 325

acg gca ttg gtc gtt ttg tgaagatgac tgaacgaacc att 1116  
 Thr Ala Leu Val Val Leu  
 330

&lt;210&gt; 436

&lt;211&gt; 331

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 436

Met Lys Val Ser Asp Ile Arg Gln Phe Ser Val Ala Asp Gln Arg Thr  
 1 5 10 15

Ile Pro Glu Ile Thr Ile Lys Ser Ile Glu Ile Phe Pro Ala Arg Glu  
 20 25 30

Leu Leu Ile Thr Glu Glu Val Ala Ser Arg Ala Glu Ser Leu Ile Ser  
 35 40 45

Lys His Pro Gly Asn Pro Thr Leu Val Glu Met Leu Ser Arg Ile Ala  
 50 55 60  
 Asp Ser Gln Asp Val Asp Gly Met Glu Ala Leu Ile Pro Ala Leu Thr  
 65 70 75 80  
 Asp Thr Pro Met Val Pro Met Leu Glu Leu Met Pro Glu Asn Thr His  
 85 90 95  
 Val Leu Val Ile Ala Pro Glu Lys Val Arg Arg Arg Ile Ala Asp Leu  
 100 105 110  
 Glu Ala Thr Asp Ala Glu Phe Leu Met Ala Gly Trp Glu Ala Ala Ala  
 115 120 125  
 Met Gly Ala Asp Gly Pro Val Ala Ala Glu Gly Leu Asp Leu Glu Ala  
 130 135 140  
 Ser Ser Tyr Arg Ser Tyr Glu Ser Leu Glu Val Ser Ala Ser Lys Ser  
 145 150 155 160  
 Asp Val Arg Trp Trp Thr Phe Ala Pro Pro Gly Met Phe Glu Ala Ser  
 165 170 175  
 Glu Glu Ala Thr Leu Pro Leu Asp Phe Glu Ala Gly Pro Ala Pro Arg  
 180 185 190  
 Gly Glu Leu Pro Lys Ile Asp Ala Met Met Ala Gln Leu Leu Ala His  
 195 200 205  
 Thr Thr Gly Gly Gly Arg Ala Ala Phe Ile Ala Pro Thr Gln Gly Ala  
 210 215 220  
 Ile Lys Arg Met Val Asp Arg Phe Ala Glu Lys Gly Ile Pro Thr His  
 225 230 235 240  
 Val Ala Thr Pro Gly Trp Glu Pro Thr Pro Gly Gln Val Thr Leu Tyr  
 245 250 255  
 His Ala Leu Ser His Ala Gly Leu Val Phe Pro Lys Val Arg Lys His  
 260 265 270  
 Arg Asp Gly Ala Ala Met Pro Leu Val Val Ile Thr Glu Thr Asp Leu  
 275 280 285  
 Thr Gly Asn Arg Val Gly Asp Ile Ala Gly Arg Asn Val Asp Leu Gln  
 290 295 300  
 Asn Ala Ala Thr Arg Trp Ile Leu Trp Arg Trp Ser Gln Gly Ile Trp  
 305 310 315 320  
 Trp Phe Met Lys Pro Thr Ala Leu Val Val Leu  
 325 330

&lt;210&gt; 437

&lt;211&gt; 480

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(480)

&lt;223&gt; FRXA00737

&lt;400&gt; 437

cac	ccg	ggc	aac	ccg	acg	ctt	gtg	gag	atg	ctg	tcg	agg	att	gcg	gat	48
His	Pro	Gly	Asn	Pro	Thr	Leu	Val	Glu	Met	Leu	Ser	Arg	Ile	Ala	Asp	
1				5					10					15		
tcc	caa	gat	gtt	gat	ggc	atg	gag	gcg	ttg	att	ccg	gcg	ctg	acg	gat	96
Ser	Gln	Asp	Val	Asp	Gly	Met	Glu	Ala	Leu	Ile	Pro	Ala	Leu	Thr	Asp	
			20					25					30			
acg	ccg	atg	gtt	ccg	atg	ctg	gag	ctc	atg	ccg	gaa	aac	acc	cat	gtg	144
Thr	Pro	Met	Val	Pro	Met	Leu	Glu	Leu	Met	Pro	Glu	Asn	Thr	His	Val	
		35					40					45				
ttg	gtg	att	gct	ccg	gag	aag	gtg	cgc	cga	cgc	att	gcg	gat	ctg	gaa	192
Leu	Val	Ile	Ala	Pro	Glu	Lys	Val	Arg	Arg	Arg	Ile	Ala	Asp	Leu	Glu	
	50					55					60					
gca	acc	gat	gct	gag	ttt	ttg	atg	gct	ggc	tgg	gaa	gca	gct	gcg	atg	240
Ala	Thr	Asp	Ala	Glu	Phe	Leu	Met	Ala	Gly	Trp	Glu	Ala	Ala	Ala	Met	
65					70					75					80	
ggc	gct	gat	ggc	cca	gtg	gct	gcg	gaa	ggc	ctg	gac	ttg	gaa	gct	tct	288
Gly	Ala	Asp	Gly	Pro	Val	Ala	Ala	Glu	Gly	Leu	Asp	Leu	Glu	Ala	Ser	
				85					90					95		
agc	tat	cgc	agt	tat	gaa	agt	ttg	gag	gtt	tct	gcg	tcg	aaa	agc	gat	336
Ser	Tyr	Arg	Ser	Tyr	Glu	Ser	Leu	Glu	Val	Ser	Ala	Ser	Lys	Ser	Asp	
			100					105					110			
gtg	cgt	tgg	tgg	act	ttc	gcg	ccg	ccg	ggc	atg	ttt	gag	gcc	tcg	gag	384
Val	Arg	Trp	Trp	Thr	Phe	Ala	Pro	Pro	Gly	Met	Phe	Glu	Ala	Ser	Glu	
		115					120					125				
gag	gcg	acg	ctg	ccg	ctt	gat	ttt	gaa	gcc	ggg	ccg	gcg	ccg	cgc	ggc	432
Glu	Ala	Thr	Leu	Pro	Leu	Asp	Phe	Glu	Ala	Gly	Pro	Ala	Pro	Arg	Gly	
	130					135					140					
gag	ctg	ccg	aag	atc	gat	gcg	atg	atg	gcg	cag	ctg	ctt	gcg	cac	aca	480
Glu	Leu	Pro	Lys	Ile	Asp	Ala	Met	Met	Ala	Gln	Leu	Leu	Ala	His	Thr	
145				150						155					160	

&lt;210&gt; 438

&lt;211&gt; 160

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 438

His	Pro	Gly	Asn	Pro	Thr	Leu	Val	Glu	Met	Leu	Ser	Arg	Ile	Ala	Asp	
1				5					10					15		
Ser	Gln	Asp	Val	Asp	Gly	Met	Glu	Ala	Leu	Ile	Pro	Ala	Leu	Thr	Asp	
			20					25					30			
Thr	Pro	Met	Val	Pro	Met	Leu	Glu	Leu	Met	Pro	Glu	Asn	Thr	His	Val	
		35					40					45				

Leu Val Ile Ala Pro Glu Lys Val Arg Arg Arg Ile Ala Asp Leu Glu  
 50 55 60  
 Ala Thr Asp Ala Glu Phe Leu Met Ala Gly Trp Glu Ala Ala Ala Met  
 65 70 75 80  
 Gly Ala Asp Gly Pro Val Ala Ala Glu Gly Leu Asp Leu Glu Ala Ser  
 85 90 95  
 Ser Tyr Arg Ser Tyr Glu Ser Leu Glu Val Ser Ala Ser Lys Ser Asp  
 100 105 110  
 Val Arg Trp Trp Thr Phe Ala Pro Pro Gly Met Phe Glu Ala Ser Glu  
 115 120 125  
 Glu Ala Thr Leu Pro Leu Asp Phe Glu Ala Gly Pro Ala Pro Arg Gly  
 130 135 140  
 Glu Leu Pro Lys Ile Asp Ala Met Met Ala Gln Leu Leu Ala His Thr  
 145 150 155 160

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 <223> RXN01872

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 Met Gly Asn Asp Gly  
 1 5  
 gga gac ctg cga atc gac gac cta cgc agc ttc att tca gtc gct caa 163  
 Gly Asp Leu Arg Ile Asp Asp Leu Arg Ser Phe Ile Ser Val Ala Gln  
 10 15 20  
 tca ggc cac cta acc gaa act gcc caa aga tta ggc atc ccg cag ccc 211  
 Ser Gly His Leu Thr Glu Thr Ala Gln Arg Leu Gly Ile Pro Gln Pro  
 25 30 35  
 aca ctt tcc aga cga atc agc cga gtg gaa aaa cac gca ggc acc cca 259  
 Thr Leu Ser Arg Arg Ile Ser Arg Val Glu Lys His Ala Gly Thr Pro  
 40 45 50  
 ctt ttc gac cgc gcc ggc cgc aaa ctc gtc ctc aac caa cga ggc cac 307  
 Leu Phe Asp Arg Ala Gly Arg Lys Leu Val Leu Asn Gln Arg Gly His  
 55 60 65  
 gcc ttc ctc aac cac gcc agc gcc atc gtc gca gaa ttc aac tcc gcc 355  
 Ala Phe Leu Asn His Ala Ser Ala Ile Val Ala Glu Phe Asn Ser Ala  
 70 75 80 85  
 gca act gaa atc aaa cgc ctc atg gac cca gaa aaa ggc aca atc cga 403  
 Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu Lys Gly Thr Ile Arg

90										95					100					
ctg	gac	ttc	atg	cat	tcc	ttg	ggc	act	tgg	atg	gtc	ccc	gaa	ctt	atc	451				
Leu	Asp	Phe	Met	His	Ser	Leu	Gly	Thr	Trp	Met	Val	Pro	Glu	Leu	Ile					
			105					110					115							
cga	aca	ttc	cgc	gcc	gaa	cac	ccc	aac	gta	gaa	ttc	caa	ctc	cac	caa	499				
Arg	Thr	Phe	Arg	Ala	Glu	His	Pro	Asn	Val	Glu	Phe	Gln	Leu	His	Gln					
		120					125					130								
gcg	gca	gca	atg	ctc	ctg	gta	gat	cgt	gtt	ttg	gct	gat	gaa	act	gac	547				
Ala	Ala	Ala	Met	Leu	Leu	Val	Asp	Arg	Val	Leu	Ala	Asp	Glu	Thr	Asp					
		135				140					145									
ctc	gca	tta	gtt	ggc	ccc	aaa	cct	gcc	gag	gtt	ggg	acc	tct	tta	ggg	595				
Leu	Ala	Leu	Val	Gly	Pro	Lys	Pro	Ala	Glu	Val	Gly	Thr	Ser	Leu	Gly					
150					155					160					165					
tgg	gcg	cca	ctg	ctt	cgt	caa	cga	ctt	gcc	cta	gct	gtt	ccc	gca	gat	643				
Trp	Ala	Pro	Leu	Leu	Arg	Gln	Arg	Leu	Ala	Leu	Ala	Val	Pro	Ala	Asp					
			170						175					180						
cac	cgg	ctt	gcc	tcc	ttt	tct	ggc	caa	gga	gaa	ttg	ccg	ttg	att	act	691				
His	Arg	Leu	Ala	Ser	Phe	Ser	Gly	Gln	Gly	Glu	Leu	Pro	Leu	Ile	Thr					
			185					190					195							
gcg	gcg	gaa	gaa	cct	ttc	gtg	gcg	atg	cga	gca	ggg	ttc	ggc	acc	cga	739				
Ala	Ala	Glu	Glu	Pro	Phe	Val	Ala	Met	Arg	Ala	Gly	Phe	Gly	Thr	Arg					
		200					205					210								
ctc	ctc	atg	gat	gca	tta	gcc	gaa	gaa	gcc	ggg	ttt	gtt	ccc	aat	gtg	787				
Leu	Leu	Met	Asp	Ala	Leu	Ala	Glu	Glu	Ala	Gly	Phe	Val	Pro	Asn	Val					
		215				220				225										
gtt	ttc	gaa	tcc	atg	gaa	ctc	acc	acc	gtc	gca	ggg	ctt	gtc	agc	gca	835				
Val	Phe	Glu	Ser	Met	Glu	Leu	Thr	Thr	Val	Ala	Gly	Leu	Val	Ser	Ala					
230					235					240					245					
ggg	ctc	ggc	gtt	ggg	gtg	gtt	ccg	atg	gat	gat	ccc	tac	ctt	tcc	aca	883				
Gly	Leu	Gly	Val	Gly	Val	Val	Pro	Met	Asp	Asp	Pro	Tyr	Leu	Ser	Thr					
			250					255						260						
gtg	gga	atc	gtg	caa	cgc	cca	ctt	agt	cca	ccc	gct	tat	agg	gaa		928				
Val	Gly	Ile	Val	Gln	Arg	Pro	Leu	Ser	Pro	Pro	Ala	Tyr	Arg	Glu						
			265				270						275							

&lt;210&gt; 440

&lt;211&gt; 276

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 440

Met	Gly	Asn	Asp	Gly	Gly	Asp	Leu	Arg	Ile	Asp	Asp	Leu	Arg	Ser	Phe
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Ile	Ser	Val	Ala	Gln	Ser	Gly	His	Leu	Thr	Glu	Thr	Ala	Gln	Arg	Leu
			20					25					30		
Gly	Ile	Pro	Gln	Pro	Thr	Leu	Ser	Arg	Arg	Ile	Ser	Arg	Val	Glu	Lys
		35					40					45			

His Ala Gly Thr Pro Leu Phe Asp Arg Ala Gly Arg Lys Leu Val Leu  
 50 55 60  
 Asn Gln Arg Gly His Ala Phe Leu Asn His Ala Ser Ala Ile Val Ala  
 65 70 75 80  
 Glu Phe Asn Ser Ala Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu  
 85 90 95  
 Lys Gly Thr Ile Arg Leu Asp Phe Met His Ser Leu Gly Thr Trp Met  
 100 105 110  
 Val Pro Glu Leu Ile Arg Thr Phe Arg Ala Glu His Pro Asn Val Glu  
 115 120 125  
 Phe Gln Leu His Gln Ala Ala Ala Met Leu Leu Val Asp Arg Val Leu  
 130 135 140  
 Ala Asp Glu Thr Asp Leu Ala Leu Val Gly Pro Lys Pro Ala Glu Val  
 145 150 155 160  
 Gly Thr Ser Leu Gly Trp Ala Pro Leu Leu Arg Gln Arg Leu Ala Leu  
 165 170 175  
 Ala Val Pro Ala Asp His Arg Leu Ala Ser Phe Ser Gly Gln Gly Glu  
 180 185 190  
 Leu Pro Leu Ile Thr Ala Ala Glu Glu Pro Phe Val Ala Met Arg Ala  
 195 200 205  
 Gly Phe Gly Thr Arg Leu Leu Met Asp Ala Leu Ala Glu Glu Ala Gly  
 210 215 220  
 Phe Val Pro Asn Val Val Phe Glu Ser Met Glu Leu Thr Thr Val Ala  
 225 230 235 240  
 Gly Leu Val Ser Ala Gly Leu Gly Val Gly Val Val Pro Met Asp Asp  
 245 250 255  
 Pro Tyr Leu Ser Thr Val Gly Ile Val Gln Arg Pro Leu Ser Pro Pro  
 260 265 270  
 Ala Tyr Arg Glu  
 275

&lt;210&gt; 441

&lt;211&gt; 865

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(865)

&lt;223&gt; FRXA01872

&lt;400&gt; 441

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											1				5	
gga	gac	ctg	cga	atc	gac	gac	cta	cgc	agc	ttc	att	tca	gtc	gct	caa	163
Gly	Asp	Leu	Arg	Ile	Asp	Asp	Leu	Arg	Ser	Phe	Ile	Ser	Val	Ala	Gln	
				10					15					20		
tca	ggc	cac	cta	acc	gaa	act	gcc	caa	aga	tta	ggc	atc	ccg	cag	ccc	211
Ser	Gly	His	Leu	Thr	Glu	Thr	Ala	Gln	Arg	Leu	Gly	Ile	Pro	Gln	Pro	
			25					30					35			
aca	ctt	tcc	aga	cga	atc	agc	cga	gtg	gaa	aaa	cac	gca	ggc	acc	cca	259
Thr	Leu	Ser	Arg	Arg	Ile	Ser	Arg	Val	Glu	Lys	His	Ala	Gly	Thr	Pro	
		40					45					50				
ctt	ttc	gac	cgc	gcc	ggc	cgc	aaa	ctc	gtc	ctc	aac	caa	cga	ggc	cac	307
Leu	Phe	Asp	Arg	Ala	Gly	Arg	Lys	Leu	Val	Leu	Asn	Gln	Arg	Gly	His	
	55					60					65					
gcc	ttc	ctc	aac	cac	gcc	agc	gcc	atc	gtc	gca	gaa	ttc	aac	tcc	gcc	355
Ala	Phe	Leu	Asn	His	Ala	Ser	Ala	Ile	Val	Ala	Glu	Phe	Asn	Ser	Ala	
70				75					80						85	
gca	act	gaa	atc	aaa	cgc	ctc	atg	gac	cca	gaa	aaa	ggc	aca	atc	cga	403
Ala	Thr	Glu	Ile	Lys	Arg	Leu	Met	Asp	Pro	Glu	Lys	Gly	Thr	Ile	Arg	
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Leu	Asp	Phe	Met	His	Ser	Leu	Gly	Thr	Trp	Met	Val	Pro	Glu	Leu	Ile	
			105				110					115				
cga	aca	ttc	cgc	gcc	gaa	cac	ccc	aac	gta	gaa	ttc	caa	ctc	cac	caa	499
Arg	Thr	Phe	Arg	Ala	Glu	His	Pro	Asn	Val	Glu	Phe	Gln	Leu	His	Gln	
		120					125					130				
gcg	gca	gca	atg	ctc	ctg	gta	gat	cgt	gtt	ttg	gct	gat	gaa	act	gac	547
Ala	Ala	Ala	Met	Leu	Leu	Val	Asp	Arg	Val	Leu	Ala	Asp	Glu	Thr	Asp	
	135					140				145						
ctc	gca	tta	gtt	ggc	ccc	aaa	cct	gcc	gag	gtt	ggc	acc	tct	tta	ggg	595
Leu	Ala	Leu	Val	Gly	Pro	Lys	Pro	Ala	Glu	Val	Gly	Thr	Ser	Leu	Gly	
150				155					160						165	
tgg	gcg	cca	ctg	ctt	cgt	caa	cga	ctt	gcc	cta	gct	gtt	ccc	gca	gat	643
Trp	Ala	Pro	Leu	Leu	Arg	Gln	Arg	Leu	Ala	Leu	Ala	Val	Pro	Ala	Asp	
			170					175					180			
cac	cgg	ctt	gcc	tcc	ttt	tct	ggc	caa	gga	gaa	ttg	ccg	ttg	att	act	691
His	Arg	Leu	Ala	Ser	Phe	Ser	Gly	Gln	Gly	Glu	Leu	Pro	Leu	Ile	Thr	
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gcg	gcg	gaa	gaa	cct	ttc	gtg	gcg	atg	cga	gca	gg					

230                      235                      240                      245                      865

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 <212> PRT  
 <213> Corynebacterium glutamicum

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                     20                    25                    30

Gly Ile Pro Gln Pro Thr Leu Ser Arg Arg Ile Ser Arg Val Glu Lys  
                     35                    40                    45

His Ala Gly Thr Pro Leu Phe Asp Arg Ala Gly Arg Lys Leu Val Leu  
   50                    55                    60

Asn Gln Arg Gly His Ala Phe Leu Asn His Ala Ser Ala Ile Val Ala  
   65                    70                    75                    80

Glu Phe Asn Ser Ala Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu  
                     85                    90                    95

Lys Gly Thr Ile Arg Leu Asp Phe Met His Ser Leu Gly Thr Trp Met  
                     100                    105                    110

Val Pro Glu Leu Ile Arg Thr Phe Arg Ala Glu His Pro Asn Val Glu  
                     115                    120                    125

Phe Gln Leu His Gln Ala Ala Ala Met Leu Leu Val Asp Arg Val Leu  
   130                    135                    140

Ala Asp Glu Thr Asp Leu Ala Leu Val Gly Pro Lys Pro Ala Glu Val  
  145                    150                    155                    160

Gly Thr Ser Leu Gly Trp Ala Pro Leu Leu Arg Gln Arg Leu Ala Leu  
                     165                    170                    175

Ala Val Pro Ala Asp His Arg Leu Ala Ser Phe Ser Gly Gln Gly Glu  
                     180                    185                    190

Leu Pro Leu Ile Thr Ala Ala Glu Glu Pro Phe Val Ala Met Arg Ala  
                     195                    200                    205

Gly Phe Gly Thr Arg Leu Leu Met Asp Ala Leu Ala Glu Glu Ala Gly  
   210                    215                    220

Phe Val Pro Asn Val Val Phe Glu Ser Met Glu Leu Thr Thr Val Ala  
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Gly Leu Val Ser Ala Gly Leu Gly Val Gly Val Val Pro Met Asp  
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Met Thr Ser Glu Asn 5																
tcc gaa tcc cag gac att tgg cta acc gat gag caa caa gat gtg tgg 163																
Ser Glu Ser Gln Asp Ile Trp Leu Thr Asp Glu Gln Gln Asp Val Trp 20																
ctc gat gtg tgg aca atg cga atc ggc ctg cct gct cgc ttg gat gct 211																
Leu Asp Val Trp Thr Met Arg Ile Gly Leu Pro Ala Arg Leu Asp Ala 35																
caa ctg aaa gaa gct gcg ggt gtc agc cac ttt gag tac ttc acc atg 259																
Gln Leu Lys Glu Ala Ala Gly Val Ser His Phe Glu Tyr Phe Thr Met 50																
gcg cag att tct atg gcc ccg gaa cat cgg gtg cgc atg agt gag ctt 307																
Ala Gln Ile Ser Met Ala Pro Glu His Arg Val Arg Met Ser Glu Leu 65																
gct gag ctg tcc gat atg acg cta tcg cat cta tct aga gtg gtt act 355																
Ala Glu Leu Ser Asp Met Thr Leu Ser His Leu Ser Arg Val Val Thr 85																
cgc cta gaa aag gct ggc tgg gtg aag cgt gtt ccc gat cct gat gat 403																
Arg Leu Glu Lys Ala Gly Trp Val Lys Arg Val Pro Asp Pro Asp Asp 100																
ggt cgc gcc acc gtt gct gtg ctc acg gac tct ggg tgg gag aaa gtt 451																
Gly Arg Ala Thr Val Ala Val Leu Thr Asp Ser Gly Trp Glu Lys Val 115																
aaa gca aca gcc cct ggt cat gtg aag gaa gtg cgt cgt ttg gtg ttt 499																
Lys Ala Thr Ala Pro Gly His Val Lys Glu Val Arg Arg Leu Val Phe 130																
gac gat ctc act cca gaa gaa ctc aag gta atg ggc acc gca atg aag 547																
Asp Asp Leu Thr Pro Glu Glu Leu Lys Val Met Gly Thr Ala Met Lys 145																
aag att gtg aac cga ctc gat atg tcc aac agg ctg ccc cgg gtg 592																
Lys Ile Val Asn Arg Leu Asp Met Ser Asn Arg Leu Pro Arg Val 160																
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 <211> 164  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 444  
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                     20                    25                    30  
 Ala Arg Leu Asp Ala Gln Leu Lys Glu Ala Ala Gly Val Ser His Phe  
                     35                    40                    45  
 Glu Tyr Phe Thr Met Ala Gln Ile Ser Met Ala Pro Glu His Arg Val  
                     50                    55                    60  
 Arg Met Ser Glu Leu Ala Glu Leu Ser Asp Met Thr Leu Ser His Leu  
                     65                    70                    75                    80  
 Ser Arg Val Val Thr Arg Leu Glu Lys Ala Gly Trp Val Lys Arg Val  
                     85                    90                    95  
 Pro Asp Pro Asp Asp Gly Arg Ala Thr Val Ala Val Leu Thr Asp Ser  
                     100                    105                    110  
 Gly Trp Glu Lys Val Lys Ala Thr Ala Pro Gly His Val Lys Glu Val  
                     115                    120                    125  
 Arg Arg Leu Val Phe Asp Asp Leu Thr Pro Glu Glu Leu Lys Val Met  
                     130                    135                    140  
 Gly Thr Ala Met Lys Lys Ile Val Asn Arg Leu Asp Met Ser Asn Arg  
                     145                    150                    155                    160  
 Leu Pro Arg Val

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 <211> 1022  
 <212> DNA  
 <213> Corynebacterium glutamicum

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 gca ggc gtc tcc aaa tcc ttg gtt tct ctc gtg ctt cgc ggc tcc ccc 96  
 Ala Gly Val Ser Lys Ser Leu Val Ser Leu Val Leu Arg Gly Ser Pro  
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 aac gtg agc aaa gaa tcc gaa gcc gcg gtc aag acc gcg ata aaa aag 144  
 Asn Val Ser Lys Glu Ser Glu Ala Ala Val Lys Thr Ala Ile Lys Lys

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ctc	aac	tac	cag	cca	aat	cgc	gcc	gca	tca	gac	ctt	gcg	gcc	aag	cgc	192
Leu	Asn	Tyr	Gln	Pro	Asn	Arg	Ala	Ala	Ser	Asp	Leu	Ala	Ala	Lys	Arg	
	50					55					60					
acg	cag	ctc	att	gca	gtg	ctt	atc	gac	gac	tac	tcc	aac	ccg	tgg	ttc	240
Thr	Gln	Leu	Ile	Ala	Val	Leu	Ile	Asp	Asp	Tyr	Ser	Asn	Pro	Trp	Phe	
	65				70					75					80	
atc	gac	ctg	att	caa	agc	ctc	agc	gat	gtg	ctc	acc	ccc	aag	ggg	tac	288
Ile	Asp	Leu	Ile	Gln	Ser	Leu	Ser	Asp	Val	Leu	Thr	Pro	Lys	Gly	Tyr	
				85					90					95		
cga	ctg	tcc	gtc	att	gac	tca	tta	acc	tct	caa	gcc	ggc	acc	gat	ccc	336
Arg	Leu	Ser	Val	Ile	Asp	Ser	Leu	Thr	Ser	Gln	Ala	Gly	Thr	Asp	Pro	
			100					105					110			
att	acc	agt	gca	cta	tca	atg	cgc	ccc	gat	gga	atc	atc	atc	gcc	caa	384
Ile	Thr	Ser	Ala	Leu	Ser	Met	Arg	Pro	Asp	Gly	Ile	Ile	Ile	Ala	Gln	
		115					120					125				
gac	atc	ccc	gat	ttc	act	gtc	ccc	gat	tcc	cta	ccc	cca	ttt	gtc	atc	432
Asp	Ile	Pro	Asp	Phe	Thr	Val	Pro	Asp	Ser	Leu	Pro	Pro	Phe	Val	Ile	
	130					135					140					
gca	ggc	acc	aga	atc	acc	caa	gcc	agc	acc	cat	gat	tca	gtg	gcc	aac	480
Ala	Gly	Thr	Arg	Ile	Thr	Gln	Ala	Ser	Thr	His	Asp	Ser	Val	Ala	Asn	
	145				150					155					160	
gat	gac	ttc	cgg	ggc	gca	gaa	ata	gcc	aca	aaa	cac	ctc	atc	gat	ctt	528
Asp	Asp	Phe	Arg	Gly	Ala	Glu	Ile	Ala	Thr	Lys	His	Leu	Ile	Asp	Leu	
				165				170						175		
gga	cac	acc	cac	atc	gcc	cac	cta	cgc	gtg	gga	agc	ggc	gct	ggc	tta	576
Gly	His	Thr	His	Ile	Ala	His	Leu	Arg	Val	Gly	Ser	Gly	Ala	Gly	Leu	
			180					185					190			
cga	cgc	ttc	gaa	agc	ttt	gag	gca	acc	atg	cgt	gca	cat	ggc	ctg	gag	624
Arg	Arg	Phe	Glu	Ser	Phe	Glu	Ala	Thr	Met	Arg	Ala	His	Gly	Leu	Glu	
		195					200					205				
ccg	ctt	tcc	aac	gat	tac	ctc	ggc	ccc	gcc	gtt	gag	cac	gcc	ggg	tac	672
Pro	Leu	Ser	Asn	Asp	Tyr	Leu	Gly	Pro	Ala	Val	Glu	His	Ala	Gly	Tyr	
	210					215					220					
acc	gaa	acc	ctc	gca	cta	ctc	aaa	gag	cac	ccg	gag	gtc	acc	gcc	att	720
Thr	Glu	Thr	Leu	Ala	Leu	Leu	Lys	Glu	His	Pro	Glu	Val	Thr	Ala	Ile	
	225				230					235					240	
ttc	tcc	tca	aac	gac	atc	acc	gcc	atc	gga	gca	ctc	ggt	gcc	gcc	cgt	768
Phe	Ser	Ser	Asn	Asp	Ile	Thr	Ala	Ile	Gly	Ala	Leu	Gly	Ala	Ala	Arg	
				245					250					255		
gaa	cta	ggt	tta	cgc	gta	cct	gaa	gat	cta	tca	ata	atc	gga	tat	gac	816
Glu	Leu	Gly	Leu	Arg	Val	Pro	Glu	Asp	Leu	Ser	Ile	Ile	Gly	Tyr	Asp	
			260					265					270			
aac	act	ccc	ctc	gcc	caa	acc	cga	ctg	atc	aac	ctc	acc	acc	atc	gac	864
Asn	Thr	Pro	Leu	Ala	Gln	Thr	Arg	Leu	Ile	Asn	Leu	Thr	Thr	Ile	Asp	
		275					280					285				

gac aac agc atc ggc gtc ggc tac aac gcc gct ctc ttg ttg ctg agc 912  
 Asp Asn Ser Ile Gly Val Gly Tyr Asn Ala Ala Leu Leu Leu Leu Ser  
 290 295 300

atg ctt gat ccc gag gca ccc cac ccg gag atc atg cat acg ttg cag 960  
 Met Leu Asp Pro Glu Ala Pro His Pro Glu Ile Met His Thr Leu Gln  
 305 310 315 320

ccc tcg ctg att gaa cgg ggc acg tgc gcg cca cgt gga tagctacccc 1009  
 Pro Ser Leu Ile Glu Arg Gly Thr Cys Ala Pro Arg Gly  
 325 330

aaataacttg act 1022

<210> 446  
 <211> 333  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 446  
 Gln Lys Met Ser Thr Ser Arg Pro Thr Ile Tyr Asp Val Ala Lys Ala  
 1 5 10 15  
 Ala Gly Val Ser Lys Ser Leu Val Ser Leu Val Leu Arg Gly Ser Pro  
 20 25 30  
 Asn Val Ser Lys Glu Ser Glu Ala Ala Val Lys Thr Ala Ile Lys Lys  
 35 40 45  
 Leu Asn Tyr Gln Pro Asn Arg Ala Ala Ser Asp Leu Ala Ala Lys Arg  
 50 55 60  
 Thr Gln Leu Ile Ala Val Leu Ile Asp Asp Tyr Ser Asn Pro Trp Phe  
 65 70 75 80  
 Ile Asp Leu Ile Gln Ser Leu Ser Asp Val Leu Thr Pro Lys Gly Tyr  
 85 90 95  
 Arg Leu Ser Val Ile Asp Ser Leu Thr Ser Gln Ala Gly Thr Asp Pro  
 100 105 110  
 Ile Thr Ser Ala Leu Ser Met Arg Pro Asp Gly Ile Ile Ile Ala Gln  
 115 120 125  
 Asp Ile Pro Asp Phe Thr Val Pro Asp Ser Leu Pro Pro Phe Val Ile  
 130 135 140  
 Ala Gly Thr Arg Ile Thr Gln Ala Ser Thr His Asp Ser Val Ala Asn  
 145 150 155 160  
 Asp Asp Phe Arg Gly Ala Glu Ile Ala Thr Lys His Leu Ile Asp Leu  
 165 170 175  
 Gly His Thr His Ile Ala His Leu Arg Val Gly Ser Gly Ala Gly Leu  
 180 185 190  
 Arg Arg Phe Glu Ser Phe Glu Ala Thr Met Arg Ala His Gly Leu Glu  
 195 200 205

Pro Leu Ser Asn Asp Tyr Leu Gly Pro Ala Val Glu His Ala Gly Tyr  
 210 215 220  
 Thr Glu Thr Leu Ala Leu Leu Lys Glu His Pro Glu Val Thr Ala Ile  
 225 230 235 240  
 Phe Ser Ser Asn Asp Ile Thr Ala Ile Gly Ala Leu Gly Ala Ala Arg  
 245 250 255  
 Glu Leu Gly Leu Arg Val Pro Glu Asp Leu Ser Ile Ile Gly Tyr Asp  
 260 265 270  
 Asn Thr Pro Leu Ala Gln Thr Arg Leu Ile Asn Leu Thr Thr Ile Asp  
 275 280 285  
 Asp Asn Ser Ile Gly Val Gly Tyr Asn Ala Ala Leu Leu Leu Leu Ser  
 290 295 300  
 Met Leu Asp Pro Glu Ala Pro His Pro Glu Ile Met His Thr Leu Gln  
 305 310 315 320  
 Pro Ser Leu Ile Glu Arg Gly Thr Cys Ala Pro Arg Gly  
 325 330

<210> 447  
 <211> 523  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(523)  
 <223> RXN02827

<220>  
 <223> All occurrences of n = any nucleotide

<220>  
 <223> All occurrences of Xaa = any amino acid

<400> 447  
 cggtttactt ttatttatcg aatgaatcat gtacatagaa taataagcat taaagggggg 60  
 gcgggtagga agaagcagcc gtgtcgcata tgcttacttt atg tat gag cag cag 115  
 Met Tyr Glu Gln Gln  
 1 5  
 aag atc ctt aac gaa gtc agt gaa aaa cgt ctt cag gca atc aaa gat 163  
 Lys Ile Leu Asn Glu Val Ser Glu Lys Arg Leu Gln Ala Ile Lys Asp  
 10 15 20  
 ttt aca gaa ctg gga tct gga ttc aag att gcg atg cgg gat ctt tcc 211  
 Phe Thr Glu Leu Gly Ser Gly Phe Lys Ile Ala Met Arg Asp Leu Ser  
 25 30 35  
 att cgc ggt gca ggt aat ctc tta ggt gct cag cag cat gga ttt att 259  
 Ile Arg Gly Ala Gly Asn Leu Leu Gly Ala Gln Gln His Gly Phe Ile  
 40 45 50  
 gat gca gtc ggt ttc gat atg tat tct caa atg cta agc gaa gct gtt 307

```

Asp Ala Val Gly Phe Asp Met Tyr Ser Gln Met Leu Ser Glu Ala Val
  55                      60                      65

tnt cgt aaa caa gga aag aat agt caa gtg gag aag ncc nct gtt gag 355
Xaa Arg Lys Gln Gly Lys Asn Ser Gln Val Glu Lys Xaa Xaa Val Glu
  70                      75                      80                      85

atc gac cnc ggt gtc gat gcg tat cta cct gaa aca tac gtg gca gat 403
Ile Asp Xaa Gly Val Asp Ala Tyr Leu Pro Glu Thr Tyr Val Ala Asp
                      90                      95                      100

can cgg cag aaa atc gag atc tat aaa cga att cgt gaa ctt gat tcg 451
Xaa Arg Gln Lys Ile Glu Ile Tyr Lys Arg Ile Arg Glu Leu Asp Ser
                      105                      110                      115

caa gaa atg cta gat gaa cta gaa gat gat ctg ctc gac cgt ttt gga 499
Gln Glu Met Leu Asp Glu Leu Glu Asp Asp Leu Leu Asp Arg Phe Gly
                      120                      125                      130

gaa can cca gaa gaa gta gca cat 523
Glu Xaa Pro Glu Glu Val Ala His
  135                      140

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&lt;210&gt; 448

&lt;211&gt; 141

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;223&gt; All occurrences of Xaa = any amino acid

&lt;400&gt; 448

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Met Tyr Glu Gln Gln Lys Ile Leu Asn Glu Val Ser Glu Lys Arg Leu
  1                      5                      10                      15

Gln Ala Ile Lys Asp Phe Thr Glu Leu Gly Ser Gly Phe Lys Ile Ala
                      20                      25                      30

Met Arg Asp Leu Ser Ile Arg Gly Ala Gly Asn Leu Leu Gly Ala Gln
                      35                      40                      45

Gln His Gly Phe Ile Asp Ala Val Gly Phe Asp Met Tyr Ser Gln Met
                      50                      55                      60

Leu Ser Glu Ala Val Xaa Arg Lys Gln Gly Lys Asn Ser Gln Val Glu
                      65                      70                      75                      80

Lys Xaa Xaa Val Glu Ile Asp Xaa Gly Val Asp Ala Tyr Leu Pro Glu
                      85                      90                      95

Thr Tyr Val Ala Asp Xaa Arg Gln Lys Ile Glu Ile Tyr Lys Arg Ile
                      100                      105                      110

Arg Glu Leu Asp Ser Gln Glu Met Leu Asp Glu Leu Glu Asp Asp Leu
                      115                      120                      125

Leu Asp Arg Phe Gly Glu Xaa Pro Glu Glu Val Ala His
                      130                      135                      140

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<210> 450
<211> 147
<212> PRT
<213> Corynebacterium glutamicum
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&lt;400&gt; 450

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Met Ser Glu Asn Tyr Ser Lys Ile Val Val Gly Thr Asp Gly Ser Lys
 1           5           10           15

Ser Ser Leu Leu Ala Val Glu Arg Ala Ala Arg Ile Ala Ala Ala Phe
          20           25           30

Asp Ala Thr Leu Ile Ile Gly Cys Ala Tyr Tyr Glu Ser Lys Glu Asp
          35           40           45

Ala Ser Glu Thr Leu Arg Gln Asp Ser Val Thr Ile Leu Gly Asp Asp
          50           55           60

Pro Ala Arg Glu Asn Leu Asp Lys Ala Ala Asp Ala Ala Arg Ala Val
 65           70           75           80

Gly Ala Thr Ser Ile Glu Thr Glu Val Arg Thr Gly Thr Pro Val Glu
          85           90           95

Ala Leu Met Ala Ile Val Asn Asp His Gln Ala Asp Leu Leu Val Val
          100          105          110

Gly Asn Arg Gly Ile Asn Tyr Leu Thr Gly Arg Leu Leu Gly Ser Val
          115          120          125

Pro Ala Asp Val Ala Arg Gln Ser Asp Cys Asp Val Met Ile Val His
 130          135          140

Thr Val Ser
145

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&lt;210&gt; 451

&lt;211&gt; 1272

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1249)

&lt;223&gt; RXN01671

&lt;400&gt; 451

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tctaaaaaca catttttaag ccctcccggc gcagctgaaa actcagtcgc cgggagggct 60

tttttgtacc cgaatttgta cccgaattta aggaatcgct atg aat cat gtt gtt 115
                               Met Asn His Val Val
                               1           5

aat ttt gct tca cat ttg gaa gac gca gcc ctg aag caa gcc gaa gct 163
Asn Phe Ala Ser His Leu Glu Asp Ala Ala Leu Lys Gln Ala Glu Ala
          10           15           20

act gcc acc atg ccg ttt att tac ccg cat gtg gcg ttg atg cct gat 211
Thr Ala Thr Met Pro Phe Ile Tyr Pro His Val Ala Leu Met Pro Asp
          25           30           35

gct cac ttt ggg ctg ggt tcg tcg gtg gga acg gtg ttc ggc acc aag 259
Ala His Phe Gly Leu Gly Ser Ser Val Gly Thr Val Phe Gly Thr Lys
          40           45           50

```

ggt gcg atc att ccg gcg gct gtg ggt gtg gat ata ggt tgc gga atg	307
Gly Ala Ile Ile Pro Ala Ala Val Gly Val Asp Ile Gly Cys Gly Met	
55 60 65	
ata gga gtg tgt acc aat tac acg gcc tct gac ctg gag gga cgt gat	355
Ile Gly Val Cys Thr Asn Tyr Thr Ala Ser Asp Leu Glu Gly Arg Asp	
70 75 80 85	
ttg gtg acg ctt cgg gat tac atc gag cgg gtg att ccg ttg tct cct	403
Leu Val Thr Leu Arg Asp Tyr Ile Glu Arg Val Ile Pro Leu Ser Pro	
90 95 100	
gga aat tac aat tcc acc acc ttg aag gaa acc gcg aag gtg aag gtc	451
Gly Asn Tyr Asn Ser Thr Thr Leu Lys Glu Thr Ala Lys Val Lys Val	
105 110 115	
gcg gag ttg gag gaa ctc gcg gag cgc gat ggt gta gat ttg tcg cac	499
Ala Glu Leu Glu Glu Leu Ala Glu Arg Asp Gly Val Asp Leu Ser His	
120 125 130	
tct ccg acg tgg aag cgc cag ttg ggt tcg ctt ggt gga ggt aat cac	547
Ser Pro Thr Trp Lys Arg Gln Leu Gly Ser Leu Gly Gly Gly Asn His	
135 140 145	
ttc att gag ttg tgt ctt gat gag ttg gat cgg gtg tgg atg ttt ttg	595
Phe Ile Glu Leu Cys Leu Asp Glu Leu Asp Arg Val Trp Met Phe Leu	
150 155 160 165	
cac tct ggt tcc cgc ggt gtg ggt aac aag att gcc cag aag cac atc	643
His Ser Gly Ser Arg Gly Val Gly Asn Lys Ile Ala Gln Lys His Ile	
170 175 180	
aag atc gcg cag gcc gag tgt aag aat gag gag ctt ccc gat aag gat	691
Lys Ile Ala Gln Ala Glu Cys Lys Asn Glu Glu Leu Pro Asp Lys Asp	
185 190 195	
ctt gcg tac ttg acc gag ggg act gag gag ttt gag tct tac atc aag	739
Leu Ala Tyr Leu Thr Glu Gly Thr Glu Glu Phe Glu Ser Tyr Ile Lys	
200 205 210	
gaa ctg aat tgg gcg cag cgt ttt gcg ttc ctc aac agg gaa gaa atg	787
Glu Leu Asn Trp Ala Gln Arg Phe Ala Phe Leu Asn Arg Glu Glu Met	
215 220 225	
atg gac aga ttc gca cgg gag ctg ggt ttt ttc gtc gac aag cag ctt	835
Met Asp Arg Phe Ala Arg Glu Leu Gly Phe Phe Val Asp Lys Gln Leu	
230 235 240 245	
gaa gag gtc gag cgc atc aac tgc cac cat aac tac acg gtc cag gag	883
Glu Glu Val Glu Arg Ile Asn Cys His His Asn Tyr Thr Val Gln Glu	
250 255 260	
gag cac tac ggc gag acc att tgg ctc acc cgt aag ggt gcc gtg ttg	931
Glu His Tyr Gly Glu Thr Ile Trp Leu Thr Arg Lys Gly Ala Val Leu	
265 270 275	
gcg gac gaa ggc acg ccg gcg ttg att ccg ggg tcg atg ggc acc gcg	979
Ala Asp Glu Gly Thr Pro Ala Leu Ile Pro Gly Ser Met Gly Thr Ala	
280 285 290	
tcg tac gtg ggc agt ggc aag ggc aac gcc gag gca ctg cgg tcg gcg	1027

Ser Tyr Val Gly Ser Gly Lys Gly Asn Ala Glu Ala Leu Arg Ser Ala  
 295 300 305  
 ccg cat ggg gcg ggc cgg agg atg tcg cgc aac cag gct aaa aag cgc 1075  
 Pro His Gly Ala Gly Arg Arg Met Ser Arg Asn Gln Ala Lys Lys Arg 325  
 310 315 320  
 ttc tcg acg gcc gac ctg gat tct cgg atg gcg ggc atc gtc tac cgg 1123  
 Phe Ser Thr Ala Asp Leu Asp Ser Arg Met Ala Gly Ile Val Tyr Arg 340  
 330 335  
 ccc ggc aag gag tgg atc gat gaa att ccc gac gct tac aaa gac atc 1171  
 Pro Gly Lys Glu Trp Ile Asp Glu Ile Pro Asp Ala Tyr Lys Asp Ile 355  
 345 350  
 gat cag gtg atg gcc gat gct gcc gat ttg gtg aca att cgc cat aaa 1219  
 Asp Gln Val Met Ala Asp Ala Ala Asp Leu Val Thr Ile Arg His Lys 370  
 360 365  
 ttg cgc cag atc gtc aac gtg aaa ggc acc taaagcgcac tacggtaaag tgc 1272  
 Leu Arg Gln Ile Val Asn Val Lys Gly Thr 380  
 375 380

<210> 452

<211> 383

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 452

Met Asn His Val Val Asn Phe Ala Ser His Leu Glu Asp Ala Ala Leu  
 1 5 10 15  
 Lys Gln Ala Glu Ala Thr Ala Thr Met Pro Phe Ile Tyr Pro His Val  
 20 25 30  
 Ala Leu Met Pro Asp Ala His Phe Gly Leu Gly Ser Ser Val Gly Thr  
 35 40 45  
 Val Phe Gly Thr Lys Gly Ala Ile Ile Pro Ala Ala Val Gly Val Asp  
 50 55 60  
 Ile Gly Cys Gly Met Ile Gly Val Cys Thr Asn Tyr Thr Ala Ser Asp  
 65 70 75 80  
 Leu Glu Gly Arg Asp Leu Val Thr Leu Arg Asp Tyr Ile Glu Arg Val  
 85 90 95  
 Ile Pro Leu Ser Pro Gly Asn Tyr Asn Ser Thr Thr Leu Lys Glu Thr  
 100 105 110  
 Ala Lys Val Lys Val Ala Glu Leu Glu Glu Leu Ala Glu Arg Asp Gly  
 115 120 125  
 Val Asp Leu Ser His Ser Pro Thr Trp Lys Arg Gln Leu Gly Ser Leu  
 130 135 140  
 Gly Gly Gly Asn His Phe Ile Glu Leu Cys Leu Asp Glu Leu Asp Arg  
 145 150 155 160  
 Val Trp Met Phe Leu His Ser Gly Ser Arg Gly Val Gly Asn Lys Ile

165						170						175					
Ala	Gln	Lys	His	Ile	Lys	Ile	Ala	Gln	Ala	Glu	Cys	Lys	Asn	Glu	Glu		
			180					185					190				
Leu	Pro	Asp	Lys	Asp	Leu	Ala	Tyr	Leu	Thr	Glu	Gly	Thr	Glu	Glu	Phe		
		195					200					205					
Glu	Ser	Tyr	Ile	Lys	Glu	Leu	Asn	Trp	Ala	Gln	Arg	Phe	Ala	Phe	Leu		
	210						215				220						
Asn	Arg	Glu	Glu	Met	Met	Asp	Arg	Phe	Ala	Arg	Glu	Leu	Gly	Phe	Phe		
225				230						235					240		
Val	Asp	Lys	Gln	Leu	Glu	Glu	Val	Glu	Arg	Ile	Asn	Cys	His	His	Asn		
			245					250						255			
Tyr	Thr	Val	Gln	Glu	Glu	His	Tyr	Gly	Glu	Thr	Ile	Trp	Leu	Thr	Arg		
			260					265					270				
Lys	Gly	Ala	Val	Leu	Ala	Asp	Glu	Gly	Thr	Pro	Ala	Leu	Ile	Pro	Gly		
		275					280					285					
Ser	Met	Gly	Thr	Ala	Ser	Tyr	Val	Gly	Ser	Gly	Lys	Gly	Asn	Ala	Glu		
	290						295				300						
Ala	Leu	Arg	Ser	Ala	Pro	His	Gly	Ala	Gly	Arg	Arg	Met	Ser	Arg	Asn		
305					310					315					320		
Gln	Ala	Lys	Lys	Arg	Phe	Ser	Thr	Ala	Asp	Leu	Asp	Ser	Arg	Met	Ala		
			325						330					335			
Gly	Ile	Val	Tyr	Arg	Pro	Gly	Lys	Glu	Trp	Ile	Asp	Glu	Ile	Pro	Asp		
		340					345					350					
Ala	Tyr	Lys	Asp	Ile	Asp	Gln	Val	Met	Ala	Asp	Ala	Ala	Asp	Leu	Val		
		355					360					365					
Thr	Ile	Arg	His	Lys	Leu	Arg	Gln	Ile	Val	Asn	Val	Lys	Gly	Thr			
	370						375				380						

&lt;210&gt; 453

&lt;211&gt; 1137

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1114)

&lt;223&gt; RXS00671

&lt;400&gt; 453

gccccgggtg cacaggaatc ttctgatttt ccaaacatcc ttcattggttt tagaaacctt 60

taccgacgtc	aaatagcggc	cgctactcaa	ggagagttca	atg	ctc	att	tca	cag	115
				Met	Leu	Ile	Ser	Gln	
				1				5	

cgc	cca	acc	atc	acc	gag	gaa	ttt	gtt	aat	aac	gca	cgt	tcc	cgg	ttt	163
Arg	Pro	Thr	Ile	Thr	Glu	Glu	Phe	Val	Asn	Asn	Ala	Arg	Ser	Arg	Phe	

				10					15					20		
gtc	atc	gag	cca	ctg	gag	cca	ggt	ttt	ggc	tac	acc	ctc	ggt	aac	tcc	211
Val	Ile	Glu	Pro	Leu	Glu	Pro	Gly	Phe	Gly	Tyr	Thr	Leu	Gly	Asn	Ser	
				25					30					35		
ctg	cgc	cgt	acc	ctg	ctg	tcc	tcc	att	cct	gga	gca	gca	gta	acc	agc	259
Leu	Arg	Arg	Thr	Leu	Leu	Ser	Ser	Ile	Pro	Gly	Ala	Ala	Val	Thr	Ser	
				40					45					50		
gtc	aag	att	gac	ggt	gta	ctc	cac	gag	ttc	acc	acc	atc	agc	ggt	gtt	307
Val	Lys	Ile	Asp	Gly	Val	Leu	His	Glu	Phe	Thr	Thr	Ile	Ser	Gly	Val	
				55					60					65		
aag	gaa	gat	gtc	tct	gac	atc	atc	ttg	aac	atc	aag	gga	ttg	gtt	ttg	355
Lys	Glu	Asp	Val	Ser	Asp	Ile	Ile	Leu	Asn	Ile	Lys	Gly	Leu	Val	Leu	
				70					75					80		
tct	tct	gat	tcc	gat	gag	cca	gtt	gtt	atg	cag	ctg	gtc	aag	gaa	ggc	403
Ser	Ser	Asp	Ser	Asp	Glu	Pro	Val	Val	Met	Gln	Leu	Val	Lys	Glu	Gly	
				90					95					100		
cca	gga	gtt	gta	act	gca	ggt	gac	att	cag	cca	cca	gca	ggc	gtg	gag	451
Pro	Gly	Val	Val	Thr	Ala	Gly	Asp	Ile	Gln	Pro	Pro	Ala	Gly	Val	Glu	
				105					110					115		
atc	cac	aac	ccg	gat	ctg	cac	att	gca	acc	ctg	aac	gag	acc	gcc	aag	499
Ile	His	Asn	Pro	Asp	Leu	His	Ile	Ala	Thr	Leu	Asn	Glu	Thr	Ala	Lys	
				120					125					130		
att	gag	atc	gag	ctc	atc	gtc	gag	cgt	gga	cgt	ggc	tac	gtt	ccc	gca	547
Ile	Glu	Ile	Glu	Leu	Ile	Val	Glu	Arg	Gly	Arg	Gly	Tyr	Val	Pro	Ala	
				135					140					145		
act	gtt	act	gca	acc	ggt	gga	gag	atc	ggc	cgc	att	ccg	gtc	gat	cag	595
Thr	Val	Thr	Ala	Thr	Gly	Gly	Glu	Ile	Gly	Arg	Ile	Pro	Val	Asp	Gln	
				150					155					160		
atc	tac	tcc	cca	gta	ctg	aag	gtc	agc	tac	aag	gtt	gaa	gct	act	cgt	643
Ile	Tyr	Ser	Pro	Val	Leu	Lys	Val	Ser	Tyr	Lys	Val	Glu	Ala	Thr	Arg	
				170					175					180		
gtt	gag	cag	cgc	acc	gac	ttt	gac	aag	ctg	gtc	atc	gac	gtt	gag	acc	691
Val	Glu	Gln	Arg	Thr	Asp	Phe	Asp	Lys	Leu	Val	Ile	Asp	Val	Glu	Thr	
				185					190					195		
aag	aac	tct	att	acc	gca	cgt	gac	gcc	ctg	gcg	tcg	gca	ggt	aag	acc	739
Lys	Asn	Ser	Ile	Thr	Ala	Arg	Asp	Ala	Leu	Ala	Ser	Ala	Gly	Lys	Thr	
				200					205					210		
ctg	gtt	gag	ctg	ttc	ggc	ctc	gca	cgc	gag	ctg	aac	atc	gca	gcc	gag	787
Leu	Val	Glu	Leu	Phe	Gly	Leu	Ala	Arg	Glu	Leu	Asn	Ile	Ala	Ala	Glu	
				215					220					225		
ggc	atc	gag	atc	gga	cca	tct	cct	cag	gag	acc	gag	tac	atc	gct	gcc	835
Gly	Ile	Glu	Ile	Gly	Pro	Ser	Pro	Gln	Glu	Thr	Glu	Tyr	Ile	Ala	Ala	
				230					235					240		
tac	agc	atg	cca	atc	gag	gat	ctg	gac	ttc	tct	gtc	cgt	tcc	tac	aac	883
Tyr	Ser	Met	Pro	Ile	Glu	Asp	Leu	Asp	Phe	Ser	Val	Arg	Ser	Tyr	Asn	
				250					255					260		

tgc ctc aag cgc gaa gac atc cac acc gtg ggt gaa ctc gca gag cgc 931  
 Cys Leu Lys Arg Glu Asp Ile His Thr Val Gly Glu Leu Ala Glu Arg  
 265 270 275  
  
 gct gag tcc gat ttg ctg gat atc cgc aac ttc gga cag aag tcg atc 979  
 Ala Glu Ser Asp Leu Leu Asp Ile Arg Asn Phe Gly Gln Lys Ser Ile  
 280 285 290  
  
 aac gag gta aag atc aag ctt gct ggc ctg ggt ctg acc ctg aag gat 1027  
 Asn Glu Val Lys Ile Lys Leu Ala Gly Leu Gly Leu Thr Leu Lys Asp  
 295 300 305  
  
 gct cct gaa gac ttc gat cct tca act ctt gaa ggt tat gac gcc gaa 1075  
 Ala Pro Glu Asp Phe Asp Pro Ser Thr Leu Glu Gly Tyr Asp Ala Glu  
 310 315 320 325  
  
 act ggt ggc tac atc gat gtc gag gcg gaa gat tcc gag taagtcgcat 1124  
 Thr Gly Gly Tyr Ile Asp Val Glu Ala Glu Asp Ser Glu  
 330 335  
  
 ggtccaattc atg 1137

<210> 454  
 <211> 338  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 454  
 Met Leu Ile Ser Gln Arg Pro Thr Ile Thr Glu Glu Phe Val Asn Asn  
 1 5 10 15  
  
 Ala Arg Ser Arg Phe Val Ile Glu Pro Leu Glu Pro Gly Phe Gly Tyr  
 20 25 30  
  
 Thr Leu Gly Asn Ser Leu Arg Arg Thr Leu Leu Ser Ser Ile Pro Gly  
 35 40 45  
  
 Ala Ala Val Thr Ser Val Lys Ile Asp Gly Val Leu His Glu Phe Thr  
 50 55 60  
  
 Thr Ile Ser Gly Val Lys Glu Asp Val Ser Asp Ile Ile Leu Asn Ile  
 65 70 75 80  
  
 Lys Gly Leu Val Leu Ser Ser Asp Ser Asp Glu Pro Val Val Met Gln  
 85 90 95  
  
 Leu Val Lys Glu Gly Pro Gly Val Val Thr Ala Gly Asp Ile Gln Pro  
 100 105 110  
  
 Pro Ala Gly Val Glu Ile His Asn Pro Asp Leu His Ile Ala Thr Leu  
 115 120 125  
  
 Asn Glu Thr Ala Lys Ile Glu Ile Glu Leu Ile Val Glu Arg Gly Arg  
 130 135 140  
  
 Gly Tyr Val Pro Ala Thr Val Thr Ala Thr Gly Gly Glu Ile Gly Arg  
 145 150 155 160  
  
 Ile Pro Val Asp Gln Ile Tyr Ser Pro Val Leu Lys Val Ser Tyr Lys

165. 170 175  
 Val Glu Ala Thr Arg Val Glu Gln Arg Thr Asp Phe Asp Lys Leu Val  
 180 185 190  
 Ile Asp Val Glu Thr Lys Asn Ser Ile Thr Ala Arg Asp Ala Leu Ala  
 195 200 205  
 Ser Ala Gly Lys Thr Leu Val Glu Leu Phe Gly Leu Ala Arg Glu Leu  
 210 215 220  
 Asn Ile Ala Ala Glu Gly Ile Glu Ile Gly Pro Ser Pro Gln Glu Thr  
 225 230 235 240  
 Glu Tyr Ile Ala Ala Tyr Ser Met Pro Ile Glu Asp Leu Asp Phe Ser  
 245 250 255  
 Val Arg Ser Tyr Asn Cys Leu Lys Arg Glu Asp Ile His Thr Val Gly  
 260 265 270  
 Glu Leu Ala Glu Arg Ala Glu Ser Asp Leu Leu Asp Ile Arg Asn Phe  
 275 280 285  
 Gly Gln Lys Ser Ile Asn Glu Val Lys Ile Lys Leu Ala Gly Leu Gly  
 290 295 300  
 Leu Thr Leu Lys Asp Ala Pro Glu Asp Phe Asp Pro Ser Thr Leu Glu  
 305 310 315 320  
 Gly Tyr Asp Ala Glu Thr Gly Gly Tyr Ile Asp Val Glu Ala Glu Asp  
 325 330 335  
 Ser Glu

<210> 455  
 <211> 1077  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1054)  
 <223> RXS02760

<400> 455  
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 ggggttttagg gtcgatagat aggttgggag aacacgcatt atg agc gat gag aac 115  
 Met Ser Asp Glu Asn  
 1 5  
 att aac gag ttt gag cag gac gag gat ctg aac ttc ggc gcg agc ttt 163  
 Ile Asn Glu Phe Glu Gln Asp Glu Asp Leu Asn Phe Gly Ala Ser Phe  
 10 15 20  
 agt gat gaa ttc gca gat gac gat ttc gat gca gaa gca gac gta gaa 211  
 Ser Asp Glu Phe Ala Asp Asp Asp Phe Asp Ala Glu Ala Asp Val Glu  
 25 30 35

gca gat gct gct gca gag gcc tct gcc ctg gaa gct gag cag gat ctg	259
Ala Asp Ala Ala Ala Glu Ala Ser Ala Leu Glu Ala Glu Gln Asp Leu	
40 45 50	
gaa gaa gag acc cta gat gct cca gaa gaa gcc gca gaa gaa gct cct	307
Glu Glu Glu Thr Leu Asp Ala Pro Glu Glu Ala Ala Glu Glu Ala Pro	
55 60 65	
gct gct gca gag tcc gaa gct cca gta gaa gag gac gaa gag gct gac	355
Ala Ala Ala Glu Ser Glu Ala Pro Val Glu Glu Asp Glu Glu Ala Asp	
70 75 80 85	
agc ctt gct cag gcg gct gct gca ctt ggt gac acc gat gag cag gac	403
Ser Leu Ala Gln Ala Ala Ala Leu Gly Asp Thr Asp Glu Gln Asp	
90 95 100	
gcg gat gca gag tac aag gct cgt ctg cgt aag ttc act cgt gag ctg	451
Ala Asp Ala Glu Tyr Lys Ala Arg Leu Arg Lys Phe Thr Arg Glu Leu	
105 110 115	
aag aag cag cct ggt gtt tgg tac atc att cag tgc tac tcc ggc tac	499
Lys Lys Gln Pro Gly Val Trp Tyr Ile Ile Gln Cys Tyr Ser Gly Tyr	
120 125 130	
gag aac aag gtg aag gcg aac ctt gac atg cgt gct cag acc ctt gag	547
Glu Asn Lys Val Lys Ala Asn Leu Asp Met Arg Ala Gln Thr Leu Glu	
135 140 145	
gtt gag gat gac atc ttt gag gtt gtt gtt cct atc gag cag gtc act	595
Val Glu Asp Asp Ile Phe Glu Val Val Val Pro Ile Glu Gln Val Thr	
150 155 160 165	
gag atc cgt gat ggt aag cgc aag ctg gtt aag cgt aag ttg ctg ccg	643
Glu Ile Arg Asp Gly Lys Arg Lys Leu Val Lys Arg Lys Leu Leu Pro	
170 175 180	
ggc tac gtt ttg gtc cgc atg gac atg aat gac cgc gtg tgg tct gtt	691
Gly Tyr Val Leu Val Arg Met Asp Met Asn Asp Arg Val Trp Ser Val	
185 190 195	
gtt cgc gat aca cct ggt gtg acc agc ttt gtg ggt aac gag ggc aat	739
Val Arg Asp Thr Pro Gly Val Thr Ser Phe Val Gly Asn Glu Gly Asn	
200 205 210	
gca act cct gtg aag cac cgc gat gtt gcg aag ttc ttg atg cct cag	787
Ala Thr Pro Val Lys His Arg Asp Val Ala Lys Phe Leu Met Pro Gln	
215 220 225	
gag cag gct gtt gtc acc ggt gag gct gct gct gcg gct gcc gag ggt	835
Glu Gln Ala Val Val Thr Gly Glu Ala Ala Ala Ala Ala Ala Glu Gly	
230 235 240 245	
gag cag gtt gtg gct atg cct acc gat acc aag aag cct cag gtt gct	883
Glu Gln Val Val Ala Met Pro Thr Asp Thr Lys Lys Pro Gln Val Ala	
250 255 260	
gtg gac ttc act gtt ggt gag gct gtg acc att ctg act ggt gct ttc	931
Val Asp Phe Thr Val Gly Glu Ala Val Thr Ile Leu Thr Gly Ala Phe	
265 270 275	
gct tct gtt tct gca acg att tct tct atc gat cct gag ctg cag aag	979

Ala Ser Val Ser Ala Thr Ile Ser Ser Ile Asp Pro Glu Leu Gln Lys  
 280 285 290

ctg gaa gtt ttg gtg tcc atc ttt ggt cgt gaa act cct gtt gat ctc 1027  
 Leu Glu Val Leu Val Ser Ile Phe Gly Arg Glu Thr Pro Val Asp Leu  
 295 300 305

agc ttc gac cag gtt gag aag gtt agc tagtagctaa actgcaccac tta 1077  
 Ser Phe Asp Gln Val Glu Lys Val Ser  
 310 315

&lt;210&gt; 456

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 456

Met Ser Asp Glu Asn Ile Asn Glu Phe Glu Gln Asp Glu Asp Leu Asn  
 1 5 10 15

Phe Gly Ala Ser Phe Ser Asp Glu Phe Ala Asp Asp Asp Phe Asp Ala  
 20 25 30

Glu Ala Asp Val Glu Ala Asp Ala Ala Ala Glu Ala Ser Ala Leu Glu  
 35 40 45

Ala Glu Gln Asp Leu Glu Glu Glu Thr Leu Asp Ala Pro Glu Glu Ala  
 50 55 60

Ala Glu Glu Ala Pro Ala Ala Ala Glu Ser Glu Ala Pro Val Glu Glu  
 65 70 75 80

Asp Glu Glu Ala Asp Ser Leu Ala Gln Ala Ala Ala Ala Leu Gly Asp  
 85 90 95

Thr Asp Glu Gln Asp Ala Asp Ala Glu Tyr Lys Ala Arg Leu Arg Lys  
 100 105 110

Phe Thr Arg Glu Leu Lys Lys Gln Pro Gly Val Trp Tyr Ile Ile Gln  
 115 120 125

Cys Tyr Ser Gly Tyr Glu Asn Lys Val Lys Ala Asn Leu Asp Met Arg  
 130 135 140

Ala Gln Thr Leu Glu Val Glu Asp Asp Ile Phe Glu Val Val Val Pro  
 145 150 155 160

Ile Glu Gln Val Thr Glu Ile Arg Asp Gly Lys Arg Lys Leu Val Lys  
 165 170 175

Arg Lys Leu Leu Pro Gly Tyr Val Leu Val Arg Met Asp Met Asn Asp  
 180 185 190

Arg Val Trp Ser Val Val Arg Asp Thr Pro Gly Val Thr Ser Phe Val  
 195 200 205

Gly Asn Glu Gly Asn Ala Thr Pro Val Lys His Arg Asp Val Ala Lys  
 210 215 220

Phe Leu Met Pro Gln Glu Gln Ala Val Val Thr Gly Glu Ala Ala Ala

225		230		235		240
Ala Ala Ala Glu Gly Glu Gln Val Val Ala Met Pro Thr Asp Thr Lys						
	245			250		255
Lys Pro Gln Val Ala Val Asp Phe Thr Val Gly Glu Ala Val Thr Ile						
	260			265		270
Leu Thr Gly Ala Phe Ala Ser Val Ser Ala Thr Ile Ser Ser Ile Asp						
	275			280		285
Pro Glu Leu Gln Lys Leu Glu Val Leu Val Ser Ile Phe Gly Arg Glu						
	290			295		300
Thr Pro Val Asp Leu Ser Phe Asp Gln Val Glu Lys Val Ser						
305		310		315		

&lt;210&gt; 457

&lt;211&gt; 662

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(648)

&lt;223&gt; RXS02830

&lt;400&gt; 457

cgg cgg ctg gaa gac agc ctt ggc gtg tcg ctg ttt gaa cgg gcc ggg	48
Arg Arg Leu Glu Asp Ser Leu Gly Val Ser Leu Phe Glu Arg Ala Gly	
1 5 10 15	
cgc ggg ctg gcg ctg aca ggg gcg ggc gat cag ctt ttg tcg cag gcg	96
Arg Gly Leu Ala Leu Thr Gly Ala Gly Asp Gln Leu Leu Ser Gln Ala	
20 25 30	
cgc cgc ctg atc gcc ctg aac gac gag gta tac gcc cgc ttg aac gcc	144
Arg Arg Leu Ile Ala Leu Asn Asp Glu Val Tyr Ala Arg Leu Asn Ala	
35 40 45	
ggt gcc tac gag ggc gag gtg acg ctg ggc gtg cct caa gac gtg atc	192
Gly Ala Tyr Glu Gly Glu Val Thr Leu Gly Val Pro Gln Asp Val Ile	
50 55 60	
tac ccc gtc atc ccg cgc gtc ttg cag caa ttc gcc cgc gat ttt ccc	240
Tyr Pro Val Ile Pro Arg Val Leu Gln Gln Phe Ala Arg Asp Phe Pro	
65 70 75 80	
cgc gtg caa att cac ctg atc tcg aac ttc acg ctg atg ctg aaa gaa	288
Arg Val Gln Ile His Leu Ile Ser Asn Phe Thr Leu Met Leu Lys Glu	
85 90 95	
cag ttc cgc cgc ggc gaa atc gac gtg atg ctg acg acc gag gac gag	336
Gln Phe Arg Arg Gly Glu Ile Asp Val Met Leu Thr Thr Glu Asp Glu	
100 105 110	
ctg ggc gag ggc ggc gag acg ctg gcc cag cgc gag ctg atc tgg gtc	384
Leu Gly Glu Gly Gly Glu Thr Leu Ala Gln Arg Glu Leu Ile Trp Val	
115 120 125	

ggc gca ccg ggc ggg tgc gcg tgg acc cgc agg ccg ctg ccc ttg gcg 432  
 Gly Ala Pro Gly Gly Ser Ala Trp Thr Arg Arg Pro Leu Pro Leu Ala  
 130 135 140

ttt gaa cgc gcc tgc att ttc cgg tct ttc gtg cag cgc cgc ttg gat 480  
 Phe Glu Arg Ala Cys Ile Phe Arg Ser Phe Val Gln Arg Arg Leu Asp  
 145 150 155 160

gcc aac agc atc gat tgg cag atg gtg gtc agc agc gaa tcc aca cgg 528  
 Ala Asn Ser Ile Asp Trp Gln Met Val Val Ser Ser Glu Ser Thr Arg  
 165 170 175

aca att gaa gcg acc gtc agt gcc gat ctg gcg gtg cat acc tat atc 576  
 Thr Ile Glu Ala Thr Val Ser Ala Asp Leu Ala Val His Thr Tyr Ile  
 180 185 190

gag ggg gcc gag ccg gcg cac ctc gag cgt att gcc aca acg gcg ccc 624  
 Glu Gly Ala Glu Pro Ala His Leu Glu Arg Ile Ala Thr Thr Ala Pro  
 195 200 205

tgc cgg aac tac gtc ttt caa cat taacctctat tatg 662  
 Cys Arg Asn Tyr Val Phe Gln His  
 210 215

&lt;210&gt; 458

&lt;211&gt; 216

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 458

Arg Arg Leu Glu Asp Ser Leu Gly Val Ser Leu Phe Glu Arg Ala Gly  
 1 5 10 15

Arg Gly Leu Ala Leu Thr Gly Ala Gly Asp Gln Leu Leu Ser Gln Ala  
 20 25 30

Arg Arg Leu Ile Ala Leu Asn Asp Glu Val Tyr Ala Arg Leu Asn Ala  
 35 40 45

Gly Ala Tyr Glu Gly Glu Val Thr Leu Gly Val Pro Gln Asp Val Ile  
 50 55 60

Tyr Pro Val Ile Pro Arg Val Leu Gln Gln Phe Ala Arg Asp Phe Pro  
 65 70 75 80

Arg Val Gln Ile His Leu Ile Ser Asn Phe Thr Leu Met Leu Lys Glu  
 85 90 95

Gln Phe Arg Arg Gly Glu Ile Asp Val Met Leu Thr Thr Glu Asp Glu  
 100 105 110

Leu Gly Glu Gly Gly Glu Thr Leu Ala Gln Arg Glu Leu Ile Trp Val  
 115 120 125

Gly Ala Pro Gly Gly Ser Ala Trp Thr Arg Arg Pro Leu Pro Leu Ala  
 130 135 140

Phe Glu Arg Ala Cys Ile Phe Arg Ser Phe Val Gln Arg Arg Leu Asp  
 145 150 155 160

Ala Asn Ser Ile Asp Trp Gln Met Val Val Ser Ser Glu Ser Thr Arg  
                                   165                                  170                                  175

Thr Ile Glu Ala Thr Val Ser Ala Asp Leu Ala Val His Thr Tyr Ile  
                                   180                                  185                                  190

Glu Gly Ala Glu Pro Ala His Leu Glu Arg Ile Ala Thr Thr Ala Pro  
                                   195                                  200                                  205

Cys Arg Asn Tyr Val Phe Gln His  
                                   210                                  215

<210> 459

<211> 1123

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1093)

<223> RXS03207

<400> 459

ccccaatgtg ggggtgttaa gaactccata aaagcgcttg ggaacttttt gtggaagcag 60

tccgttgaac ctcttgaacc gcgaatttag gaggccagtt atg aca gca ccg tcc 115  
   Met Thr Ala Pro Ser  
   1  5

acg cag gat ctc gca acg act gaa cgt gag gta gat ccc ggc agc aga 163  
   Thr Gln Asp Leu Ala Thr Thr Glu Arg Glu Val Asp Pro Gly Ser Arg  
                                   10                                  15                                  20

agg ggc caa acc aac gac aat ccc tcg cag gac ctt gtt cgc gtt tac 211  
   Arg Gly Gln Thr Asn Asp Asn Pro Ser Gln Asp Leu Val Arg Val Tyr  
                                   25                                  30                                  35

ctc aac ggc atc ggc aaa act gcc ttg ctt acc gcg gag gat gaa gtt 259  
   Leu Asn Gly Ile Gly Lys Thr Ala Leu Leu Thr Ala Glu Asp Glu Val  
                                   40                                  45                                  50

gag ctc gca cag acc att gag gtt ggc ctt tat gca gag cac ctt ctg 307  
   Glu Leu Ala Gln Thr Ile Glu Val Gly Leu Tyr Ala Glu His Leu Leu  
                                   55                                  60                                  65

aaa aac tct gaa gag cca ctc acc cgc gcc atg aag cgc gat cta aag 355  
   Lys Asn Ser Glu Glu Pro Leu Thr Arg Ala Met Lys Arg Asp Leu Lys  
                                   70                                  75                                  80                                  85

gtt ctt gcc aag gac ggc aag aag gct cgt tcc cac ctc ctc gag gca 403  
   Val Leu Ala Lys Asp Gly Lys Lys Ala Arg Ser His Leu Leu Glu Ala  
                                   90                                  95                                  100

aac ctg cgc ctg gtg gtg tcc ctt gct aag cgc tac acc ggc cgc ggc 451  
   Asn Leu Arg Leu Val Val Ser Leu Ala Lys Arg Tyr Thr Gly Arg Gly  
                                   105                                  110                                  115

atg cca ctg ctg gat ctt atc cag gag ggc aac ctc gga ctg atc cgc 499  
   Met Pro Leu Leu Asp Leu Ile Gln Glu Gly Asn Leu Gly Leu Ile Arg  
                                   120                                  125                                  130

gcg atg gaa aag ttt gat tac tcc aag ggc ttt aag ttc tcc acc tac 547  
Ala Met Glu Lys Phe Asp Tyr Ser Lys Gly Phe Lys Phe Ser Thr Tyr  
135 140 145

gca acc tgg tgg atc cgc cag gca atc acc cgc ggc atg gca gat cag 595  
Ala Thr Trp Trp Ile Arg Gln Ala Ile Thr Arg Gly Met Ala Asp Gln  
150 155 160 165

tcc cgc acc atc cgc ctc cca gtc cac ctt gtg gag cag gtg aac aag 643  
Ser Arg Thr Ile Arg Leu Pro Val His Leu Val Glu Gln Val Asn Lys  
170 175 180

ctt tcc cgc atc aag cgc gag ttg tac cag cac ttg ggc cgt gaa gcc 691  
Leu Ser Arg Ile Lys Arg Glu Leu Tyr Gln His Leu Gly Arg Glu Ala  
185 190 195

acc aat gag gaa ctc gca gaa gag tcc ggc att gaa gag tcc aag att 739  
Thr Asn Glu Glu Leu Ala Glu Glu Ser Gly Ile Glu Glu Ser Lys Ile  
200 205 210

gaa atg ctg ctt cgt cag tct cgc gat cca gtg agc ttg gac atg cca 787  
Glu Met Leu Leu Arg Gln Ser Arg Asp Pro Val Ser Leu Asp Met Pro  
215 220 225

gtc ggc gcc gat gaa gaa gct cct ttg ggt gac ttc att gag gat tct 835  
Val Gly Ala Asp Glu Glu Ala Pro Leu Gly Asp Phe Ile Glu Asp Ser  
230 235 240 245

gag gcc acc gat gca gaa tcc gca gtg gtt gct tcc atg cgc cac tcc 883  
Glu Ala Thr Asp Ala Glu Ser Ala Val Val Ala Ser Met Arg His Ser  
250 255 260

gat atc cgc gcg gtc ctt aac act ctc gag cca cgc gag cag gat gtc 931  
Asp Ile Arg Ala Val Leu Asn Thr Leu Glu Pro Arg Glu Gln Asp Val  
265 270 275

atc cgt ttg cgc tac ggc ctc gat gac ggt gtg cca cgc acc ctt gat 979  
Ile Arg Leu Arg Tyr Gly Leu Asp Asp Gly Val Pro Arg Thr Leu Asp  
280 285 290

cag att ggt cgc cgc ttc gga ctg tcc cgt gag cgc gtc cgc cag ata 1027  
Gln Ile Gly Arg Arg Phe Gly Leu Ser Arg Glu Arg Val Arg Gln Ile  
295 300 305

gag cgt gaa gtc atg agt aag ctc cgc gat gga gag cgc gca tca cgt 1075  
Glu Arg Glu Val Met Ser Lys Leu Arg Asp Gly Glu Arg Ala Ser Arg  
310 315 320 325

ctt cgt gag tac gcc cag taaaagcgtg aactaacaat cgaagcgtcg 1123  
Leu Arg Glu Tyr Ala Gln  
330

&lt;210&gt; 460

&lt;211&gt; 331

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 460

Met Thr Ala Pro Ser Thr Gln Asp Leu Ala Thr Thr Glu Arg Glu Val

1	5	10	15
Asp Pro Gly Ser Arg Arg Gly Gln Thr Asn Asp Asn Pro Ser Gln Asp	20	25	30
Leu Val Arg Val Tyr Leu Asn Gly Ile Gly Lys Thr Ala Leu Leu Thr	35	40	45
Ala Glu Asp Glu Val Glu Leu Ala Gln Thr Ile Glu Val Gly Leu Tyr	50	55	60
Ala Glu His Leu Leu Lys Asn Ser Glu Glu Pro Leu Thr Arg Ala Met	65	70	75
Lys Arg Asp Leu Lys Val Leu Ala Lys Asp Gly Lys Lys Ala Arg Ser	85	90	95
His Leu Leu Glu Ala Asn Leu Arg Leu Val Val Ser Leu Ala Lys Arg	100	105	110
Tyr Thr Gly Arg Gly Met Pro Leu Leu Asp Leu Ile Gln Glu Gly Asn	115	120	125
Leu Gly Leu Ile Arg Ala Met Glu Lys Phe Asp Tyr Ser Lys Gly Phe	130	135	140
Lys Phe Ser Thr Tyr Ala Thr Trp Trp Ile Arg Gln Ala Ile Thr Arg	145	150	155
Gly Met Ala Asp Gln Ser Arg Thr Ile Arg Leu Pro Val His Leu Val	165	170	175
Glu Gln Val Asn Lys Leu Ser Arg Ile Lys Arg Glu Leu Tyr Gln His	180	185	190
Leu Gly Arg Glu Ala Thr Asn Glu Glu Leu Ala Glu Glu Ser Gly Ile	195	200	205
Glu Glu Ser Lys Ile Glu Met Leu Leu Arg Gln Ser Arg Asp Pro Val	210	215	220
Ser Leu Asp Met Pro Val Gly Ala Asp Glu Glu Ala Pro Leu Gly Asp	225	230	235
Phe Ile Glu Asp Ser Glu Ala Thr Asp Ala Glu Ser Ala Val Val Ala	245	250	255
Ser Met Arg His Ser Asp Ile Arg Ala Val Leu Asn Thr Leu Glu Pro	260	265	270
Arg Glu Gln Asp Val Ile Arg Leu Arg Tyr Gly Leu Asp Asp Gly Val	275	280	285
Pro Arg Thr Leu Asp Gln Ile Gly Arg Arg Phe Gly Leu Ser Arg Glu	290	295	300
Arg Val Arg Gln Ile Glu Arg Glu Val Met Ser Lys Leu Arg Asp Gly	305	310	315
Glu Arg Ala Ser Arg Leu Arg Glu Tyr Ala Gln	325	330	



170 175 180 690

ggt ccg gtg cgc aag ggc aag aaa taatcacgaa taggggtttaa gga  
 Gly Pro Val Arg Lys Gly Lys Lys  
 185

<210> 462  
 <211> 189  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 462

Val	Val	Arg	Tyr	Val	Lys	Phe	Ser	Arg	Thr	Ala	Asn	Arg	Gly	Val	His
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Ile	Ser	Ala	Glu	Ala	Arg	Ile	Asn	Glu	Arg	Ile	Arg	Val	Pro	Glu	Val
			20					25					30		
Arg	Leu	Val	Gly	Pro	Asn	Gly	Glu	Gln	Val	Gly	Ile	Val	Arg	Ile	Glu
		35					40					45			
Asp	Ala	Arg	Lys	Leu	Ala	Phe	Asp	Ala	Asp	Leu	Asp	Leu	Val	Glu	Val
	50					55						60			
Ala	Pro	Asn	Ala	Lys	Pro	Pro	Val	Cys	Lys	Ile	Met	Asp	Tyr	Gly	Lys
	65				70					75					80
Phe	Lys	Tyr	Glu	Ala	Ala	Gln	Lys	Ala	Arg	Glu	Ser	Arg	Lys	Asn	Gln
				85					90					95	
Gln	Gln	Thr	Val	Val	Lys	Glu	Gln	Lys	Leu	Arg	Pro	Lys	Ile	Asp	Asp
			100					105					110		
His	Asp	Tyr	Glu	Thr	Lys	Lys	Asn	Asn	Val	Ile	Arg	Phe	Leu	Glu	Lys
		115					120					125			
Gly	Ser	Lys	Val	Lys	Val	Thr	Ile	Met	Phe	Arg	Gly	Arg	Glu	Gln	Ala
		130				135					140				
Arg	Pro	Glu	Leu	Gly	Tyr	Arg	Leu	Leu	Glu	Arg	Leu	Ala	Asn	Asp	Val
	145				150					155					160
Val	Asp	Phe	Gly	Ile	Val	Glu	Thr	Arg	Ala	Lys	Gln	Asp	Gly	Arg	Asn
			165						170					175	
Met	Thr	Met	Val	Leu	Gly	Pro	Val	Arg	Lys	Gly	Lys	Lys			
			180					185							

<210> 463  
 <211> 3135  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(3112)  
 <223> RXN01496

<400> 463

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taagggcctt cgaacctctg gcaagaacta gaggagagaa gtg ccc gga aag cta																115
Val Pro Gly Lys Leu																5
cgt gta cat gag ctt gct aag caa ctc ggt att acc agc aag gaa cta																163
Arg Val His Glu Leu Ala Lys Gln Leu Gly Ile Thr Ser Lys Glu Leu																20
ctt gcc acc ctt aag gat aaa ggc gag ttt gtt aaa acc gca tca tcc																211
Leu Ala Thr Leu Lys Asp Lys Gly Glu Phe Val Lys Thr Ala Ser Ser																35
aca att gaa ccc cca gtt gtg aag agg atg cag gag cac tac ggt tcg																259
Thr Ile Glu Pro Pro Val Val Lys Arg Met Gln Glu His Tyr Gly Ser																50
agc ggt tcg gat aag tcc gac acc gct gcg aag cct gca gcg gca aag																307
Ser Gly Ser Asp Lys Ser Asp Thr Ala Ala Lys Pro Ala Ala Ala Lys																65
cct gct gcg cca aaa cca gct gcg tca gca gct cca aag cca ggt gct																355
Pro Ala Ala Pro Lys Pro Ala Ala Ser Ala Ala Pro Lys Pro Gly Ala																85
cca gca aaa cct gca gca cct gca gca aag cct gcc cca gct gct cct																403
Pro Ala Lys Pro Ala Ala Pro Ala Ala Lys Pro Ala Pro Ala Ala Pro																100
tct gca gct tct gca gca aag cca ggc gca gca cct aag cca ggc gtt																451
Ser Ala Ala Ser Ala Ala Lys Pro Gly Ala Ala Pro Lys Pro Gly Val																115
cag gca aag cct gca gca gcc gct aag cca ggc gct cca gca aag cca																499
Gln Ala Lys Pro Ala Ala Ala Ala Lys Pro Pro Gly Ala Pro Ala Lys Pro																130
gca gca cct gca gct cct tct gcc gct aag tca ggt tca gct tca aag																547
Ala Ala Pro Ala Ala Pro Ser Ala Ala Lys Ser Gly Ser Ala Ser Lys																145
cct gca gca gca gct aag cca gca ttt tct ggc cca act cca ggc gat																595
Pro Ala Ala Ala Ala Lys Pro Ala Phe Ser Gly Pro Thr Pro Gly Asp																165
gca tct aag aag gca gag cca gca gct aag cca ggc gcg gaa gca cct																643
Ala Ser Lys Lys Ala Glu Pro Ala Ala Lys Pro Gly Ala Glu Ala Pro																180
cgc cca ggc ggc atg cca cgt cca atg ggc aag cct gct cca aag cca																691
Arg Pro Gly Met Pro Arg Pro Met Gly Lys Pro Ala Pro Lys Pro																195
ggc gca cgt gca cca cgt gta gct aac aac cca ttc tcc acc ggt ggt																739
Gly Ala Arg Ala Pro Arg Val Ala Asn Asn Pro Phe Ser Thr Gly Gly																210
ggc gag cgt cca gct cct cgc cca ggt ggc ggc cca cgt cct ggt ggc																787
Gly Glu Arg Pro Ala Pro Arg Pro Gly Gly Gly Pro Arg Pro Gly Gly																225

gga cct cgc cca ggc ggt gga cca cgt cca cag ggc cag ggt cgt cca	835
Gly Pro Arg Pro Gly Gly Gly Pro Arg Pro Gln Gly Gln Gly Arg Pro	
230 235 240 245	
ggt ggc cag cga gat ggt cag cgc gac gga cag cgt gat ggt cag ggt	883
Gly Gly Gln Arg Asp Gly Gln Arg Asp Gly Gln Arg Asp Gly Gln Gly	
250 255 260	
aac cgc ggc ggt cag cgt caa ggc gct ggc gca ggt gga cca cgc cca	931
Asn Arg Gly Gly Gln Arg Gln Gly Ala Gly Ala Gly Gly Pro Arg Pro	
265 270 275	
cag ggt gga cca cgc cct cag ggc ggt tca cgc cca cag ggt ggc tcc	979
Gln Gly Gly Pro Arg Pro Gln Gly Gly Ser Arg Pro Gln Gly Gly Ser	
280 285 290	
gct cag ggt gct cag gga gca cct tcc cag gag cgt caa ggt ggc gga	1027
Ala Gln Gly Ala Gln Gly Ala Pro Ser Gln Glu Arg Gln Gly Gly Gly	
295 300 305	
cgt cgt cca tcc cca gca atg atg cct cca acc cca ggt cag atg cct	1075
Arg Arg Pro Ser Pro Ala Met Met Pro Pro Thr Pro Gly Gln Met Pro	
310 315 320 325	
gct aag gca cct ggc aag ggt ggt cgt ggt ggc caa gcc ggc ggt ggc	1123
Ala Lys Ala Pro Gly Lys Gly Gly Arg Gly Gly Gln Ala Gly Gly Gly	
330 335 340	
gct ggt ggc gga ttc aac cgt ggt ggc gga acc ggt ggc ggc gca ggc	1171
Ala Gly Gly Gly Phe Asn Arg Gly Gly Gly Thr Gly Gly Gly Ala Gly	
345 350 355	
cgt ggc ggt cgt cgt ggc ggt acc gca ggt gca ttc ggc cgt cca ggt	1219
Arg Gly Gly Arg Arg Gly Gly Thr Ala Gly Ala Phe Gly Arg Pro Gly	
360 365 370	
ggt gct cca cgc agg gga cgt aag tcg aag cgt cag aag cgc aac gag	1267
Gly Ala Pro Arg Arg Gly Arg Lys Ser Lys Arg Gln Lys Arg Asn Glu	
375 380 385	
tac gaa tca atg cag gca ccg aac gtc att ggt ggc gtt cgt ttg cca	1315
Tyr Glu Ser Met Gln Ala Pro Asn Val Ile Gly Gly Val Arg Leu Pro	
390 395 400 405	
gac ggc aag ggt gca acc atc cgc ctc gcg cgc ggt gca tct ttg gct	1363
Asp Gly Lys Gly Ala Thr Ile Arg Leu Ala Arg Gly Ala Ser Leu Ala	
410 415 420	
gac ttc gct gac aag atc ggc gca gac gca gca gca ttg gtt cag gct	1411
Asp Phe Ala Asp Lys Ile Gly Ala Asp Ala Ala Ala Leu Val Gln Ala	
425 430 435	
ctg ttc aac ttg ggt gaa atg gtc acc gca act gca tcg gtt tct gat	1459
Leu Phe Asn Leu Gly Glu Met Val Thr Ala Thr Ala Ser Val Ser Asp	
440 445 450	
gaa acc ttg cag ctg ctc ggt gag gaa atg aac tac aag gtt cag gtt	1507
Glu Thr Leu Gln Leu Leu Gly Glu Glu Met Asn Tyr Lys Val Gln Val	
455 460 465	

gtt tcc cca gaa gat gaa gac cgt gag ctg ctc gaa agc ttc gac ctt	1555
Val Ser Pro Glu Asp Glu Asp Arg Glu Leu Leu Glu Ser Phe Asp Leu	
470 475 480 485	
cag ttc ggt gag gac gaa ggt ggc gag gct gac ctt gct aag cgt cct	1603
Gln Phe Gly Glu Asp Glu Gly Gly Glu Ala Asp Leu Ala Lys Arg Pro	
490 495 500	
cca gtg gtt acc gtc atg ggt cac gtt gac cac ggt aag act cgt ttg	1651
Pro Val Val Thr Val Met Gly His Val Asp His Gly Lys Thr Arg Leu	
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Leu Asp Thr Ile Arg Lys Ala Asn Val Gly Ser Asp Glu Ala Gly Gly	
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att acc cag ggc att ggt gca tac cag gtc aag gta aat gtc gag gac	1747
Ile Thr Gln Gly Ile Gly Ala Tyr Gln Val Lys Val Asn Val Glu Asp	
535 540 545	
act gag cgc acg atc acc ttc ctg gat acc cca ggt cac gag gcc ttc	1795
Thr Glu Arg Thr Ile Thr Phe Leu Asp Thr Pro Gly His Glu Ala Phe	
550 555 560 565	
acc gca atg cgt gcc cgt ggt gca aag tcc aca gat atc gcg gtt ctg	1843
Thr Ala Met Arg Ala Arg Gly Ala Lys Ser Thr Asp Ile Ala Val Leu	
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gtt gtt gca gca gac gac ggc gtt atg cct cag act gtg gaa gca atc	1891
Val Val Ala Ala Asp Asp Gly Val Met Pro Gln Thr Val Glu Ala Ile	
585 590 595	
aac cac gct aag gct gca gat gta cca atc gtg gtt gca gtg aac aag	1939
Asn His Ala Lys Ala Ala Asp Val Pro Ile Val Val Ala Val Asn Lys	
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att gat aag cca gaa gct tct cca gag aag atc cgt ggt cag ctg acc	1987
Ile Asp Lys Pro Glu Ala Ser Pro Glu Lys Ile Arg Gly Gln Leu Thr	
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Glu Tyr Gly Leu Ile Pro Glu Glu Tyr Gly Gly Asp Thr Ile Phe Val	
630 635 640 645	
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Asp Ile Ser Ala Lys Gln Gly Leu Asn Ile Asp Glu Leu Leu Ala Ser	
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gtc tgc ctg acc gca gac gct gag ctt gac ctt gtt gct aac cca gaa	2131
Val Cys Leu Thr Ala Asp Ala Glu Leu Asp Leu Val Ala Asn Pro Glu	
665 670 675	
atg gac gca cag ggt gtt gca att gaa gct cac ctc gac cgt ggt cgt	2179
Met Asp Ala Gln Gly Val Ala Ile Glu Ala His Leu Asp Arg Gly Arg	
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Gly Pro Val Ala Thr Val Ile Val Gln Arg Gly Thr Leu Arg Val Gly	
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Asp 710	Ser	Ile	Val	Ala	Gly 715	Asp	Thr	Tyr	Gly	Arg 720	Val	Arg	Arg	Met	Val 725	
gac	gaa	tac	gga	cgc	gac	gtt	gaa	gag	gcc	gga	cct	tcc	cgt	cct	gtt	2323
Asp	Glu	Tyr	Gly	Arg 730	Asp	Val	Glu	Glu	Ala 735	Gly	Pro	Ser	Arg	Pro 740	Val	
cag	gtt	cag	ggt	ctt	aac	ggt	gtc	cca	ggc	gcc	ggc	gac	aac	ctt	ctg	2371
Gln	Val	Gln	Gly 745	Leu	Asn	Gly	Val	Pro 750	Gly	Ala	Gly	Asp	Asn 755	Leu	Leu	
gtt	gtt	gaa	gat	gac	cgc	att	gca	cgt	cag	att	gct	aac	cag	cgc	aac	2419
Val	Val	Glu 760	Asp	Asp	Arg	Ile	Ala 765	Arg	Gln	Ile	Ala	Asn 770	Gln	Arg	Asn	
gcc	cgc	aag	cgt	aac	gct	ctg	gca	gca	cgc	tcc	cgt	aag	cgc	gtc	tcc	2467
Ala	Arg	Lys	Arg	Asn	Ala 780	Leu	Ala	Ala	Arg	Ser	Arg 785	Lys	Arg	Val	Ser	
ctc	gag	gat	ctg	gat	tca	gtt	ctt	aag	gaa	cat	agc	acc	ctt	aac	ctc	2515
Leu	Glu	Asp	Leu	Asp	Ser 795	Val	Leu	Lys	Glu	His 800	Ser	Thr	Leu	Asn	Leu 805	
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Ile	Leu	Lys	Gly	Asp 810	Asn	Ala	Gly	Ser 815	Val	Glu	Ala	Leu	Glu 820	Glu	Ala	
ttg	cta	aag	att	gag	atg	gac	gat	gaa	gtc	cag	ctc	aac	atc	atc	gac	2611
Leu	Leu	Lys	Ile 825	Glu	Met	Asp	Asp	Glu 830	Val	Gln	Leu	Asn 835	Ile	Ile	Asp	
cgc	ggt	gtg	ggt	gca	gtt	acc	cag	acc	aac	gtc	acc	ctt	gca	gct	gca	2659
Arg	Gly	Val 840	Gly	Ala	Val	Thr	Gln 845	Thr	Asn	Val	Thr	Leu 850	Ala	Ala	Ala	
tcc	gac	gct	gtc	atc	atc	gcc	ttc	aac	gtt	cgc	gct	gaa	ggt	aag	gca	2707
Ser	Asp	Ala	Val	Ile	Ile	Ala 860	Phe	Asn	Val	Arg	Ala 865	Glu	Gly	Lys	Ala	
act	gag	gaa	gca	aac	gca	gaa	ggc	gtc	gat	gtt	cgt	tac	tac	acg	atc	2755
Thr	Glu	Glu	Ala	Asn	Ala 875	Glu	Gly	Val	Asp	Val 880	Arg	Tyr	Tyr	Thr	Ile 885	
atc	tac	cgt	gct	atc	gaa	gag	gtc	gag	gcg	gcc	ctc	aag	ggc	atg	ctc	2803
Ile	Tyr	Arg	Ala	Ile 890	Glu	Glu	Val	Glu	Ala 895	Ala	Leu	Lys	Gly	Met 900	Leu	
aag	cca	atc	tac	gaa	gag	cgc	gtt	atc	gga	cat	gct	gag	atc	cgt	gcg	2851
Lys	Pro	Ile	Tyr 905	Glu	Glu	Arg	Val 910	Ile	Gly	His	Ala	Glu	Ile 915	Arg	Ala	
atc	ttc	aag	gct	tcc	tct	gtc	ggc	ctc	atc	gca	ggt	tgc	atg	gtt	gaa	2899
Ile	Phe	Lys 920	Ala	Ser	Ser	Val	Gly 925	Leu	Ile	Ala	Gly	Cys 930	Met	Val	Glu	
gac	ggc	aag	gtg	cgc	cga	aac	gcc	aca	gtc	cgc	att	att	cgc	gac	ggc	2947
Asp	Gly 935	Lys	Val	Arg	Arg	Asn 940	Ala	Thr	Val	Arg	Ile 945	Ile	Arg	Asp	Gly	
aac	gtc	atc	gcc	gag	aat	gca	aag	atc	gtg	tcc	ctt	cgc	cgt	gag	aag	2995
Asn	Val	Ile	Ala	Glu	Asn	Ala	Lys	Ile	Val	Ser	Leu	Arg	Arg	Glu	Lys	

950	955	960	965	
gac gat gcc acc gaa gtc tct gca ggc tac gag tgc ggt atg gtt ctg				3043
Asp Asp Ala Thr Glu Val Ser Ala Gly Tyr Glu Cys Gly Met Val Leu				
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tct tac cca gac atc tcc gtc gac gac aag atc gag gtc tac gaa atg				3091
Ser Tyr Pro Asp Ile Ser Val Asp Asp Lys Ile Glu Val Tyr Glu Met				
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Val Glu Val Pro Arg Glu Ala				
1000				

<210> 464  
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 <213> Corynebacterium glutamicum

<400> 464  
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           20                    25                    30  
 Lys Thr Ala Ser Ser Thr Ile Glu Pro Pro Val Val Lys Arg Met Gln  
           35                    40                    45  
 Glu His Tyr Gly Ser Ser Gly Ser Asp Lys Ser Asp Thr Ala Ala Lys  
           50                    55                    60  
 Pro Ala Ala Ala Lys Pro Ala Ala Pro Lys Pro Ala Ala Ser Ala Ala  
           65                    70                    75                    80  
 Pro Lys Pro Gly Ala Pro Ala Lys Pro Ala Ala Pro Ala Ala Lys Pro  
                     85                    90                    95  
 Ala Pro Ala Ala Pro Ser Ala Ala Ser Ala Ala Lys Pro Gly Ala Ala  
                     100                    105                    110  
 Pro Lys Pro Gly Val Gln Ala Lys Pro Ala Ala Ala Ala Lys Pro Gly  
           115                    120                    125  
 Ala Pro Ala Lys Pro Ala Ala Pro Ala Ala Pro Ser Ala Ala Lys Ser  
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 Gly Ser Ala Ser Lys Pro Ala Ala Ala Ala Lys Pro Ala Phe Ser Gly  
           145                    150                    155                    160  
 Pro Thr Pro Gly Asp Ala Ser Lys Lys Ala Glu Pro Ala Ala Lys Pro  
                     165                    170                    175  
 Gly Ala Glu Ala Pro Arg Pro Gly Gly Met Pro Arg Pro Met Gly Lys  
                     180                    185                    190  
 Pro Ala Pro Lys Pro Gly Ala Arg Ala Pro Arg Val Ala Asn Asn Pro  
           195                    200                    205  
 Phe Ser Thr Gly Gly Gly Glu Arg Pro Ala Pro Arg Pro Gly Gly Gly

210	215	220
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Gly Gln Gly Arg Pro Gly Gly Gln Arg Asp 245	Gly Gln Arg Asp Gly Gln 250 255	
Arg Asp Gly Gln Gly Asn Arg Gly Gly Gln Arg Gln Gly Ala Gly Ala 260 265 270		
Gly Gly Pro Arg Pro Gln Gly Gly Pro Arg Pro Gln Gly Gly Ser Arg 275 280 285		
Pro Gln Gly Gly Ser Ala Gln Gly Ala Gln Gly Ala Pro Ser Gln Glu 290 295 300		
Arg Gln Gly Gly Gly Arg Arg Pro Ser Pro Ala Met Met Pro Pro Thr 305 310 315 320		
Pro Gly Gln Met Pro Ala Lys Ala Pro Gly Lys Gly Gly Arg Gly Gly 325 330 335		
Gln Ala Gly Gly Gly Ala Gly Gly Gly Phe Asn Arg Gly Gly Gly Thr 340 345 350		
Gly Gly Gly Ala Gly Arg Gly Gly Arg Arg Gly Gly Thr Ala Gly Ala 355 360 365		
Phe Gly Arg Pro Gly Gly Ala Pro Arg Arg Gly Arg Lys Ser Lys Arg 370 375 380		
Gln Lys Arg Asn Glu Tyr Glu Ser Met Gln Ala Pro Asn Val Ile Gly 385 390 395 400		
Gly Val Arg Leu Pro Asp Gly Lys Gly Ala Thr Ile Arg Leu Ala Arg 405 410 415		
Gly Ala Ser Leu Ala Asp Phe Ala Asp Lys Ile Gly Ala Asp Ala Ala 420 425 430		
Ala Leu Val Gln Ala Leu Phe Asn Leu Gly Glu Met Val Thr Ala Thr 435 440 445		
Ala Ser Val Ser Asp Glu Thr Leu Gln Leu Leu Gly Glu Glu Met Asn 450 455 460		
Tyr Lys Val Gln Val Val Ser Pro Glu Asp Glu Asp Arg Glu Leu Leu 465 470 475 480		
Glu Ser Phe Asp Leu Gln Phe Gly Glu Asp Glu Gly Gly Glu Ala Asp 485 490 495		
Leu Ala Lys Arg Pro Pro Val Val Thr Val Met Gly His Val Asp His 500 505 510		
Gly Lys Thr Arg Leu Leu Asp Thr Ile Arg Lys Ala Asn Val Gly Ser 515 520 525		
Asp Glu Ala Gly Gly Ile Thr Gln Gly Ile Gly Ala Tyr Gln Val Lys 530 535 540		

Val	Asn	Val	Glu	Asp	Thr	Glu	Arg	Thr	Ile	Thr	Phe	Leu	Asp	Thr	Pro
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Gly	His	Glu	Ala	Phe	Thr	Ala	Met	Arg	Ala	Arg	Gly	Ala	Lys	Ser	Thr
				565					570					575	
Asp	Ile	Ala	Val	Leu	Val	Val	Ala	Ala	Asp	Asp	Gly	Val	Met	Pro	Gln
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Thr	Val	Glu	Ala	Ile	Asn	His	Ala	Lys	Ala	Ala	Asp	Val	Pro	Ile	Val
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Val	Ala	Val	Asn	Lys	Ile	Asp	Lys	Pro	Glu	Ala	Ser	Pro	Glu	Lys	Ile
	610					615					620				
Arg	Gly	Gln	Leu	Thr	Glu	Tyr	Gly	Leu	Ile	Pro	Glu	Glu	Tyr	Gly	Gly
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Asp	Thr	Ile	Phe	Val	Asp	Ile	Ser	Ala	Lys	Gln	Gly	Leu	Asn	Ile	Asp
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Glu	Leu	Leu	Ala	Ser	Val	Cys	Leu	Thr	Ala	Asp	Ala	Glu	Leu	Asp	Leu
			660					665					670		
Val	Ala	Asn	Pro	Glu	Met	Asp	Ala	Gln	Gly	Val	Ala	Ile	Glu	Ala	His
		675					680					685			
Leu	Asp	Arg	Gly	Arg	Gly	Pro	Val	Ala	Thr	Val	Ile	Val	Gln	Arg	Gly
	690					695					700				
Thr	Leu	Arg	Val	Gly	Asp	Ser	Ile	Val	Ala	Gly	Asp	Thr	Tyr	Gly	Arg
705					710					715					720
Val	Arg	Arg	Met	Val	Asp	Glu	Tyr	Gly	Arg	Asp	Val	Glu	Glu	Ala	Gly
			725						730					735	
Pro	Ser	Arg	Pro	Val	Gln	Val	Gln	Gly	Leu	Asn	Gly	Val	Pro	Gly	Ala
			740					745					750		
Gly	Asp	Asn	Leu	Leu	Val	Val	Glu	Asp	Asp	Arg	Ile	Ala	Arg	Gln	Ile
		755					760					765			
Ala	Asn	Gln	Arg	Asn	Ala	Arg	Lys	Arg	Asn	Ala	Leu	Ala	Ala	Arg	Ser
	770					775					780				
Arg	Lys	Arg	Val	Ser	Leu	Glu	Asp	Leu	Asp	Ser	Val	Leu	Lys	Glu	His
785					790					795					800
Ser	Thr	Leu	Asn	Leu	Ile	Leu	Lys	Gly	Asp	Asn	Ala	Gly	Ser	Val	Glu
			805						810					815	
Ala	Leu	Glu	Glu	Ala	Leu	Leu	Lys	Ile	Glu	Met	Asp	Asp	Glu	Val	Gln
			820					825					830		
Leu	Asn	Ile	Ile	Asp	Arg	Gly	Val	Gly	Ala	Val	Thr	Gln	Thr	Asn	Val
		835					840					845			
Thr	Leu	Ala	Ala	Ala	Ser	Asp	Ala	Val	Ile	Ile	Ala	Phe	Asn	Val	Arg
	850					855					860				

Ala Glu Gly Lys Ala Thr Glu Glu Ala Asn Ala Glu Gly Val Asp Val  
865 870 875 880

Arg Tyr Tyr Thr Ile Ile Tyr Arg Ala Ile Glu Glu Val Glu Ala Ala  
885 890 895

Leu Lys Gly Met Leu Lys Pro Ile Tyr Glu Glu Arg Val Ile Gly His  
900 905 910

Ala Glu Ile Arg Ala Ile Phe Lys Ala Ser Ser Val Gly Leu Ile Ala  
915 920 925

Gly Cys Met Val Glu Asp Gly Lys Val Arg Arg Asn Ala Thr Val Arg  
930 935 940

Ile Ile Arg Asp Gly Asn Val Ile Ala Glu Asn Ala Lys Ile Val Ser  
945 950 955 960

Leu Arg Arg Glu Lys Asp Asp Ala Thr Glu Val Ser Ala Gly Tyr Glu  
965 970 975

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<210> 465

<211> 1375

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1375)

<223> FRXA00755

<400> 465

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Val Pro Gly Lys Leu 5

cgt gta cat gag ctt gct aag caa ctc ggt att acc agc aag gaa cta 163  
Arg Val His Glu Leu Ala Lys Gln Leu Gly Ile Thr Ser Lys Glu Leu 20

ctt gcc acc ctt aag gat aaa ggc gag ttt gtt aaa acc gca tca tcc 211  
Leu Ala Thr Leu Lys Asp Lys Gly Glu Phe Val Lys Thr Ala Ser Ser 35

aca att gaa ccc cca gtt gtg aag agg atg cag gag cac tac ggt tcg 259  
Thr Ile Glu Pro Pro Val Val Lys Arg Met Gln Glu His Tyr Gly Ser 50

agc ggt tcg gat aag tcc gac acc gct gcg aag cct gca gcg gca aag 307  
Ser Gly Ser Asp Lys Ser Asp Thr Ala Ala Lys Pro Ala Ala Ala Lys 65

cct gct gcg cca aaa cca gct gcg tca gca gct cca aag cca ggt gct	355
Pro Ala Ala Pro Lys Pro Ala Ala Ser Ala Ala Pro Lys Pro Gly Ala	
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cca gca aaa cct gca gca cct gca gca aag cct gcc cca gct gct cct	403
Pro Ala Lys Pro Ala Ala Pro Ala Ala Lys Pro Ala Pro Ala Ala Pro	
90 95 100	
tct gca gct tct gca gca aag cca ggc gca gca cct aag cca ggc gtt	451
Ser Ala Ala Ser Ala Ala Lys Pro Gly Ala Ala Pro Lys Pro Gly Val	
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Gln Ala Lys Pro Ala Ala Ala Ala Lys Pro Gly Ala Pro Ala Lys Pro	
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gca gca cct gca gct cct tct gcc gct aag tca ggt tca gct tca aag	547
Ala Ala Pro Ala Ala Pro Ser Ala Ala Lys Ser Gly Ser Ala Ser Lys	
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cct gca gca gca gct aag cca gca ttt tct ggc cca act cca ggc gat	595
Pro Ala Ala Ala Ala Lys Pro Ala Phe Ser Gly Pro Thr Pro Gly Asp	
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Ala Ser Lys Lys Ala Glu Pro Ala Ala Lys Pro Gly Ala Glu Ala Pro	
170 175 180	
cgc cca ggc ggc atg cca cgt cca atg ggc aag cct gct cca aag cca	691
Arg Pro Gly Gly Met Pro Arg Pro Met Gly Lys Pro Ala Pro Lys Pro	
185 190 195	
ggc gca cgt gca cca cgt gta gct aac aac cca ttc tcc acc ggt ggt	739
Gly Ala Arg Ala Pro Arg Val Ala Asn Asn Pro Phe Ser Thr Gly Gly	
200 205 210	
ggc gag cgt cca gct cct cgc cca ggt ggc ggc cca cgt cct ggt ggc	787
Gly Glu Arg Pro Ala Pro Arg Pro Gly Gly Gly Pro Arg Pro Gly Gly	
215 220 225	
gga cct cgc cca ggc ggt gga cca cgt cca cag ggc cag ggt cgt cca	835
Gly Pro Arg Pro Gly Gly Gly Pro Arg Pro Gln Gly Gln Gly Arg Pro	
230 235 240 245	
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Gly Gly Gln Arg Asp Gly Gln Arg Asp Gly Gln Arg Asp Gly Gln Gly	
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Asn Arg Gly Gly Gln Arg Gln Gly Ala Gly Ala Gly Gly Pro Arg Pro	
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Gln Gly Gly Pro Arg Pro Gln Gly Gly Ser Arg Pro Gln Gly Gly Ser	
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gct cag ggt gct cag gga gca cct tcc cag gag cgt caa ggt ggc gga	1027
Ala Gln Gly Ala Gln Gly Ala Pro Ser Gln Glu Arg Gln Gly Gly Gly	
295 300 305	
cgt cgt cca tcc cca gca atg atg cct cca acc cca ggt cag atg cct	1075

Arg 310	Arg	Pro	Ser	Pro	Ala 315	Met	Met	Pro	Pro	Thr 320	Pro	Gly	Gln	Met	Pro 325	
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tac Tyr 390	gaa Glu	tca Ser	atg Met	cag Gln	gca Ala 395	ccg Pro	aac Asn	gtc Val	att Ile	ggt Gly 400	ggc Gly	gtt Val	cgt Arg	ttg Leu	cca Pro 405	1315
gac Asp	ggc Gly	aag Lys	ggt Gly	gca Ala 410	acc Thr	atc Ile	cgc Arg	ctc Leu	gcg Ala 415	cgc Arg	ggt Gly	gca Ala	tct Ser	ttg Leu 420	gct Ala	1363
gac Asp	ttc Phe	gct Ala	gac Asp 425													1375

&lt;210&gt; 466

&lt;211&gt; 425

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 466

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Lys	Thr	Ala	Ser	Ser	Thr	Ile	Glu	Pro	Pro	Val	Val	Lys	Arg	Met	Gln	30
Glu	His	Tyr	Gly	Ser	Ser	Gly	Ser	Asp	Lys	Ser	Asp	Thr	Ala	Ala	Lys	40
Pro	Ala	Ala	Ala	Lys	Pro	Ala	Ala	Pro	Lys	Pro	Ala	Ala	Ser	Ala	Ala	50
Pro	Lys	Pro	Gly	Ala	Pro	Ala	Lys	Pro	Ala	Ala	Pro	Ala	Ala	Lys	Pro	60
Ala	Pro	Ala	Ala	Pro	Ser	Ala	Ala	Ser	Ala	Ala	Lys	Pro	Gly	Ala	Ala	70
Pro	Lys	Pro	Gly	Val	Gln	Ala	Lys	Pro	Ala	Ala	Ala	Ala	Lys	Pro	Gly	80

Ala Pro Ala Lys Pro Ala Ala Pro Ala Ala Pro Ser Ala Ala Lys Ser  
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 Pro Thr Pro Gly Asp Ala Ser Lys Lys Ala Glu Pro Ala Ala Lys Pro  
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 Gly Ala Glu Ala Pro Arg Pro Gly Gly Met Pro Arg Pro Met Gly Lys  
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 Pro Ala Pro Lys Pro Gly Ala Arg Ala Pro Arg Val Ala Asn Asn Pro  
 195 200 205  
 Phe Ser Thr Gly Gly Gly Glu Arg Pro Ala Pro Arg Pro Gly Gly Gly  
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 Arg Gln Gly Gly Gly Arg Arg Pro Ser Pro Ala Met Met Pro Pro Thr  
 305 310 315 320  
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 Phe Gly Arg Pro Gly Gly Ala Pro Arg Arg Gly Arg Lys Ser Lys Arg  
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 Gln Lys Arg Asn Glu Tyr Glu Ser Met Gln Ala Pro Asn Val Ile Gly  
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 Gly Ala Ser Leu Ala Asp Phe Ala Asp  
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&lt;210&gt; 467

&lt;211&gt; 1751

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1728)

&lt;223&gt; FRXA01496

&lt;400&gt; 467

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gtc acc gca act gca tcg gtt tct gat gaa acc ttg cag ctg ctc ggt	96
Val Thr Ala Thr Ala Ser Val Ser Asp Glu Thr Leu Gln Leu Leu Gly	
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gag gaa atg aac tac aag gtt cag gtt gtt tcc cca gaa gat gaa gac	144
Glu Glu Met Asn Tyr Lys Val Gln Val Val Ser Pro Glu Asp Glu Asp	
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cgt gag ctg ctc gaa agc ttc gac ctt cag ttc ggt gag gac gaa ggt	192
Arg Glu Leu Leu Glu Ser Phe Asp Leu Gln Phe Gly Glu Asp Glu Gly	
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Gly Glu Ala Asp Leu Ala Lys Arg Pro Pro Val Val Thr Val Met Gly	
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cac gtt gac cac ggt aag act cgt ttg ctg gat act atc cgt aag gca	288
His Val Asp His Gly Lys Thr Arg Leu Leu Asp Thr Ile Arg Lys Ala	
85 90 95	
aat gtg ggc tcc gac gaa gcc ggc ggc att acc cag ggc att ggt gca	336
Asn Val Gly Ser Asp Glu Ala Gly Gly Ile Thr Gln Gly Ile Gly Ala	
100 105 110	
tac cag gtc aag gta aat gtc gag gac act gag cgc acg atc acc ttc	384
Tyr Gln Val Lys Val Asn Val Glu Asp Thr Glu Arg Thr Ile Thr Phe	
115 120 125	
ctg gat acc cca ggt cac gag gcc ttc acc gca atg cgt gcc cgt ggt	432
Leu Asp Thr Pro Gly His Glu Ala Phe Thr Ala Met Arg Ala Arg Gly	
130 135 140	
gca aag tcc aca gat atc gcg gtt ctg gtt gtt gca gca gac gac ggc	480
Ala Lys Ser Thr Asp Ile Ala Val Leu Val Val Ala Ala Asp Asp Gly	
145 150 155 160	
gtt atg cct cag act gtg gaa gca atc aac cac gct aag gct gca gat	528
Val Met Pro Gln Thr Val Glu Ala Ile Asn His Ala Lys Ala Ala Asp	
165 170 175	
gta cca atc gtg gtt gca gtg aac aag att gat aag cca gaa gct tct	576
Val Pro Ile Val Val Ala Val Asn Lys Ile Asp Lys Pro Glu Ala Ser	
180 185 190	
cca gag aag atc cgt ggt cag ctg acc gaa tac gga ttg atc cct gaa	624
Pro Glu Lys Ile Arg Gly Gln Leu Thr Glu Tyr Gly Leu Ile Pro Glu	
195 200 205	

gag tac ggt ggc gac acc atc ttc gtt gac atc tct gca aag cag gga	672
Glu Tyr Gly Gly Asp Thr Ile Phe Val Asp Ile Ser Ala Lys Gln Gly	
210 215 220	
ctg aac atc gat gag ctg ctc gct tct gtc tgc ctg acc gca gac gct	720
Leu Asn Ile Asp Glu Leu Leu Ala Ser Val Cys Leu Thr Ala Asp Ala	
225 230 235 240	
gag ctt gac ctt gtt gct aac cca gaa atg gac gca cag ggt gtt gca	768
Glu Leu Asp Leu Val Ala Asn Pro Glu Met Asp Ala Gln Gly Val Ala	
245 250 255	
att gaa gct cac ctc gac cgt ggt cgt gga cca gtg gca acc gtt atc	816
Ile Glu Ala His Leu Asp Arg Gly Arg Gly Pro Val Ala Thr Val Ile	
260 265 270	
gtc cag cgc ggt acc ctg cgc gtc ggt gac tcc atc gtt gca ggc gat	864
Val Gln Arg Gly Thr Leu Arg Val Gly Asp Ser Ile Val Ala Gly Asp	
275 280 285	
acc tac gga cgt gtt cgc cgc atg gtg gac gaa tac gga cgc gac gtt	912
Thr Tyr Gly Arg Val Arg Arg Met Val Asp Glu Tyr Gly Arg Asp Val	
290 295 300	
gaa gag gcc gga cct tcc cgt cct gtt cag gtt cag ggt ctt aac ggt	960
Glu Glu Ala Gly Pro Ser Arg Pro Val Gln Val Gln Gly Leu Asn Gly	
305 310 315 320	
gtc cca ggc gcc ggc gac aac ctt ctg gtt gtt gaa gat gac cgc att	1008
Val Pro Gly Ala Gly Asp Asn Leu Leu Val Val Glu Asp Asp Arg Ile	
325 330 335	
gca cgt cag att gct aac cag cgc aac gcc cgc aag cgt aac gct ctg	1056
Ala Arg Gln Ile Ala Asn Gln Arg Asn Ala Arg Lys Arg Asn Ala Leu	
340 345 350	
gca gca cgc tcc cgt aag cgc gtc tcc ctc gag gat ctg gat tca gtt	1104
Ala Ala Arg Ser Arg Lys Arg Val Ser Leu Glu Asp Leu Asp Ser Val	
355 360 365	
ctt aag gaa cat agc acc ctt aac ctc att ctt aag ggc gac aac gca	1152
Leu Lys Glu His Ser Thr Leu Asn Leu Ile Leu Lys Gly Asp Asn Ala	
370 375 380	
ggt tcc gtg gaa gca ctg gaa gaa gca ttg cta aag att gag atg gac	1200
Gly Ser Val Glu Ala Leu Glu Glu Ala Leu Leu Lys Ile Glu Met Asp	
385 390 395 400	
gat gaa gtc cag ctc aac atc atc gac cgc ggt gtg ggt gca gtt acc	1248
Asp Glu Val Gln Leu Asn Ile Ile Asp Arg Gly Val Gly Ala Val Thr	
405 410 415	
cag acc aac gtc acc ctt gca gct gca tcc gac gct gtc atc atc gcc	1296
Gln Thr Asn Val Thr Leu Ala Ala Ala Ser Asp Ala Val Ile Ile Ala	
420 425 430	
ttc aac gtt cgc gct gaa ggt aag gca act gag gaa gca aac gca gaa	1344
Phe Asn Val Arg Ala Glu Gly Lys Ala Thr Glu Glu Ala Asn Ala Glu	
435 440 445	
ggc gtc gat gtt cgt tac tac acg atc atc tac cgt gct atc gaa gag	1392

Gly Val Asp Val Arg Tyr Tyr Thr Ile Ile Tyr Arg Ala Ile Glu Glu  
 450 455 460  
 gtc gag gcg gcc ctc aag ggc atg ctc aag cca atc tac gaa gag cgc 1440  
 Val Glu Ala Ala Leu Lys Gly Met Leu Lys Pro Ile Tyr Glu Glu Arg  
 465 470 475 480  
 gtt atc gga cat gct gag atc cgt gcg atc ttc aag gct tcc tct gtc 1488  
 Val Ile Gly His Ala Glu Ile Arg Ala Ile Phe Lys Ala Ser Ser Val  
 485 490 495  
 ggc ctc atc gca ggt tgc atg gtt gaa gac ggc aag gtg cgc cga aac 1536  
 Gly Leu Ile Ala Gly Cys Met Val Glu Asp Gly Lys Val Arg Arg Asn  
 500 505 510  
 gcc aca gtc cgc att att cgc gac ggc aac gtc atc gcc gag aat gca 1584  
 Ala Thr Val Arg Ile Ile Arg Asp Gly Asn Val Ile Ala Glu Asn Ala  
 515 520 525  
 aag atc gtg tcc ctt cgc cgt gag aag gac gat gcc acc gaa gtc tct 1632  
 Lys Ile Val Ser Leu Arg Arg Glu Lys Asp Asp Ala Thr Glu Val Ser  
 530 535 540  
 gca ggc tac gag tgc ggt atg gtt ctg tct tac cca gac atc tcc gtc 1680  
 Ala Gly Tyr Glu Cys Gly Met Val Leu Ser Tyr Pro Asp Ile Ser Val  
 545 550 555 560  
 gac gac aag atc gag gtc tac gaa atg gtt gag gtt cca cgc gaa gct 1728  
 Asp Asp Lys Ile Glu Val Tyr Glu Met Val Glu Val Pro Arg Glu Ala  
 565 570 575  
 taagcatttc cggctcgggg cat 1751

&lt;210&gt; 468

&lt;211&gt; 576

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 468

Ala Asp Ala Ala Ala Leu Val Gln Ala Leu Phe Asn Leu Gly Glu Met  
 1 5 10 15  
 Val Thr Ala Thr Ala Ser Val Ser Asp Glu Thr Leu Gln Leu Leu Gly  
 20 25 30  
 Glu Glu Met Asn Tyr Lys Val Gln Val Val Ser Pro Glu Asp Glu Asp  
 35 40 45  
 Arg Glu Leu Leu Glu Ser Phe Asp Leu Gln Phe Gly Glu Asp Glu Gly  
 50 55 60  
 Gly Glu Ala Asp Leu Ala Lys Arg Pro Pro Val Val Thr Val Met Gly  
 65 70 75 80  
 His Val Asp His Gly Lys Thr Arg Leu Leu Asp Thr Ile Arg Lys Ala  
 85 90 95  
 Asn Val Gly Ser Asp Glu Ala Gly Gly Ile Thr Gln Gly Ile Gly Ala  
 100 105 110

Tyr Gln Val Lys Val Asn Val Glu Asp Thr Glu Arg Thr Ile Thr Phe  
 115 120 125  
 Leu Asp Thr Pro Gly His Glu Ala Phe Thr Ala Met Arg Ala Arg Gly  
 130 135 140  
 Ala Lys Ser Thr Asp Ile Ala Val Leu Val Val Ala Ala Asp Asp Gly  
 145 150 155 160  
 Val Met Pro Gln Thr Val Glu Ala Ile Asn His Ala Lys Ala Ala Asp  
 165 170 175  
 Val Pro Ile Val Val Ala Val Asn Lys Ile Asp Lys Pro Glu Ala Ser  
 180 185 190  
 Pro Glu Lys Ile Arg Gly Gln Leu Thr Glu Tyr Gly Leu Ile Pro Glu  
 195 200 205  
 Glu Tyr Gly Gly Asp Thr Ile Phe Val Asp Ile Ser Ala Lys Gln Gly  
 210 215 220  
 Leu Asn Ile Asp Glu Leu Leu Ala Ser Val Cys Leu Thr Ala Asp Ala  
 225 230 235 240  
 Glu Leu Asp Leu Val Ala Asn Pro Glu Met Asp Ala Gln Gly Val Ala  
 245 250 255  
 Ile Glu Ala His Leu Asp Arg Gly Arg Gly Pro Val Ala Thr Val Ile  
 260 265 270  
 Val Gln Arg Gly Thr Leu Arg Val Gly Asp Ser Ile Val Ala Gly Asp  
 275 280 285  
 Thr Tyr Gly Arg Val Arg Arg Met Val Asp Glu Tyr Gly Arg Asp Val  
 290 295 300  
 Glu Glu Ala Gly Pro Ser Arg Pro Val Gln Val Gln Gly Leu Asn Gly  
 305 310 315 320  
 Val Pro Gly Ala Gly Asp Asn Leu Leu Val Val Glu Asp Asp Arg Ile  
 325 330 335  
 Ala Arg Gln Ile Ala Asn Gln Arg Asn Ala Arg Lys Arg Asn Ala Leu  
 340 345 350  
 Ala Ala Arg Ser Arg Lys Arg Val Ser Leu Glu Asp Leu Asp Ser Val  
 355 360 365  
 Leu Lys Glu His Ser Thr Leu Asn Leu Ile Leu Lys Gly Asp Asn Ala  
 370 375 380  
 Gly Ser Val Glu Ala Leu Glu Glu Ala Leu Leu Lys Ile Glu Met Asp  
 385 390 395 400  
 Asp Glu Val Gln Leu Asn Ile Ile Asp Arg Gly Val Gly Ala Val Thr  
 405 410 415  
 Gln Thr Asn Val Thr Leu Ala Ala Ala Ser Asp Ala Val Ile Ile Ala  
 420 425 430  
 Phe Asn Val Arg Ala Glu Gly Lys Ala Thr Glu Glu Ala Asn Ala Glu

435	440	445
Gly Val Asp Val Arg Tyr Tyr Thr Ile Ile Tyr Arg Ala Ile Glu Glu 450 455 460		
Val Glu Ala Ala Leu Lys Gly Met Leu Lys Pro Ile Tyr Glu Glu Arg 465 470 475 480		
Val Ile Gly His Ala Glu Ile Arg Ala Ile Phe Lys Ala Ser Ser Val 485 490 495		
Gly Leu Ile Ala Gly Cys Met Val Glu Asp Gly Lys Val Arg Arg Asn 500 505 510		
Ala Thr Val Arg Ile Ile Arg Asp Gly Asn Val Ile Ala Glu Asn Ala 515 520 525		
Lys Ile Val Ser Leu Arg Arg Glu Lys Asp Asp Ala Thr Glu Val Ser 530 535 540		
Ala Gly Tyr Glu Cys Gly Met Val Leu Ser Tyr Pro Asp Ile Ser Val 545 550 555 560		
Asp Asp Lys Ile Glu Val Tyr Glu Met Val Glu Val Pro Arg Glu Ala 565 570 575		

&lt;210&gt; 469

&lt;211&gt; 339

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(316)

&lt;223&gt; RXA00677

&lt;400&gt; 469

cctatatcga tgggtgtgcgt acatcttgag tgacgcaacc attttgaagt ggaaaaactt 60

aaggcctccc gcaggggagt gttctggaaa agcggaggat	atg gct aag gaa ggc	115
	Met Ala Lys Glu Gly	
	1 5	

gct att gaa gtt gag ggt cgc att gtc gaa cct ctg ccg aat gca atg	163
Ala Ile Glu Val Glu Gly Arg Ile Val Glu Pro Leu Pro Asn Ala Met	
10 15 20	

ttc cga gtc gag ctc gac aac gga cac aag gta ctc gcc cac atc agt	211
Phe Arg Val Glu Leu Asp Asn Gly His Lys Val Leu Ala His Ile Ser	
25 30 35	

gga aag atg cgc cag cac tac atc cgt atc ctt cct gag gac cgc gtc	259
Gly Lys Met Arg Gln His Tyr Ile Arg Ile Leu Pro Glu Asp Arg Val	
40 45 50	

gtt gta gag ctg tcg ccc tat gat ctg act cgt gga cga atc gtt tac	307
Val Val Glu Leu Ser Pro Tyr Asp Leu Thr Arg Gly Arg Ile Val Tyr	
55 60 65	

cgc tac aag taaaaataag ctttaagcct cca 339

Arg Tyr Lys  
70

<210> 470  
<211> 72  
<212> PRT  
<213> Corynebacterium glutamicum

<400> 470  
Met Ala Lys Glu Gly Ala Ile Glu Val Glu Gly Arg Ile Val Glu Pro  
1 5 10 15  
Leu Pro Asn Ala Met Phe Arg Val Glu Leu Asp Asn Gly His Lys Val  
20 25 30  
Leu Ala His Ile Ser Gly Lys Met Arg Gln His Tyr Ile Arg Ile Leu  
35 40 45  
Pro Glu Asp Arg Val Val Val Glu Leu Ser Pro Tyr Asp Leu Thr Arg  
50 55 60  
Gly Arg Ile Val Tyr Arg Tyr Lys  
65 70

<210> 471  
<211> 667  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (101)..(667)  
<223> RXN01284

<400> 471  
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gcgaaagtcg tagccaccac gaagtccagg aggacataca gtg gca aag gcg aag 115  
Val Ala Lys Ala Lys  
1 5  
ttc gag cgt acc aag ccc cac gta aac atc ggc acc atc ggt cac gtt 163  
Phe Glu Arg Thr Lys Pro His Val Asn Ile Gly Thr Ile Gly His Val  
10 15 20  
gac cac ggt aag acc acc acc acc gcg gct atc acc aag gtt ctg gct 211  
Asp His Gly Lys Thr Thr Thr Thr Ala Ala Ile Thr Lys Val Leu Ala  
25 30 35  
gac act tac cct gag ctc aac gag gct ttc gcc ttc gac tcc atc gat 259  
Asp Thr Tyr Pro Glu Leu Asn Glu Ala Phe Ala Phe Asp Ser Ile Asp  
40 45 50  
aag gct cct gag gag aag gag cgt ggc atc acg atc aac atc tcc cac 307  
Lys Ala Pro Glu Glu Lys Glu Arg Gly Ile Thr Ile Asn Ile Ser His  
55 60 65  
gtt gag tac cag act gaa aag cgc cac tac gca cac gtt gac gct cca 355  
Val Glu Tyr Gln Thr Glu Lys Arg His Tyr Ala His Val Asp Ala Pro

70	75	80	85	
ggc cac gcc gac tac atc aag aac atg att acc ggc gct gct cag atg				403
Gly His Ala Asp Tyr Ile Lys Asn Met Ile Thr Gly Ala Ala Gln Met				
	90	95	100	
gac ggc gca atc ctc gtt gtt gct gct acc gac ggc cca atg cct cag				451
Asp Gly Ala Ile Leu Val Val Ala Ala Thr Asp Gly Pro Met Pro Gln				
	105	110	115	
acc cgt gag cac gtt ctt ctt gct cgc cag gtt ggc gtt cct tac atc				499
Thr Arg Glu His Val Leu Leu Ala Arg Gln Val Gly Val Pro Tyr Ile				
	120	125	130	
ctc gtt gct ctt aac aag tgc gac atg gtt gag gat gag gaa atc atc				547
Leu Val Ala Leu Asn Lys Cys Asp Met Val Glu Asp Glu Glu Ile Ile				
	135	140	145	
gag ctc gtc gag atg gaa gtt cgt gaa ctt ctt gct gag cag gac tac				595
Glu Leu Val Glu Met Glu Val Arg Glu Leu Leu Ala Glu Gln Asp Tyr				
	150	155	160	165
gac gaa gag gct cca att gtt cac atc tcc gct ctg aag gct ctt gag				643
Asp Glu Glu Ala Pro Ile Val His Ile Ser Ala Leu Lys Ala Leu Glu				
	170	175	180	
ggc gac gag aag tgg ggc aag cag				667
Gly Asp Glu Lys Trp Gly Lys Gln				
	185			

&lt;210&gt; 472

&lt;211&gt; 189

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 472

Val Ala Lys Ala Lys Phe Glu Arg Thr Lys Pro His Val Asn Ile Gly				
1	5	10	15	
Thr Ile Gly His Val Asp His Gly Lys Thr Thr Thr Thr Ala Ala Ile				
	20	25	30	
Thr Lys Val Leu Ala Asp Thr Tyr Pro Glu Leu Asn Glu Ala Phe Ala				
	35	40	45	
Phe Asp Ser Ile Asp Lys Ala Pro Glu Glu Lys Glu Arg Gly Ile Thr				
	50	55	60	
Ile Asn Ile Ser His Val Glu Tyr Gln Thr Glu Lys Arg His Tyr Ala				
	65	70	75	80
His Val Asp Ala Pro Gly His Ala Asp Tyr Ile Lys Asn Met Ile Thr				
	85	90	95	
Gly Ala Ala Gln Met Asp Gly Ala Ile Leu Val Val Ala Ala Thr Asp				
	100	105	110	
Gly Pro Met Pro Gln Thr Arg Glu His Val Leu Leu Ala Arg Gln Val				
	115	120	125	

Gly Val Pro Tyr Ile Leu Val Ala Leu Asn Lys Cys Asp Met Val Glu  
 130 135 140

Asp Glu Glu Ile Ile Glu Leu Val Glu Met Glu Val Arg Glu Leu Leu  
 145 150 155 160

Ala Glu Gln Asp Tyr Asp Glu Glu Ala Pro Ile Val His Ile Ser Ala  
 165 170 175

Leu Lys Ala Leu Glu Gly Asp Glu Lys Trp Gly Lys Gln  
 180 185

<210> 473

<211> 507

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(507)

<223> FRXA01284

<400> 473

ggt gac cac ggt aag acc acc acc acc gcg gct atc acc aag gtt ctg	48
Val Asp His Gly Lys Thr Thr Thr Thr Ala Ala Ile Thr Lys Val Leu	
1 5 10 15	
gct gac act tac cct gag ctg aac cag gct ttc gcc ttc gac tcc atc	96
Ala Asp Thr Tyr Pro Glu Leu Asn Gln Ala Phe Ala Phe Asp Ser Ile	
20 25 30	
gat aag gct cct gag gag aag gag cgt ggc atc acg atc aac atc tcc	144
Asp Lys Ala Pro Glu Glu Lys Glu Arg Gly Ile Thr Ile Asn Ile Ser	
35 40 45	
cac gtt gag tac cag act gaa aag cgc cac tac gca cac gtt gac gct	192
His Val Glu Tyr Gln Thr Glu Lys Arg His Tyr Ala His Val Asp Ala	
50 55 60	
cca ggc cac gcc gac tac atc aag aac atg att acc ggc gct gct cag	240
Pro Gly His Ala Asp Tyr Ile Lys Asn Met Ile Thr Gly Ala Ala Gln	
65 70 75 80	
atg gac ggc gca atc ctg gtt gtt gct gct acc gac ggc cca atg cct	288
Met Asp Gly Ala Ile Leu Val Val Ala Ala Thr Asp Gly Pro Met Pro	
85 90 95	
cag acc cgt gag cac gtt ctt ctt gct cgc cag gtt ggc gtt cct tac	336
Gln Thr Arg Glu His Val Leu Leu Ala Arg Gln Val Gly Val Pro Tyr	
100 105 110	
atc ctg gtt gct ctt aac aag tgc gac atg gtt gag gat gag gaa atc	384
Ile Leu Val Ala Leu Asn Lys Cys Asp Met Val Glu Asp Glu Glu Ile	
115 120 125	
atc gag ctg gtc gag atg gaa gtt cgt gaa ctt ctt gct gag cag gac	432
Ile Glu Leu Val Glu Met Glu Val Arg Glu Leu Leu Ala Glu Gln Asp	
130 135 140	
tac gac gaa gag gct cca att gtt cac atc tcc gct ctg aag gct ctt	480

Tyr Asp Glu Glu Ala Pro Ile Val His Ile Ser Ala Leu Lys Ala Leu  
 145 150 155 160

gag ggc gac gag aag tgg ggc aag cag  
 Glu Gly Asp Glu Lys Trp Gly Lys Gln  
 165

507

<210> 474  
 <211> 169  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 474  
 Val Asp His Gly Lys Thr Thr Thr Thr Ala Ala Ile Thr Lys Val Leu  
 1 5 10 15  
 Ala Asp Thr Tyr Pro Glu Leu Asn Gln Ala Phe Ala Phe Asp Ser Ile  
 20 25 30  
 Asp Lys Ala Pro Glu Glu Lys Glu Arg Gly Ile Thr Ile Asn Ile Ser  
 35 40 45  
 His Val Glu Tyr Gln Thr Glu Lys Arg His Tyr Ala His Val Asp Ala  
 50 55 60  
 Pro Gly His Ala Asp Tyr Ile Lys Asn Met Ile Thr Gly Ala Ala Gln  
 65 70 75 80  
 Met Asp Gly Ala Ile Leu Val Val Ala Ala Thr Asp Gly Pro Met Pro  
 85 90 95  
 Gln Thr Arg Glu His Val Leu Leu Ala Arg Gln Val Gly Val Pro Tyr  
 100 105 110  
 Ile Leu Val Ala Leu Asn Lys Cys Asp Met Val Glu Asp Glu Glu Ile  
 115 120 125  
 Ile Glu Leu Val Glu Met Glu Val Arg Glu Leu Leu Ala Glu Gln Asp  
 130 135 140  
 Tyr Asp Glu Glu Ala Pro Ile Val His Ile Ser Ala Leu Lys Ala Leu  
 145 150 155 160  
 Glu Gly Asp Glu Lys Trp Gly Lys Gln  
 165

<210> 475  
 <211> 684  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(661)  
 <223> RXA00138

<400> 475  
 cctcatcggtg gtgtaatcta ggtgagctaa tcggtctgcg cgtttttcaa gcactttgcg 60



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<210> 477
<211> 480
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(457)  
<223> RXA00331
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<400> 477															
cagcgccgac	cagcaagcga	agtactgacc	cagatttacg	aagaagtgct	ccccacctc	60									
taaaatgcct gttccggcac ttcccttcgg ggaaacagct						atg gtt ggc cac atg	115								
						Met Val Gly His Met									
						1 5									
tcg aat gat cac cca tac tcc ccc gca aaa cgc gtc gga aat ttc atc															163
Ser Asn Asp His	Pro Tyr Ser Pro	Ala Lys Arg	Val Gly Asn Phe	Ile											
					10 15 20										
ttc gtc tcc ggc gct ctt tca gta gac aag gac tac caa cca gtc gtc															211
Phe Val Ser Gly	Ala Leu Ser Val	Asp Lys Asp Tyr	Gln Pro Val Val												
					25 30 35										
ggt cgt aaa gaa gca gtt gat gca gca ctt gaa cgc atg cgt gaa cgc															259

Gly Arg Lys Glu Ala Val Asp Ala Ala Leu Glu Arg Met Arg Glu Arg  
           40                          45                          50  
 ctc gcc acc gct ggt ggt gaa ctc aaa gac gtt gtg aaa ctc act tac 307  
 Leu Ala Thr Ala Gly Gly Glu Leu Lys Asp Val Val Lys Leu Thr Tyr  
       55                          60                          65  
 ttt gtc acc gac atc agc ctg cgc gaa gaa tgc aac gag caa ttc cga 355  
 Phe Val Thr Asp Ile Ser Leu Arg Glu Glu Cys Asn Glu Gln Phe Arg  
       70                          75                          80                          85  
 gag cat ttc ctc gaa ggc cgc ccg gca cgc tct ttc gtg ggt gca tca 403  
 Glu His Phe Leu Glu Gly Arg Pro Ala Arg Ser Phe Val Gly Ala Ser  
                           90                          95                          100  
 tcg ctt cct tat ggt gca act gtg gaa att gat gcg att gcg atg atc 451  
 Ser Leu Pro Tyr Gly Ala Thr Val Glu Ile Asp Ala Ile Ala Met Ile  
           105                          110                          115  
 gag gac taaccagagc atttttcgca cga 480  
 Glu Asp

<210> 478  
 <211> 119  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 478  
 Met Val Gly His Met Ser Asn Asp His Pro Tyr Ser Pro Ala Lys Arg  
       1                          5                          10                          15  
 Val Gly Asn Phe Ile Phe Val Ser Gly Ala Leu Ser Val Asp Lys Asp  
           20                          25                          30  
 Tyr Gln Pro Val Val Gly Arg Lys Glu Ala Val Asp Ala Ala Leu Glu  
           35                          40                          45  
 Arg Met Arg Glu Arg Leu Ala Thr Ala Gly Gly Glu Leu Lys Asp Val  
       50                          55                          60  
 Val Lys Leu Thr Tyr Phe Val Thr Asp Ile Ser Leu Arg Glu Glu Cys  
       65                          70                          75                          80  
 Asn Glu Gln Phe Arg Glu His Phe Leu Glu Gly Arg Pro Ala Arg Ser  
           85                          90                          95  
 Phe Val Gly Ala Ser Ser Leu Pro Tyr Gly Ala Thr Val Glu Ile Asp  
           100                          105                          110  
 Ala Ile Ala Met Ile Glu Asp  
       115

<210> 479  
 <211> 570  
 <212> DNA  
 <213> Corynebacterium glutamicum  
 <220>

&lt;221&gt; CDS

&lt;222&gt; (1)..(570)

&lt;223&gt; RXA02822

&lt;400&gt; 479

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ggt acc gag gtt agc cat ccc gcc cat ggt gcg tgg agc cag ttc aag      48
Gly Thr Glu Val Ser His Pro Ala His Gly Ala Trp Ser Gln Phe Lys
  1                               5          10          15

ttt gaa ggt ggc gtg cac cgt gtt cag cgt gtg cct gtt act gaa tct      96
Phe Glu Gly Gly Val His Arg Val Gln Arg Val Pro Val Thr Glu Ser
                20          25          30

cag gga cgc atc cag acc tct gct gct ggt gtc ttg gtt tac cca gaa      144
Gln Gly Arg Ile Gln Thr Ser Ala Ala Gly Val Leu Val Tyr Pro Glu
                35          40          45

cca gat gag gtg gaa aac gtt gag atc gat gag aag gat att cgc gtc      192
Pro Asp Glu Val Glu Asn Val Glu Ile Asp Glu Lys Asp Ile Arg Val
                50          55          60

gat gtg tac cgt tcc tca ggt aag ggt ggt cag ggc gtt aac acc act      240
Asp Val Tyr Arg Ser Ser Gly Lys Gly Gly Gln Gly Val Asn Thr Thr
  65                70          75          80

gac tcc gct gtg cgt att acc cac ttg cca act ggt ttg gtg gtg acc      288
Asp Ser Ala Val Arg Ile Thr His Leu Pro Thr Gly Leu Val Val Thr
                85          90          95

tgt cag aag gag cgc tcc cag att cag aac cgt gcg cgt gcg atg cag      336
Cys Gln Lys Glu Arg Ser Gln Ile Gln Asn Arg Ala Arg Ala Met Gln
                100          105          110

gtt ttg gct gcc cgt tta cag gcg atg aag gaa gag gaa gcg gcg gct      384
Val Leu Ala Ala Arg Leu Gln Ala Met Lys Glu Glu Glu Ala Ala Ala
                115          120          125

gag gct gct acg gga cgt gct gcg cag att cgc acc atg gac cgc tct      432
Glu Ala Ala Thr Gly Arg Ala Ala Gln Ile Arg Thr Met Asp Arg Ser
                130          135          140

gag cgc atc cgt acc tac aac tgg ccg gaa aac cgc atc agc gat cac      480
Glu Arg Ile Arg Thr Tyr Asn Trp Pro Glu Asn Arg Ile Ser Asp His
                145          150          155          160

cgt att ggt ttt aag gcg aac aac ctt gat tcg gtt ctc gat ggt gaa      528
Arg Ile Gly Phe Lys Ala Asn Asn Leu Asp Ser Val Leu Asp Gly Glu
                165          170          175

ttg gat gat ctg ttc acc gcg ttg cag gct gct gag cgt gca      570
Leu Asp Asp Leu Phe Thr Ala Leu Gln Ala Ala Glu Arg Ala
                180          185          190

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&lt;210&gt; 480

&lt;211&gt; 190

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 480

Gly Thr Glu Val Ser His Pro Ala His Gly Ala Trp Ser Gln Phe Lys

1	5	10	15
Phe Glu Gly Gly Val His Arg Val Gln Arg Val Pro Val Thr Glu Ser	20	25	30
Gln Gly Arg Ile Gln Thr Ser Ala Ala Gly Val Leu Val Tyr Pro Glu	35	40	45
Pro Asp Glu Val Glu Asn Val Glu Ile Asp Glu Lys Asp Ile Arg Val	50	55	60
Asp Val Tyr Arg Ser Ser Gly Lys Gly Gly Gln Gly Val Asn Thr Thr	65	70	75
Asp Ser Ala Val Arg Ile Thr His Leu Pro Thr Gly Leu Val Val Thr	85	90	95
Cys Gln Lys Glu Arg Ser Gln Ile Gln Asn Arg Ala Arg Ala Met Gln	100	105	110
Val Leu Ala Ala Arg Leu Gln Ala Met Lys Glu Glu Glu Ala Ala Ala	115	120	125
Glu Ala Ala Thr Gly Arg Ala Ala Gln Ile Arg Thr Met Asp Arg Ser	130	135	140
Glu Arg Ile Arg Thr Tyr Asn Trp Pro Glu Asn Arg Ile Ser Asp His	145	150	155
Arg Ile Gly Phe Lys Ala Asn Asn Leu Asp Ser Val Leu Asp Gly Glu	165	170	175
Leu Asp Asp Leu Phe Thr Ala Leu Gln Ala Ala Glu Arg Ala	180	185	190

&lt;210&gt; 481

&lt;211&gt; 480

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(457)

&lt;223&gt; RXA00011

&lt;400&gt; 481

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gtcgatgtct accgctctc cggcccaggt ggtcagtcca	gtg aac acc acc gac	115
	Val Asn Thr Thr Asp	
	1 5	

tct gcc gtg cgc ctg acc cac atc cca acc ggc atc gtg gtg acc tgc	163
Ser Ala Val Arg Leu Thr His Ile Pro Thr Gly Ile Val Val Thr Cys	
10 15 20	

caa aac gag aaa tca cag atc caa aac aag gca tcc gcg atg cgt gtt	211
Gln Asn Glu Lys Ser Gln Ile Gln Asn Lys Ala Ser Ala Met Arg Val	
25 30 35	

ctc cag gca aaa ctg ctt gag cgt aaa cgc cag gaa gaa cgc gcc gaa 259  
 Leu Gln Ala Lys Leu Leu Glu Arg Lys Arg Gln Glu Glu Arg Ala Glu  
           40                                  45                                  50

atg gat gcc ctc gga gct gga ggc aat gca tcc tgg ggt aac caa atg 307  
 Met Asp Ala Leu Gly Ala Gly Gly Asn Ala Ser Trp Gly Asn Gln Met  
           55                                  60                                  65

cgt tcc tac gtg ctg cac cct tat caa atg gtg aag gat ctg cgc acc 355  
 Arg Ser Tyr Val Leu His Pro Tyr Gln Met Val Lys Asp Leu Arg Thr  
           70                                  75                                  80                                  85

aac ttt gaa gtc aac gat ccg caa aaa gtc ctt gac ggc gat atc gat 403  
 Asn Phe Glu Val Asn Asp Pro Gln Lys Val Leu Asp Gly Asp Ile Asp  
                                   90                                  95                                  100

ggc ctt ttg gaa gca ggt att cgc tgg cga atg gct gag agc cag tcg 451  
 Gly Leu Leu Glu Ala Gly Ile Arg Trp Arg Met Ala Glu Ser Gln Ser  
                   105                                  110                                  115

gcg gaa taaaggttg ttttctggca gaa 480  
 Ala Glu

<210> 482  
 <211> 119  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 482  
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Ile Val Val Thr Cys Gln Asn Glu Lys Ser Gln Ile Gln Asn Lys Ala  
                   20                                  25                                  30

Ser Ala Met Arg Val Leu Gln Ala Lys Leu Leu Glu Arg Lys Arg Gln  
                   35                                  40                                  45

Glu Glu Arg Ala Glu Met Asp Ala Leu Gly Ala Gly Gly Asn Ala Ser  
                   50                                  55                                  60

Trp Gly Asn Gln Met Arg Ser Tyr Val Leu His Pro Tyr Gln Met Val  
                   65                                  70                                  75                                  80

Lys Asp Leu Arg Thr Asn Phe Glu Val Asn Asp Pro Gln Lys Val Leu  
                   85                                  90                                  95

Asp Gly Asp Ile Asp Gly Leu Leu Glu Ala Gly Ile Arg Trp Arg Met  
                   100                                  105                                  110

Ala Glu Ser Gln Ser Ala Glu  
                   115

<210> 483  
 <211> 999  
 <212> DNA  
 <213> Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(976)

&lt;223&gt; RXA00012

&lt;400&gt; 483

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gttctaagaa tcacaatcgg tgcgggtaat atgtgcaatc atg cgt ccc gaa ttt 115
                                         Met Arg Pro Glu Phe
                                         1           5

tct gca gaa ctc tcc gag cta gac agc acg ctg aca acc att gaa aaa 163
Ser Ala Glu Leu Ser Glu Leu Asp Ser Thr Leu Thr Thr Ile Glu Lys
                        10                        15                        20

gtg ctg aac ccg caa gag atg tct gac cga gtc aga gaa ctt gaa gct 211
Val Leu Asn Pro Gln Glu Met Ser Asp Arg Val Arg Glu Leu Glu Ala
                        25                        30                        35

caa gca gct gac ccg tct ctg tgg gat gac cct gac cat gca cag caa 259
Gln Ala Ala Asp Pro Ser Leu Trp Asp Asp Pro Asp His Ala Gln Gln
                        40                        45                        50

gtc acc tct gag ctg tcc cac gtc cag gcg gag ctg cgc aaa att acc 307
Val Thr Ser Glu Leu Ser His Val Gln Ala Glu Leu Arg Lys Ile Thr
                        55                        60                        65

gat ctg cgc cag cgc atc gaa gat ctg ccc atc atg gtg gaa ctc gca 355
Asp Leu Arg Gln Arg Ile Glu Asp Leu Pro Ile Met Val Glu Leu Ala
                        70                        75                        80                        85

gag gaa gaa gac ggc gat acc tcc atc gcg gaa gaa gaa ctc gcc gat 403
Glu Glu Glu Asp Gly Asp Thr Ser Ile Ala Glu Glu Glu Leu Ala Asp
                        90                        95                        100

ctg cgt tct ctg atc gat gcg ttg gaa gta aag acc atg ctg tcg ggt 451
Leu Arg Ser Leu Ile Asp Ala Leu Glu Val Lys Thr Met Leu Ser Gly
                        105                        110                        115

gaa tat gat gct cgc gag gca gtg atc aat att cga tcc ggt gcc ggt 499
Glu Tyr Asp Ala Arg Glu Ala Val Ile Asn Ile Arg Ser Gly Ala Gly
                        120                        125                        130

ggg gtc gat gct gcg gac tgg gct gaa atg ctc atg cgc atg tac acc 547
Gly Val Asp Ala Ala Asp Trp Ala Glu Met Leu Met Arg Met Tyr Thr
                        135                        140                        145

cgc tgg gcg gaa aag aac ggc cac aaa gta gat att tac gat att tcc 595
Arg Trp Ala Glu Lys Asn Gly His Lys Val Asp Ile Tyr Asp Ile Ser
                        150                        155                        160                        165

tac gcc gaa gaa gcc ggc atc aaa tcc gcc acc ttc gtg gtc cac ggc 643
Tyr Ala Glu Glu Ala Gly Ile Lys Ser Ala Thr Phe Val Val His Gly
                        170                        175                        180

gac tac atg tac ggc cag ctc tcc gtg gag caa ggc gca cac cgc ctc 691
Asp Tyr Met Tyr Gly Gln Leu Ser Val Glu Gln Gly Ala His Arg Leu
                        185                        190                        195

gtg cgc atc agt cct ttt gat aac cag ggc agg cgc caa acc tcc ttc 739

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Val	Arg	Ile	Ser	Pro	Phe	Asp	Asn	Gln	Gly	Arg	Arg	Gln	Thr	Ser	Phe		
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gcc	gag	gta	gaa	gtt	ctt	ccc	gtg	gtg	gaa	aaa	gtg	gac	tcc	atc	gac	787	
Ala	Glu	Val	Glu	Val	Leu	Pro	Val	Val	Glu	Lys	Val	Asp	Ser	Ile	Asp		
	215					220				225							
atc	cct	gat	gcc	gat	gtt	cgc	gtc	gat	gtc	tac	cgc	tcc	tcc	ggc	cca	835	
Ile	Pro	Asp	Ala	Asp	Val	Arg	Val	Asp	Val	Tyr	Arg	Ser	Ser	Gly	Pro		
230					235					240					245		
ggg	ggg	cag	tcc	agt	gaa	cac	cac	cga	ctc	tgc	cgt	gcg	cct	gac	cca	883	
Gly	Gly	Gln	Ser	Ser	Glu	His	His	Arg	Leu	Cys	Arg	Ala	Pro	Asp	Pro		
				250					255					260			
cat	ccc	aac	cgg	cat	cgt	ggg	gac	ctg	cca	aaa	cga	gaa	atc	aca	gat	931	
His	Pro	Asn	Arg	His	Arg	Gly	Asp	Leu	Pro	Lys	Arg	Glu	Ile	Thr	Asp		
			265					270					275				
cca	aaa	caa	ggc	atc	cgc	gat	gcg	tgt	tct	cca	ggc	aaa	act	gct		976	
Pro	Lys	Gln	Gly	Ile	Arg	Asp	Ala	Cys	Ser	Pro	Gly	Lys	Thr	Ala			
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 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 484																	
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			20				25						30				
Arg	Glu	Leu	Glu	Ala	Gln	Ala	Ala	Asp	Pro	Ser	Leu	Trp	Asp	Asp	Pro		
		35					40					45					
Asp	His	Ala	Gln	Gln	Val	Thr	Ser	Glu	Leu	Ser	His	Val	Gln	Ala	Glu		
	50					55					60						
Leu	Arg	Lys	Ile	Thr	Asp	Leu	Arg	Gln	Arg	Ile	Glu	Asp	Leu	Pro	Ile		
65					70					75					80		
Met	Val	Glu	Leu	Ala	Glu	Glu	Glu	Asp	Gly	Asp	Thr	Ser	Ile	Ala	Glu		
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Glu	Glu	Leu	Ala	Asp	Leu	Arg	Ser	Leu	Ile	Asp	Ala	Leu	Glu	Val	Lys		
		100						105					110				
Thr	Met	Leu	Ser	Gly	Glu	Tyr	Asp	Ala	Arg	Glu	Ala	Val	Ile	Asn	Ile		
		115					120					125					
Arg	Ser	Gly	Ala	Gly	Gly	Val	Asp	Ala	Ala	Asp	Trp	Ala	Glu	Met	Leu		
		130				135					140						
Met	Arg	Met	Tyr	Thr	Arg	Trp	Ala	Glu	Lys	Asn	Gly	His	Lys	Val	Asp		
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Leu	Arg	Ser	Phe	Tyr	Thr	Pro	Glu	Gln	Ala	Ile	Glu	Arg	Glu	Gly	Asp	
1				5					10					15		
gtc	tgg	aaa	gcc	gcc	acc	gaa	gaa	gca	gaa	ctc	ctc	gca	gct	gac	ggc	96
Val	Trp	Lys	Ala	Ala	Thr	Glu	Glu	Ala	Glu	Leu	Leu	Ala	Ala	Asp	Gly	
			20					25					30			
gcc	gtc	cac	gac	cag	gaa	ctc	ttc	ctc	aac	tgc	acc	acc	tcc	cca	ctg	144
Ala	Val	His	Asp	Gln	Glu	Leu	Phe	Leu	Asn	Cys	Thr	Thr	Ser	Pro	Leu	
		35					40					45				
atc	ttc	gcc	tcc	gcg	atg	ctc	aac	ttc	ggc	gtc	cac	caa	atc	ctg	gac	192
Ile	Phe	Ala	Ser	Ala	Met	Leu	Asn	Phe	Gly	Val	His	Gln	Ile	Leu	Asp	
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acc	ctc	tgc	caa	ctc	gca	cca	tcc	ccc	gcc	ggc	cgc	gac	gca	gac	ccc	240
Thr	Leu	Cys	Gln	Leu	Ala	Pro	Ser	Pro	Ala	Gly	Arg	Asp	Ala	Asp	Pro	
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aaa	gcc	ctc	gaa	gcc	gcc	acc	tcc	gca	atg	gac	gac	cac	cgc	gac	acc	288

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Val Trp Lys Ala Ala Thr Glu Glu Ala Glu Leu Leu Ala Ala Asp Gly  
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Ala Val His Asp Gln Glu Leu Phe Leu Asn Cys Thr Thr Ser Pro Leu  
35 40 45  
Ile Phe Ala Ser Ala Met Leu Asn Phe Gly Val His Gln Ile Leu Asp  
50 55 60

Thr Leu Cys Gln Leu Ala Pro Ser Pro Ala Gly Arg Asp Ala Asp Pro  
 65 70 75 80  
 Lys Ala Leu Glu Ala Ala Thr Ser Ala Met Asp Asp His Arg Asp Thr  
 85 90 95  
 Thr Asp Asp Phe Ser Gly Val Val Phe Lys Val Gln Ala Gly Met Asp  
 100 105 110  
 Lys Asn His Arg Asp Thr Leu Ala Phe Met Arg Val Val Ser Gly Glu  
 115 120 125  
 Phe Asp Arg Gly Met Gln Val Thr His Ser Gln Ser Gly Arg Ser Phe  
 130 135 140  
 Ser Thr Lys Tyr Ala Leu Thr Val Phe Gly Arg Thr Arg Ser Thr Val  
 145 150 155 160  
 Glu Thr Ala Phe Pro Gly Asp Ile Val Gly Leu Val Asn Ala Gly Ala  
 165 170 175  
 Leu Ala Pro Gly Asp Thr Ile Phe Glu Gly Arg Lys Ile Gln Tyr Pro  
 180 185 190  
 Pro Met Pro Lys Phe Ala Pro Glu His Phe Arg Ile Leu Arg Ala Lys  
 195 200 205  
 Ser Leu Gly Lys Tyr Lys Gln Phe Arg Lys Ala Leu Glu Gln Leu Asp  
 210 215 220  
 Ser Glu Gly Val Val Gln Ile Leu Lys Asn Asp Leu Arg Gly Asp Ala  
 225 230 235 240  
 Asn Pro Gly His Gly Arg Cys  
 245

<210> 487  
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 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(672)  
 <223> FRXA01926

<400> 487  
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 gtc tgg aaa gcc gcc acc gaa gaa gca gaa ctc ctc gca gct gac ggc 96  
 Val Trp Lys Ala Ala Thr Glu Glu Ala Glu Leu Leu Ala Ala Asp Gly  
 20 25 30  
 gcc gtc cac gac cag gaa ctc ttc ctc aac tgc acc acc tcc cca ctg 144  
 Ala Val His Asp Gln Glu Leu Phe Leu Asn Cys Thr Thr Ser Pro Leu  
 35 40 45

atc ttc gcc tcc gcg atg ctc aac ttc ggc gtc cac caa atc ctg gac 192  
 Ile Phe Ala Ser Ala Met Leu Asn Phe Gly Val His Gln Ile Leu Asp  
 50 55 60

acc ctc tgc caa ctc gca cca tcc ccc gcc ggc cgc gac gca gac ccc 240  
 Thr Leu Cys Gln Leu Ala Pro Ser Pro Ala Gly Arg Asp Ala Asp Pro  
 65 70 75 80

aaa gcc ctc gaa gcc gcc acc tcc gca atg gac gac cac cgc gac acc 288  
 Lys Ala Leu Glu Ala Ala Thr Ser Ala Met Asp Asp His Arg Asp Thr  
 85 90 95

acc gac gac ttc tcc ggc gtc gtc ttc aaa gtc caa gcc ggc atg gac 336  
 Thr Asp Asp Phe Ser Gly Val Val Phe Lys Val Gln Ala Gly Met Asp  
 100 105 110

aaa aac cac cgc gat acc ctc gcc ttc atg cgc gtc gtc tcc ggc gaa 384  
 Lys Asn His Arg Asp Thr Leu Ala Phe Met Arg Val Val Ser Gly Glu  
 115 120 125

ttc gac cgc ggc atg caa gtc acc cac tcc caa tcc ggc cgc agc ttc 432  
 Phe Asp Arg Gly Met Gln Val Thr His Ser Gln Ser Gly Arg Ser Phe  
 130 135 140

tcc acc aaa tac gcc ctc acc gtc ttc ggc cgc acc cgc tct acc gtc 480  
 Ser Thr Lys Tyr Ala Leu Thr Val Phe Gly Arg Thr Arg Ser Thr Val  
 145 150 155 160

gaa acc gcc ttc ccc ggc gac atc gtc ggc ctc gtc aac gcc ggc gcc 528  
 Glu Thr Ala Phe Pro Gly Asp Ile Val Gly Leu Val Asn Ala Gly Ala  
 165 170 175

ctc gca cca ggc gac acc atc ttc gaa ggc cga aaa atc caa tac cca 576  
 Leu Ala Pro Gly Asp Thr Ile Phe Glu Gly Arg Lys Ile Gln Tyr Pro  
 180 185 190

cca atg cca aaa ttc gcg cca gaa cac ttc cgc atc ctg cgc gcc aaa 624  
 Pro Met Pro Lys Phe Ala Pro Glu His Phe Arg Ile Leu Arg Ala Lys  
 195 200 205

tca ctc ggc aaa tac aaa cag ttc cgc aaa gcc ctc gag cag ctg gac 672  
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 <213> Corynebacterium glutamicum

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Val Trp Lys Ala Ala Thr Glu Glu Ala Glu Leu Leu Ala Ala Asp Gly  
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Ala Val His Asp Gln Glu Leu Phe Leu Asn Cys Thr Thr Ser Pro Leu  
 35 40 45

Ile Phe Ala Ser Ala Met Leu Asn Phe Gly Val His Gln Ile Leu Asp



ggc cgc aaa gcc acc gtt tcc gac tgg atg gaa atg gaa aaa gac cgc 307  
 Gly Arg Lys Ala Thr Val Ser Asp Trp Met Glu Met Glu Lys Asp Arg  
     55                    60                    65

ggc atc tcc atc gcc tcc tcc gca ctc caa ttc gag tac gca cca gaa 355  
 Gly Ile Ser Ile Ala Ser Ser Ala Leu Gln Phe Glu Tyr Ala Pro Glu  
     70                    75                    80                    85

ggc cac gca ggc gag ccc ttc atg atc aac ctc gtg gac acc cca ggc 403  
 Gly His Ala Gly Glu Pro Phe Met Ile Asn Leu Val Asp Thr Pro Gly  
                     90                    95                    100

cac gcc gac ttc tcc gaa gac acc tac cgc gtc ctc atg gcc gtc gac 451  
 His Ala Asp Phe Ser Glu Asp Thr Tyr Arg Val Leu Met Ala Val Asp  
                     105                    110                    115

gca gca gtc atg ctt atg cac tcc gtc 478  
 Ala Ala Val Met Leu Met His Ser Val  
             120                    125

<210> 490

<211> 126

<212> PRT

<213> Corynebacterium glutamicum

<400> 490

Met Ser Asn Ala Asn Ser Asp Thr Thr Ala Ala Glu Ala His Arg Arg  
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Arg Thr Phe Ala Val Ile Ala His Pro Asp Ala Gly Lys Ser Thr Leu  
             20                    25                    30

Thr Glu Ala Leu Ala Leu His Ala His Ile Ile Ser Glu Ala Gly Ala  
             35                    40                    45

Thr His Gly Lys Ala Gly Arg Lys Ala Thr Val Ser Asp Trp Met Glu  
             50                    55                    60

Met Glu Lys Asp Arg Gly Ile Ser Ile Ala Ser Ser Ala Leu Gln Phe  
     65                    70                    75                    80

Glu Tyr Ala Pro Glu Gly His Ala Gly Glu Pro Phe Met Ile Asn Leu  
                     85                    90                    95

Val Asp Thr Pro Gly His Ala Asp Phe Ser Glu Asp Thr Tyr Arg Val  
             100                    105                    110

Leu Met Ala Val Asp Ala Ala Val Met Leu Met His Ser Val  
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<210> 491

<211> 394

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (17)..(394)

&lt;223&gt; FRXA02002

&lt;400&gt; 491

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        1             5             10

gca cat cgc cgc aga aca ttc gcc gta atc gca cac ccc gac gcc ggt 100
Ala His Arg Arg Arg Thr Phe Ala Val Ile Ala His Pro Asp Ala Gly
      15             20             25

aaa tcc acc ctc acc gag gca ttg gcg ctg cat gca cac atc atc tcc 148
Lys Ser Thr Leu Thr Glu Ala Leu Ala Leu His Ala His Ile Ile Ser
      30             35             40

gaa gcc ggc gcc acc cac ggc aaa gca ggc cgc aaa gcc acc gtt tcc 196
Glu Ala Gly Ala Thr His Gly Lys Ala Gly Arg Lys Ala Thr Val Ser
      45             50             55

gac tgg atg gaa atg gaa aaa gac cgc ggc atc tcc atc gcc tcc tcc 244
Asp Trp Met Glu Met Glu Lys Asp Arg Gly Ile Ser Ile Ala Ser Ser
      65             70             75

gca ctc caa ttc gag tac gca cca gaa ggc cac gca ggc gag ccc ttc 292
Ala Leu Gln Phe Glu Tyr Ala Pro Glu Gly His Ala Gly Glu Pro Phe
      80             85             90

atg atc aac ctc gtg gac acc cca ggc cac gcc gac ttc tcc gaa gac 340
Met Ile Asn Leu Val Asp Thr Pro Gly His Ala Asp Phe Ser Glu Asp
      95             100            105

acc tac cgc gtc ctc atg gcc gtc gac gca gca gtc atg ctt atg cac 388
Thr Tyr Arg Val Leu Met Ala Val Asp Ala Ala Val Met Leu Met His
      110            115            120

tcc gtc 394
Ser Val
125

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&lt;210&gt; 492

&lt;211&gt; 126

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 492

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Met Ser Asn Ala Asn Pro Asp Thr Thr Ala Ala Glu Ala His Arg Arg
  1             5             10             15

Arg Thr Phe Ala Val Ile Ala His Pro Asp Ala Gly Lys Ser Thr Leu
      20             25             30

Thr Glu Ala Leu Ala Leu His Ala His Ile Ile Ser Glu Ala Gly Ala
      35             40             45

Thr His Gly Lys Ala Gly Arg Lys Ala Thr Val Ser Asp Trp Met Glu
      50             55             60

Met Glu Lys Asp Arg Gly Ile Ser Ile Ala Ser Ser Ala Leu Gln Phe
      65             70             75             80

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<400> 493															
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gggttaaate atctgcggaa agcatgctta gaatgttgcc atg act gtc cga cca 115															
Met Thr Val Arg Pro 5															
atc gtt att cat gga gat cct gtt ctc cac aac cct acc cag ctt gtt 163															
Ile Val Ile His Gly Asp Pro Val Leu His Asn Pro Thr Gln Leu Val 20															
act gag gat gtc tct gaa ctg cag gaa cta att gca gat atg tac gag 211															
Thr Glu Asp Val Ser Glu Leu Gln Glu Leu Ile Ala Asp Met Tyr Glu 35															
acg atg gat gtc gcc aat ggt gtg ggt ctt gcg gcc aac cag att ggt 259															
Thr Met Asp Val Ala Asn Gly Val Gly Leu Ala Ala Asn Gln Ile Gly 50															
gtg tcc aag cgc att ttt gtt tat gac tgt cct gat gat gag ggc gtg 307															
Val Ser Lys Arg Ile Phe Val Tyr Asp Cys Pro Asp Asp Glu Gly Val 65															
atg cac aag ggt tgt ttc atc aat cct gtg ttg gaa acc tct gaa atc 355															
Met His Lys Gly Cys Phe Ile Asn Pro Val Leu Glu Thr Ser Glu Ile 85															
cca gag acc atg cct gcc gat gat ggc tcc gac gag gaa ggc tgc ctg 403															
Pro Glu Thr Met Pro Ala Asp Asp Gly Ser Asp Glu Glu Gly Cys Leu 100															
tct gtt cct ggc gag ggc ttc ccc act ggc cgt gct cat tgg gcg aag 451															
Ser Val Pro Gly Glu Gly Phe Pro Thr Gly Arg Ala His Trp Ala Lys 115															
gtt act gga ctg aat gaa aag ggc gag gaa gtt tct gtt gag gct gag 499															
Val Thr Gly Leu Asn Glu Lys Gly Glu Glu Val Ser Val Glu Ala Glu 130															
ggg ttc ttg gct cgt tgc ttc cag cat gag gtt ggc cac ctt gat ggt 547															
Gly Phe Leu Ala Arg Cys Phe Gln His Glu Val Gly His Leu Asp Gly															

135	140	145	
ttc ttg tac acc gat	gtg ttg att ggt	cgg tgg aag cgc atg gct aag	595
Phe Leu Tyr Thr Asp	Val Leu Ile Gly Arg	Trp Lys Arg Met Ala Lys	
150	155	160 165	
aag gct att aag gcc aat ggg tgg act gag cct ggt ttg acc tgg atg			643
Lys Ala Ile Lys	Ala Asn Gly Trp Thr	Glu Pro Gly Leu Thr Trp Met	
	170	175 180	
ccg ggt gaa gat gag gat cct ttc ggg cat gac gcc tat gtc ttc ccc			691
Pro Gly Glu Asp Glu Asp Pro Phe Gly His Asp Ala Tyr Val Phe Pro			
	185	190 195	
gtt tcc gca gcc aga aac ctg ccg tcg gcg atc gtg ttg ttg cac gtc			739
Val Ser Ala Ala Arg Asn Leu Pro Ser Ala Ile Val Leu Leu His Val			
	200 205	210	

&lt;210&gt; 494

&lt;211&gt; 213

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 494

Met Thr Val Arg Pro Ile Val Ile His Gly Asp Pro Val Leu His Asn	
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Pro Thr Gln Leu Val Thr Glu Asp Val Ser Glu Leu Gln Glu Leu Ile	
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Ala Asp Met Tyr Glu Thr Met Asp Val Ala Asn Gly Val Gly Leu Ala	
35 40 45	
Ala Asn Gln Ile Gly Val Ser Lys Arg Ile Phe Val Tyr Asp Cys Pro	
50 55 60	
Asp Asp Glu Gly Val Met His Lys Gly Cys Phe Ile Asn Pro Val Leu	
65 70 75 80	
Glu Thr Ser Glu Ile Pro Glu Thr Met Pro Ala Asp Asp Gly Ser Asp	
85 90 95	
Glu Glu Gly Cys Leu Ser Val Pro Gly Glu Gly Phe Pro Thr Gly Arg	
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Ala His Trp Ala Lys Val Thr Gly Leu Asn Glu Lys Gly Glu Glu Val	
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Gly Leu Thr Trp Met Pro Gly Glu Asp Glu Asp Pro Phe Gly His Asp	
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 Thr Met Glu Asp Ala Gly Gly Val Gly Leu Ala Ala Asn Gln Val Gly  
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 Thr Gln Thr Gly Lys Glu Gly Cys Leu Ser Ile Pro Asp Val Ser Ala  
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 Glu Thr Thr Arg Tyr Glu Thr Val Arg Leu Ser Gly Gln Asp Arg Asp  
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 Gly Asn Pro Val Gly Phe Val Ala Asn Gly Leu Leu Ala Arg Cys Ile  
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 Gln His Glu Thr Asp His Leu Asp Gly Val Leu Phe Leu Lys Arg Leu  
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 Ala Asn Gln Val Gly Val Leu Arg Arg Val Phe Val Phe Asp Thr Ser  
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 His Gln Glu Gly Gly Leu Arg Gly His Val Ile Asn Pro Val Trp Glu  
 65 70 75 80  
 Pro Leu Thr Glu Asp Thr Gln Thr Gly Lys Glu Gly Cys Leu Ser Ile  
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 Pro Asp Val Ser Ala Glu Thr Thr Arg Tyr Glu Thr Val Arg Leu Ser  
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Leu	Ile	Ser	Asp	Thr	Glu	Trp	Arg	Glu	Arg	Leu	Thr	Pro	Gln	Glu	Phe	
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His	Val	Leu	Arg	Glu	Ala	Gly	Thr	Glu	Pro	Pro	His	Val	Gly	Glu	Tyr	
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Thr	Asn	Thr	Thr	Thr	Glu	Gly	Val	Tyr	Ser	Cys	Arg	Ala	Cys	Gly	Glu	
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Glu	Leu	Phe	Arg	Ser	Thr	Glu	Lys	Phe	Glu	Ser	His	Cys	Gly	Trp	Pro	
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Ser	Phe	Phe	Ser	Pro	Leu	Ala	Gly	Asp	Lys	Ile	Ile	Glu	Lys	Glu	Asp	
	70				75					80					85	
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Leu	Ser	Leu	Gly	Met	Arg	Arg	Val	Glu	Ile	Leu	Cys	Ala	Asn	Cys	Gly	
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Ser	His	Met	Gly	His	Val	Phe	Glu	Gly	Glu	Gly	Tyr	Asp	Thr	Pro	Thr	
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 His Cys Gly Trp Pro Ser Phe Phe Ser Pro Leu Ala Gly Asp Lys Ile  
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 Cys Ala Asn Cys Gly Ser His Met Gly His Val Phe Glu Gly Glu Gly  
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 His Tyr Glu Val Asp Glu Arg Lys Lys Thr Val Gly Val Lys Glu Glu  
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Gly Val Glu Tyr Val Glu Asp Gln Leu Gly Ile Asp Asn Leu Tyr Ala	
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Gln Glu Leu Phe Thr Arg Asp Lys Asp Tyr Ile Val Arg Asn Gly Glu	
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Val Met Ile Val Asp Gly Phe Thr Gly Arg Val Leu Ala Gly Arg Arg	
70 75 80 85	
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Tyr Asn Glu Gly Met His Gln Ala Ile Glu Ala Lys Glu Arg Val Glu	
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Ile Lys Asn Glu Asn Gln Thr Leu Ala Thr Val Thr Leu Gln Asn Tyr	
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Phe Arg Leu Tyr Thr Lys Leu Ala Gly Met Thr Gly Thr Ala Glu Thr	
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Glu Ala Ala Glu Leu Asn Gln Ile Tyr Lys Leu Asp Val Ile Ala Ile	
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Pro Thr Asn Arg Pro Asn Gln Arg Glu Asp Leu Thr Asp Leu Val Tyr	
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Lys Thr Gln Glu Ala Lys Phe Ala Ala Val Val Asp Asp Ile Ala Glu	
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Arg Thr Glu Lys Gly Gln Pro Val Leu Val Gly Thr Val Ser Val Glu	
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Arg Ser Glu Tyr Leu Ser Gln Leu Leu Thr Lys Arg Gly Ile Lys His	
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Asn Val Leu Asn Ala Lys His His Glu Gln Glu Ala Gln Ile Val Ala	
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Gln Ala Gly Leu Pro Gly Ala Val Thr Val Ala Thr Asn Met Ala Gly	
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Arg Gly Thr Asp Ile Val Leu Gly Gly Asn Pro Glu Ile Leu Leu Asp	
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Met	Met	Asn	Arg	Leu	Asn	Val	Pro	Asp	Asp	Val	Pro	Ile	Glu	Ser	Lys	
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acc	gtc	acc	aac	tcc	atc	aag	ggc	gcc	caa	gct	cag	gtg	gag	aac	cag	1267
Thr	Val	Thr	Asn	Ser	Ile	Lys	Gly	Ala	Gln	Ala	Gln	Val	Glu	Asn	Gln	
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Asn	Phe	Glu	Met	Arg	Lys	Asn	Val	Leu	Lys	Tyr	Asp	Glu	Val	Met	Asn	
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gaa	cag	cgc	aag	gtt	atc	tac	agc	gag	cga	cgc	gaa	atc	ctc	gaa	tcc	1363
Glu	Gln	Arg	Lys	Val	Ile	Tyr	Ser	Glu	Arg	Arg	Glu	Ile	Leu	Glu	Ser	
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Ala	Asp	Ile	Ser	Arg	Tyr	Ile	Gln	Asn	Met	Ile	Glu	Glu	Thr	Val	Ser	
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Ala	Tyr	Val	Asp	Gly	Ala	Thr	Ala	Asn	Gly	Tyr	Val	Glu	Asp	Trp	Asp	
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Leu	Asp	Lys	Leu	Trp	Asn	Ala	Leu	Glu	Ala	Leu	Tyr	Asp	Pro	Ser	Ile	
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 Lys Trp Arg Glu His Leu Tyr Glu Met Asp Tyr Leu Lys Glu Gly Ile  
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&lt;210&gt; 502

&lt;211&gt; 606

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 502

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 Asn Ala Ile Lys Ala Gln Glu Leu Phe Thr Arg Asp Lys Asp Tyr Ile  
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 Val Arg Asn Gly Glu Val Met Ile Val Asp Gly Phe Thr Gly Arg Val  
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 Lys Glu Arg Val Glu Ile Lys Asn Glu Asn Gln Thr Leu Ala Thr Val  
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 Thr Leu Gln Asn Tyr Phe Arg Leu Tyr Thr Lys Leu Ala Gly Met Thr  
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 Gly Thr Ala Glu Thr Glu Ala Ala Glu Leu Asn Gln Ile Tyr Lys Leu  
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Asp Val Ile Ala Ile Pro Thr Asn Arg Pro Asn Gln Arg Glu Asp Leu  
 145 150 155 160  
 Thr Asp Leu Val Tyr Lys Thr Gln Glu Ala Lys Phe Ala Ala Val Val  
 165 170 175  
 Asp Asp Ile Ala Glu Arg Thr Glu Lys Gly Gln Pro Val Leu Val Gly  
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 Thr Val Ser Val Glu Arg Ser Glu Tyr Leu Ser Gln Leu Leu Thr Lys  
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 Arg Gly Ile Lys His Asn Val Leu Asn Ala Lys His His Glu Gln Glu  
 210 215 220  
 Ala Gln Ile Val Ala Gln Ala Gly Leu Pro Gly Ala Val Thr Val Ala  
 225 230 235 240  
 Thr Asn Met Ala Gly Arg Gly Thr Asp Ile Val Leu Gly Gly Asn Pro  
 245 250 255  
 Glu Ile Leu Leu Asp Ile Lys Leu Arg Glu Arg Gly Leu Asp Pro Phe  
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 Met Lys Gln Arg Cys Glu Glu Arg Gly Asp Lys Val Arg Glu Ala Gly  
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 Pro Ile Glu Ser Lys Thr Val Thr Asn Ser Ile Lys Gly Ala Gln Ala  
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 Gln Val Glu Asn Gln Asn Phe Glu Met Arg Lys Asn Val Leu Lys Tyr  
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 Asp Glu Val Met Asn Glu Gln Arg Lys Val Ile Tyr Ser Glu Arg Arg  
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 Glu Glu Thr Val Ser Ala Tyr Val Asp Gly Ala Thr Ala Asn Gly Tyr  
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 Tyr Asp Pro Ser Ile Asn Trp Thr Asp Leu Val Glu Gly Ser Glu Tyr

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Gly Lys Pro Gly Glu Leu Ser Ala Glu Asp Leu Arg Thr Ala Leu Val						
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Asn Asp Ala His Ala Glu Tyr Ala Lys Leu Glu Glu Ala Val Ser Ala						
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Ile Gly Gly Glu Ala Gln Ile Arg Asn Ile Glu Arg Met Val Leu Met						
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Pro Val Ile Asp Thr Lys Trp Arg Glu His Leu Tyr Glu Met Asp Tyr						
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Leu Lys Glu Gly Ile Gly Leu Arg Ala Met Ala Gln Arg Asp Pro Leu						
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Val Glu Tyr Gln Lys Glu Gly Gly Asp Met Phe Asn Gly Met Lys Asp						
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Gly Ile Lys Glu Glu Thr Val Arg Gln Leu Phe Leu Ser Ala Ser Ser						
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&lt;210&gt; 503

&lt;211&gt; 832

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(832)

&lt;223&gt; FRXA00124

&lt;400&gt; 503

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Met Thr Lys Asp Val	
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His Tyr Glu Val Asp Glu Arg Lys Lys Thr Val Gly Val Lys Glu Glu	
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Pro Glu His Ser Gln Leu Val Ser Tyr Leu Asn Asn Ala Ile Lys Ala	
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Gln Glu Leu Phe Thr Arg Asp Lys Asp Tyr Ile Val Arg Asn Gly Glu	
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Tyr	Asn	Glu	Gly	Met	His	Gln	Ala	Ile	Glu	Ala	Lys	Glu	Arg	Val	Glu	
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Ile	Lys	Asn	Glu	Asn	Gln	Thr	Leu	Ala	Thr	Val	Thr	Leu	Gln	Asn	Tyr	
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Phe	Arg	Leu	Tyr	Thr	Lys	Leu	Ala	Gly	Met	Thr	Gly	Thr	Ala	Glu	Thr	
		120					125					130				
gaa	gca	gca	gag	ctc	aac	cag	atc	tac	aag	ctc	gac	gtc	atc	gcg	atc	547
Glu	Ala	Ala	Glu	Leu	Asn	Gln	Ile	Tyr	Lys	Leu	Asp	Val	Ile	Ala	Ile	
	135					140					145					
cca	acc	aac	cga	cca	aac	cag	cgc	gaa	gac	ttg	acc	gac	ttg	gtg	tac	595
Pro	Thr	Asn	Arg	Pro	Asn	Gln	Arg	Glu	Asp	Leu	Thr	Asp	Leu	Val	Tyr	
					155					160					165	
aaa	acc	caa	gag	gct	aag	ttc	gca	gca	gtc	gtc	gac	gac	atc	gca	gaa	643
Lys	Thr	Gln	Glu	Ala	Lys	Phe	Ala	Ala	Val	Val	Asp	Asp	Ile	Ala	Glu	
				170					175					180		
cgc	acc	gaa	aag	ggc	caa	cca	gtc	ctc	gtc	ggg	acc	gtc	tcc	gtc	gag	691
Arg	Thr	Glu	Lys	Gly	Gln	Pro	Val	Leu	Val	Gly	Thr	Val	Ser	Val	Glu	
			185					190					195			
cgc	tcc	gaa	tac	ctc	tcc	cag	ctg	ttg	acc	aaa	cga	ggc	atc	aag	cac	739
Arg	Ser	Glu	Tyr	Leu	Ser	Gln	Leu	Leu	Thr	Lys	Arg	Gly	Ile	Lys	His	
		200					205					210				
aac	gtc	ctc	aat	gcg	aag	cac	cac	gag	cag	gaa	gca	cag	atc	gtt	gct	787
Asn	Val	Leu	Asn	Ala	Lys	His	His	Glu	Gln	Glu	Ala	Gln	Ile	Val	Ala	
	215					220					225					
cag	gca	ggg	ctt	cca	ggc	gcc	gtc	acc	gtt	gcc	acc	aac	atg	gcg		832
Gln	Ala	Gly	Leu	Pro	Gly	Ala	Val	Thr	Val	Ala	Thr	Asn	Met	Ala		
	230				235					240						

&lt;210&gt; 504

&lt;211&gt; 244

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 504

Met	Thr	Lys	Asp	Val	His	Tyr	Glu	Val	Asp	Glu	Arg	Lys	Lys	Thr	Val	
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Gly	Val	Lys	Glu	Glu	Gly	Val	Glu	Tyr	Val	Glu	Asp	Gln	Leu	Gly	Ile	
			20					25					30			
Asp	Asn	Leu	Tyr	Ala	Pro	Glu	His	Ser	Gln	Leu	Val	Ser	Tyr	Leu	Asn	
		35					40					45				
Asn	Ala	Ile	Lys	Ala	Gln	Glu	Leu	Phe	Thr	Arg	Asp	Lys	Asp	Tyr	Ile	
	50					55					60					

Val Arg Asn Gly Glu Val Met Ile Val Asp Gly Phe Thr Gly Arg Val  
 65 70 75 80  
 Leu Ala Gly Arg Arg Tyr Asn Glu Gly Met His Gln Ala Ile Glu Ala  
 85 90 95  
 Lys Glu Arg Val Glu Ile Lys Asn Glu Asn Gln Thr Leu Ala Thr Val  
 100 105 110  
 Thr Leu Gln Asn Tyr Phe Arg Leu Tyr Thr Lys Leu Ala Gly Met Thr  
 115 120 125  
 Gly Thr Ala Glu Thr Glu Ala Ala Glu Leu Asn Gln Ile Tyr Lys Leu  
 130 135 140  
 Asp Val Ile Ala Ile Pro Thr Asn Arg Pro Asn Gln Arg Glu Asp Leu  
 145 150 155 160  
 Thr Asp Leu Val Tyr Lys Thr Gln Glu Ala Lys Phe Ala Ala Val Val  
 165 170 175  
 Asp Asp Ile Ala Glu Arg Thr Glu Lys Gly Gln Pro Val Leu Val Gly  
 180 185 190  
 Thr Val Ser Val Glu Arg Ser Glu Tyr Leu Ser Gln Leu Leu Thr Lys  
 195 200 205  
 Arg Gly Ile Lys His Asn Val Leu Asn Ala Lys His His Glu Gln Glu  
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 Ala Gln Ile Val Ala Gln Ala Gly Leu Pro Gly Ala Val Thr Val Ala  
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 Thr Asn Met Ala

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 Glu Ala Gly Gly Leu Tyr Val Leu Gly Thr Glu Arg His Glu Ser Arg  
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 cgc atc gac aac cag ctg cgc ggt cgt tct gca cgt cag ggc gac cca 96  
 Arg Ile Asp Asn Gln Leu Arg Gly Arg Ser Ala Arg Gln Gly Asp Pro  
 20 25 30  
 gga tcc acc cgc ttc tat ctc tct atg cgc gac gac ctg atg gtt cgc 144  
 Gly Ser Thr Arg Phe Tyr Leu Ser Met Arg Asp Asp Leu Met Val Arg  
 35 40 45

ttc gtc ggc cca acc atg gaa aac atg atg aac agg ctc aac gtc cca	192
Phe Val Gly Pro Thr Met Glu Asn Met Met Asn Arg Leu Asn Val Pro	
50 55 60	
gac gat gtg ccc atc gaa tcc aaa acc gtc acc aac tcc atc aag ggc	240
Asp Asp Val Pro Ile Glu Ser Lys Thr Val Thr Asn Ser Ile Lys Gly	
65 70 75 80	
gcc caa gct cag gtg gag aac cag aac ttc gaa atg cgt aag aac gtt	288
Ala Gln Ala Gln Val Glu Asn Gln Asn Phe Glu Met Arg Lys Asn Val	
85 90 95	
ctg aag tac gac gaa gtc atg aac gaa cag cgc aag gtt atc tac agc	336
Leu Lys Tyr Asp Glu Val Met Asn Glu Gln Arg Lys Val Ile Tyr Ser	
100 105 110	
gag cga cgc gaa atc ctc gaa tcc gca gac atc tcc cgc tac atc caa	384
Glu Arg Arg Glu Ile Leu Glu Ser Ala Asp Ile Ser Arg Tyr Ile Gln	
115 120 125	
aac atg atc gaa gaa aca gtc agc gca tac gtc gac ggc gcc acc gcc	432
Asn Met Ile Glu Glu Thr Val Ser Ala Tyr Val Asp Gly Ala Thr Ala	
130 135 140	
aac ggc tac gtc gaa gac tgg gac ctc gac aaa ctc tgg aac gcc ctc	480
Asn Gly Tyr Val Glu Asp Trp Asp Leu Asp Lys Leu Trp Asn Ala Leu	
145 150 155 160	
gaa gcc ctc tac gac cca tcg atc aac tgg acc gac ctc gtc gaa ggc	528
Glu Ala Leu Tyr Asp Pro Ser Ile Asn Trp Thr Asp Leu Val Glu Gly	
165 170 175	
agc gaa tac ggc aaa cca ggg gag ctg tcc gcc gaa gat cta cgc acc	576
Ser Glu Tyr Gly Lys Pro Gly Glu Leu Ser Ala Glu Asp Leu Arg Thr	
180 185 190	
gca ctc gtc aac gac gcc cac gcc gaa tac gca aaa ctc gaa gaa gcc	624
Ala Leu Val Asn Asp Ala His Ala Glu Tyr Ala Lys Leu Glu Glu Ala	
195 200 205	
gta tcc gca atc ggc ggc gaa gca cag atc cgc aac atc gaa cga atg	672
Val Ser Ala Ile Gly Gly Glu Ala Gln Ile Arg Asn Ile Glu Arg Met	
210 215 220	
gtg ctc atg cca gtc atc gac acc aaa tgg cgc gaa cac ctc tac gaa	720
Val Leu Met Pro Val Ile Asp Thr Lys Trp Arg Glu His Leu Tyr Glu	
225 230 235 240	
atg gac tac ctg aaa gaa ggc atc ggc ctg cgc gca atg gca cag cgc	768
Met Asp Tyr Leu Lys Glu Gly Ile Gly Leu Arg Ala Met Ala Gln Arg	
245 250 255	
gac cca ctg gtc gaa tac caa aag gaa ggc ggc gac atg ttc aac ggc	816
Asp Pro Leu Val Glu Tyr Gln Lys Glu Gly Gly Asp Met Phe Asn Gly	
260 265 270	
atg aaa gac ggc atc aag gaa gaa acc gtc cgc cag ctc ttc ctc tcc	864
Met Lys Asp Gly Ile Lys Glu Glu Thr Val Arg Gln Leu Phe Leu Ser	
275 280 285	
gca agc agt tca tca agc aag acg cgg aag tcg ctg act aac tca gaa	912

Ala Ser Ser Ser Ser Ser Lys Thr Arg Lys Ser Leu Thr Asn Ser Glu  
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ccc tgaaattcag catccgccac atg  
 Pro  
 305

938

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 <212> PRT  
 <213> Corynebacterium glutamicum

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 Arg Ile Asp Asn Gln Leu Arg Gly Arg Ser Ala Arg Gln Gly Asp Pro  
 20 25 30  
 Gly Ser Thr Arg Phe Tyr Leu Ser Met Arg Asp Asp Leu Met Val Arg  
 35 40 45  
 Phe Val Gly Pro Thr Met Glu Asn Met Met Asn Arg Leu Asn Val Pro  
 50 55 60  
 Asp Asp Val Pro Ile Glu Ser Lys Thr Val Thr Asn Ser Ile Lys Gly  
 65 70 75 80  
 Ala Gln Ala Gln Val Glu Asn Gln Asn Phe Glu Met Arg Lys Asn Val  
 85 90 95  
 Leu Lys Tyr Asp Glu Val Met Asn Glu Gln Arg Lys Val Ile Tyr Ser  
 100 105 110  
 Glu Arg Arg Glu Ile Leu Glu Ser Ala Asp Ile Ser Arg Tyr Ile Gln  
 115 120 125  
 Asn Met Ile Glu Glu Thr Val Ser Ala Tyr Val Asp Gly Ala Thr Ala  
 130 135 140  
 Asn Gly Tyr Val Glu Asp Trp Asp Leu Asp Lys Leu Trp Asn Ala Leu  
 145 150 155 160  
 Glu Ala Leu Tyr Asp Pro Ser Ile Asn Trp Thr Asp Leu Val Glu Gly  
 165 170 175  
 Ser Glu Tyr Gly Lys Pro Gly Glu Leu Ser Ala Glu Asp Leu Arg Thr  
 180 185 190  
 Ala Leu Val Asn Asp Ala His Ala Glu Tyr Ala Lys Leu Glu Glu Ala  
 195 200 205  
 Val Ser Ala Ile Gly Gly Glu Ala Gln Ile Arg Asn Ile Glu Arg Met  
 210 215 220  
 Val Leu Met Pro Val Ile Asp Thr Lys Trp Arg Glu His Leu Tyr Glu  
 225 230 235 240  
 Met Asp Tyr Leu Lys Glu Gly Ile Gly Leu Arg Ala Met Ala Gln Arg  
 245 250 255

Asp Pro Leu Val Glu Tyr Gln Lys Glu Gly Gly Asp Met Phe Asn Gly  
260 265 270

Met Lys Asp Gly Ile Lys Glu Glu Thr Val Arg Gln Leu Phe Leu Ser  
275 280 285

Ala Ser Ser Ser Ser Ser Lys Thr Arg Lys Ser Leu Thr Asn Ser Glu  
290 295 300

Pro  
305

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<211> 888

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<223> RXA00125

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gttatcattt ccgtatcgct atttataagg acgactgctc gtg ttt gga ttg tcc 115  
Val Phe Gly Leu Ser  
1 5

aag gtg ctc cgc gtc ggc gaa ggc cgt gcc gtg aag cga ctt cac aag 163  
Lys Val Leu Arg Val Gly Glu Gly Arg Ala Val Lys Arg Leu His Lys  
10 15 20

atc gct gac cag gtt atc gcg ctt gaa gat aag ttc gcc aac cta acc 211  
Ile Ala Asp Gln Val Ile Ala Leu Glu Asp Lys Phe Ala Asn Leu Thr  
25 30 35

gat gag gag ctc aag gca aaa aca gcc gag ttc aaa gaa cgc atc gct 259  
Asp Glu Glu Leu Lys Ala Lys Thr Ala Glu Phe Lys Glu Arg Ile Ala  
40 45 50

ggc ggt gaa gga ctc gac gaa atc ttc ctc gaa gcg ttc gca aca gcc 307  
Gly Gly Glu Gly Leu Asp Glu Ile Phe Leu Glu Ala Phe Ala Thr Ala  
55 60 65

cgt gaa gca gct tgg cgt gtg ctc ggc cag aag cac tac cat gta caa 355  
Arg Glu Ala Ala Trp Arg Val Leu Gly Gln Lys His Tyr His Val Gln  
70 75 80 85

atc atg ggt ggc gca gcg ctg cac ttt ggc aac gtc gcc gaa atg cgc 403  
Ile Met Gly Gly Ala Ala Leu His Phe Gly Asn Val Ala Glu Met Arg  
90 95 100

acc ggc gaa ggc aaa acc ctc acc tgc gtg ctt cca gca tat ttg aac 451  
Thr Gly Glu Gly Lys Thr Leu Thr Cys Val Leu Pro Ala Tyr Leu Asn  
105 110 115

gca ctt gaa gga aaa ggc gtc cac gtt gtc acc gtc aat gat tac cta 499  
Ala Leu Glu Gly Lys Gly Val His Val Val Thr Val Asn Asp Tyr Leu

120	125	130	
gca aaa cgt gac gca gaa atg atg ggc cgt gtg cac cgc tac tta ggc			547
Ala Lys Arg Asp Ala Glu Met Met Gly Arg Val His Arg Tyr Leu Gly			
135	140	145	
ctc gaa gtg gga gta atc ctc tct gac atg cgc cca gac gag cgc cgc			595
Leu Glu Val Gly Val Ile Leu Ser Asp Met Arg Pro Asp Glu Arg Arg			
150	155	160	165
gaa gcc tac gct gcc gac att acc tac ggc acc aac aac gaa ctc ggc			643
Glu Ala Tyr Ala Ala Asp Ile Thr Tyr Gly Thr Asn Asn Glu Leu Gly			
	170	175	180
ttc gac tac ctg cgc gac aac atg gca cgc tcc cta agc gac ctc gtg			691
Phe Asp Tyr Leu Arg Asp Asn Met Ala Arg Ser Leu Ser Asp Leu Val			
	185	190	195
cag cgt gga cac aac tac gcc att gtc gac gaa gta gac tcc atc ctc			739
Gln Arg Gly His Asn Tyr Ala Ile Val Asp Glu Val Asp Ser Ile Leu			
	200	205	210
atc gac gaa gcc cgc acc cca ctg att atc tcc ggg acc agt aga cgg			787
Ile Asp Glu Ala Arg Thr Pro Leu Ile Ile Ser Gly Thr Ser Arg Arg			
	215	220	225
cac atc gca gtt cta caa cgt ctt cgc aca gat cgt ccc acg cat gac			835
His Ile Ala Val Leu Gln Arg Leu Arg Thr Asp Arg Pro Thr His Asp			
230	235	240	245
caa gga cgt tca cta cga agt cga cga acg taaaaagacc gtcggtgtga aag			888
Gln Gly Arg Ser Leu Arg Ser Arg Arg Thr			
	250	255	

&lt;210&gt; 508

&lt;211&gt; 255

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 508

Val Phe Gly Leu Ser Lys Val Leu Arg Val Gly Glu Gly Arg Ala Val
1 5 10 15

Lys Arg Leu His Lys Ile Ala Asp Gln Val Ile Ala Leu Glu Asp Lys
20 25 30

Phe Ala Asn Leu Thr Asp Glu Glu Leu Lys Ala Lys Thr Ala Glu Phe
35 40 45

Lys Glu Arg Ile Ala Gly Gly Glu Gly Leu Asp Glu Ile Phe Leu Glu
50 55 60

Ala Phe Ala Thr Ala Arg Glu Ala Ala Trp Arg Val Leu Gly Gln Lys
65 70 75 80

His Tyr His Val Gln Ile Met Gly Gly Ala Ala Leu His Phe Gly Asn
85 90 95

Val Ala Glu Met Arg Thr Gly Glu Gly Lys Thr Leu Thr Cys Val Leu
100 105 110

Pro Ala Tyr Leu Asn Ala Leu Glu Gly Lys Gly Val His Val Val Thr  
 115 120 125

Val Asn Asp Tyr Leu Ala Lys Arg Asp Ala Glu Met Met Gly Arg Val  
 130 135 140

His Arg Tyr Leu Gly Leu Glu Val Gly Val Ile Leu Ser Asp Met Arg  
 145 150 155 160

Pro Asp Glu Arg Arg Glu Ala Tyr Ala Ala Asp Ile Thr Tyr Gly Thr  
 165 170 175

Asn Asn Glu Leu Gly Phe Asp Tyr Leu Arg Asp Asn Met Ala Arg Ser  
 180 185 190

Leu Ser Asp Leu Val Gln Arg Gly His Asn Tyr Ala Ile Val Asp Glu  
 195 200 205

Val Asp Ser Ile Leu Ile Asp Glu Ala Arg Thr Pro Leu Ile Ile Ser  
 210 215 220

Gly Thr Ser Arg Arg His Ile Ala Val Leu Gln Arg Leu Arg Thr Asp  
 225 230 235 240

Arg Pro Thr His Asp Gln Gly Arg Ser Leu Arg Ser Arg Arg Thr  
 245 250 255

<210> 509  
 <211> 1443  
 <212> DNA  
 <213> Corynebacterium glutamicum

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 <223> RXA00687

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aaatatgtgg gtttaagtgc tgaggaggcc aggaggataa gtg tcc gcc att att 115  
 Val Ser Ala Ile Ile  
 1 5

cag gca ttc aag gac gcc gat ctg cgt aag aag att ttc ttc act atc 163  
 Gln Ala Phe Lys Asp Ala Asp Leu Arg Lys Lys Ile Phe Phe Thr Ile  
 10 15 20

gca atg atc gtt cta tac cgc atc ggt gcg cag atc cct tcc ccg gga 211  
 Ala Met Ile Val Leu Tyr Arg Ile Gly Ala Gln Ile Pro Ser Pro Gly  
 25 30 35

gtt gac tac gca acg att agt ggt cgt ctg cgt gac ttg act cag gat 259  
 Val Asp Tyr Ala Thr Ile Ser Gly Arg Leu Arg Asp Leu Thr Gln Asp  
 40 45 50

cag tca agc gtt tat tcg ctg att aac ctg ttt tcc ggt gga gcg ctg 307  
 Gln Ser Ser Val Tyr Ser Leu Ile Asn Leu Phe Ser Gly Gly Ala Leu  
 55 60 65

ttg cag ctg tcc att ttt gct att ggt atc atg ccg tac atc acg gcg	355
Leu Gln Leu Ser Ile Phe Ala Ile Gly Ile Met Pro Tyr Ile Thr Ala	
70 75 80 85	
tct att atc gtg cag ctg ctg act gtg gtt att cca cac ttt gag gag	403
Ser Ile Ile Val Gln Leu Leu Thr Val Val Ile Pro His Phe Glu Glu	
90 95 100	
ttg aag aag gaa ggc cag tct ggc cag gcc aag atg atg cag tac acc	451
Leu Lys Lys Glu Gly Gln Ser Gly Gln Ala Lys Met Met Gln Tyr Thr	
105 110 115	
agg tac tta acg gtt gct ttg gcg ttg ctg cag tct tca ggc att gtc	499
Arg Tyr Leu Thr Val Ala Leu Ala Leu Leu Gln Ser Ser Gly Ile Val	
120 125 130	
gcg ttg gcg gac cgt gag cag ctg ctt ggc gca ggt att cgt gtg ctg	547
Ala Leu Ala Asp Arg Glu Gln Leu Leu Gly Ala Gly Ile Arg Val Leu	
135 140 145	
tcg gct gat cgc aac ttc ttc gat ctc att gtt ttg gtc atc acc atg	595
Ser Ala Asp Arg Asn Phe Phe Asp Leu Ile Val Leu Val Ile Thr Met	
150 155 160 165	
act gca ggt gcg gtg ctt gtg atg tgg atg ggt gag ctc atc acg gaa	643
Thr Ala Gly Ala Val Leu Val Met Trp Met Gly Glu Leu Ile Thr Glu	
170 175 180	
aag ggc gtg ggc aat ggt atg tcg ttg ctg att ttc gct ggt atc gca	691
Lys Gly Val Gly Asn Gly Met Ser Leu Leu Ile Phe Ala Gly Ile Ala	
185 190 195	
act cgc ctc cca act gat ggc atg aac att ctg ggt aac tcc ggc ggc	739
Thr Arg Leu Pro Thr Asp Gly Met Asn Ile Leu Gly Asn Ser Gly Gly	
200 205 210	
gtg gtt ttc gct gtt gtt ctg gct tcc gtt ctg atc ctg gtc att ggt	787
Val Val Phe Ala Val Val Leu Ala Ser Val Leu Ile Leu Val Ile Gly	
215 220 225	
gtt gta ttc gtt gag cag ggc cag cgt cgt att cca gtg cag tac gca	835
Val Val Phe Val Glu Gln Gly Gln Arg Arg Ile Pro Val Gln Tyr Ala	
230 235 240 245	
aag cgc atg gtg gga cgt cgc cag tac ggt ggt tct tcc act tac ctg	883
Lys Arg Met Val Gly Arg Arg Gln Tyr Gly Gly Ser Ser Thr Tyr Leu	
250 255 260	
cca ttg aag gtc aac caa gct ggt gtt atc cca gtg atc ttc gcg tct	931
Pro Leu Lys Val Asn Gln Ala Gly Val Ile Pro Val Ile Phe Ala Ser	
265 270 275	
tcg ctg att tac atg cca gtg ctg att act cag atc gtg aac tct ggt	979
Ser Leu Ile Tyr Met Pro Val Leu Ile Thr Gln Ile Val Asn Ser Gly	
280 285 290	
tcg ctg gaa gtg tct gat aac tgg tgg cag cgc aac atc att gcg cac	1027
Ser Leu Glu Val Ser Asp Asn Trp Trp Gln Arg Asn Ile Ile Ala His	
295 300 305	

ctg cag acg cct tct tcc tgg cag tac att gtt ttg tac ttt gca ctg 1075  
 Leu Gln Thr Pro Ser Ser Trp Gln Tyr Ile Val Leu Tyr Phe Ala Leu 325  
 310 315 320

acc atc ttc ttc tct tac ttc tat gtt tcc gtt cag tat gat cca gct 1123  
 Thr Ile Phe Phe Ser Tyr Phe Tyr Val Ser Val Gln Tyr Asp Pro Ala 340  
 330 335

gag cag gct gaa aac atg aag aag tac ggt gga ttt atc cct ggt att 1171  
 Glu Gln Ala Glu Asn Met Lys Lys Tyr Gly Gly Phe Ile Pro Gly Ile 355  
 345 350

cgt ccg ggc cgc ccg act gct gag tac ttg gga ttc gtc atg aac cgc 1219  
 Arg Pro Gly Arg Pro Thr Ala Glu Tyr Leu Gly Phe Val Met Asn Arg 370  
 360 365

ctg ctg ttt gtt ggt tcc ctg tac ctg gct gtc att gct gtg ctg cca 1267  
 Leu Leu Phe Val Gly Ser Leu Tyr Leu Ala Val Ile Ala Val Leu Pro 385  
 375 380

aac att atg ctg gat cta ggt gtt gac gcc ggt tcg gcc gga gca act 1315  
 Asn Ile Met Leu Asp Leu Gly Val Asp Ala Gly Ser Ala Gly Ala Thr 405  
 390 395 400

cca ttc ggc gga acc gca atc ttg att ctt gta tct gtt gca ctg acc 1363  
 Pro Phe Gly Gly Thr Ala Ile Leu Ile Leu Val Ser Val Ala Leu Thr 420  
 410 415

aca gtg aag cag att gag agc cag ctc ctg caa agc aac tac gaa gga 1411  
 Thr Val Lys Gln Ile Glu Ser Gln Leu Leu Gln Ser Asn Tyr Glu Gly 435  
 425 430

ctt cta aaa taatgcgact cgtactcctc gga 1443  
 Leu Leu Lys 440

&lt;210&gt; 510

&lt;211&gt; 440

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 510

Val Ser Ala Ile Ile Gln Ala Phe Lys Asp Ala Asp Leu Arg Lys Lys  
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Ile Phe Phe Thr Ile Ala Met Ile Val Leu Tyr Arg Ile Gly Ala Gln  
 20 25 30

Ile Pro Ser Pro Gly Val Asp Tyr Ala Thr Ile Ser Gly Arg Leu Arg  
 35 40 45

Asp Leu Thr Gln Asp Gln Ser Ser Val Tyr Ser Leu Ile Asn Leu Phe  
 50 55 60

Ser Gly Gly Ala Leu Leu Gln Leu Ser Ile Phe Ala Ile Gly Ile Met  
 65 70 75 80

Pro Tyr Ile Thr Ala Ser Ile Ile Val Gln Leu Leu Thr Val Val Ile  
 85 90 95

Pro His Phe Glu Glu Leu Lys Lys Glu Gly Gln Ser Gly Gln Ala Lys  
 100 105 110  
 Met Met Gln Tyr Thr Arg Tyr Leu Thr Val Ala Leu Ala Leu Leu Gln  
 115 120 125  
 Ser Ser Gly Ile Val Ala Leu Ala Asp Arg Glu Gln Leu Leu Gly Ala  
 130 135 140  
 Gly Ile Arg Val Leu Ser Ala Asp Arg Asn Phe Phe Asp Leu Ile Val  
 145 150 155 160  
 Leu Val Ile Thr Met Thr Ala Gly Ala Val Leu Val Met Trp Met Gly  
 165 170 175  
 Glu Leu Ile Thr Glu Lys Gly Val Gly Asn Gly Met Ser Leu Leu Ile  
 180 185 190  
 Phe Ala Gly Ile Ala Thr Arg Leu Pro Thr Asp Gly Met Asn Ile Leu  
 195 200 205  
 Gly Asn Ser Gly Gly Val Val Phe Ala Val Val Leu Ala Ser Val Leu  
 210 215 220  
 Ile Leu Val Ile Gly Val Val Phe Val Glu Gln Gly Gln Arg Arg Ile  
 225 230 235 240  
 Pro Val Gln Tyr Ala Lys Arg Met Val Gly Arg Arg Gln Tyr Gly Gly  
 245 250 255  
 Ser Ser Thr Tyr Leu Pro Leu Lys Val Asn Gln Ala Gly Val Ile Pro  
 260 265 270  
 Val Ile Phe Ala Ser Ser Leu Ile Tyr Met Pro Val Leu Ile Thr Gln  
 275 280 285  
 Ile Val Asn Ser Gly Ser Leu Glu Val Ser Asp Asn Trp Trp Gln Arg  
 290 295 300  
 Asn Ile Ile Ala His Leu Gln Thr Pro Ser Ser Trp Gln Tyr Ile Val  
 305 310 315 320  
 Leu Tyr Phe Ala Leu Thr Ile Phe Phe Ser Tyr Phe Tyr Val Ser Val  
 325 330 335  
 Gln Tyr Asp Pro Ala Glu Gln Ala Glu Asn Met Lys Lys Tyr Gly Gly  
 340 345 350  
 Phe Ile Pro Gly Ile Arg Pro Gly Arg Pro Thr Ala Glu Tyr Leu Gly  
 355 360 365  
 Phe Val Met Asn Arg Leu Leu Phe Val Gly Ser Leu Tyr Leu Ala Val  
 370 375 380  
 Ile Ala Val Leu Pro Asn Ile Met Leu Asp Leu Gly Val Asp Ala Gly  
 385 390 395 400  
 Ser Ala Gly Ala Thr Pro Phe Gly Gly Thr Ala Ile Leu Ile Leu Val  
 405 410 415  
 Ser Val Ala Leu Thr Thr Val Lys Gln Ile Glu Ser Gln Leu Leu Gln

420

425

430

Ser Asn Tyr Glu Gly Leu Leu Lys  
 435 440

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 <223> RXA02260

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 Met Ala Leu Thr Leu  
 1 5  
 caa atc atc ctc gtc gtc gcc agc ctg ctc atg acg gtt ttc gtc ttg 163  
 Gln Ile Ile Leu Val Val Ala Ser Leu Leu Met Thr Val Phe Val Leu  
 10 15 20  
 ctg cac aag ggc aaa ggc ggc gga ctc tcc agc ctc ttc ggt ggc ggt 211  
 Leu His Lys Gly Lys Gly Gly Gly Leu Ser Ser Leu Phe Gly Gly Gly  
 25 30 35  
 gtg cag tcc aat ctt tcg ggc tcc act gtt gtt gaa aag aac ctg gat 259  
 Val Gln Ser Asn Leu Ser Gly Ser Thr Val Val Glu Lys Asn Leu Asp  
 40 45 50  
 cgc gtc acc att ttg gtt gcc gtt atc tgg att gtg tgc att gtc gca 307  
 Arg Val Thr Ile Leu Val Ala Val Ile Trp Ile Val Cys Ile Val Ala  
 55 60 65  
 ctc aac ctc atc cag act tat tca taagacacga gcttaaaaag agc 354  
 Leu Asn Leu Ile Gln Thr Tyr Ser  
 70 75

<210> 512  
 <211> 77  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 512  
 Met Ala Leu Thr Leu Gln Ile Ile Leu Val Val Ala Ser Leu Leu Met  
 1 5 10 15  
 Thr Val Phe Val Leu Leu His Lys Gly Lys Gly Gly Gly Leu Ser Ser  
 20 25 30  
 Leu Phe Gly Gly Gly Val Gln Ser Asn Leu Ser Gly Ser Thr Val Val  
 35 40 45  
 Glu Lys Asn Leu Asp Arg Val Thr Ile Leu Val Ala Val Ile Trp Ile  
 50 55 60

Val Cys Ile Val Ala Leu Asn Leu Ile Gln Thr Tyr Ser  
 65 70 75

<210> 513  
 <211> 819  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(796)  
 <223> RXN00046

<400> 513  
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 acctaaaacg ctgttctcaa cacaggagtt tccttaaata atg gac tta aat act 115  
 Met Asp Leu Asn Thr 5  
 caa cgc tca aag ctc tac gca cag ctt caa ggc cag ctc att gtt tcc 163  
 Gln Arg Ser Lys Leu Tyr Ala Gln Leu Gln Gly Gln Leu Ile Val Ser 20  
 10 15  
 gtg caa gct ccc gac ggc cat gcc atg cga gat acc cat acg ctc acc 211  
 Val Gln Ala Pro Asp Gly His Ala Met Arg Asp Thr His Thr Leu Thr 35  
 25 30  
 cat gtg gcc gca gcc tgt gtc gat ggc ggt gct cct gcc att cgc tgt 259  
 His Val Ala Ala Ala Cys Val Asp Gly Gly Ala Pro Ala Ile Arg Cys 50  
 40 45  
 ggc ggt tac ggc ggt ttg gaa gat atc cgt tca atc tcc aac cgt gtc 307  
 Gly Gly Tyr Gly Gly Leu Glu Asp Ile Arg Ser Ile Ser Asn Arg Val 65  
 55 60  
 gac gtt ccc gtt ttc gga ctc acc aaa gaa ggc tcc gaa gga gtt tac 355  
 Asp Val Pro Val Phe Gly Leu Thr Lys Glu Gly Ser Glu Gly Val Tyr 85  
 70 75 80  
 atc acc cca acc agg gat tcc gtt cga gca gtg gca gaa tcc ggc gcc 403  
 Ile Thr Pro Thr Arg Asp Ser Val Arg Ala Val Ala Glu Ser Gly Ala 100  
 90 95  
 act gta gtc tgc gcg gat gca act ttc cga cct agg cct gac ggc tcc 451  
 Thr Val Val Cys Ala Asp Ala Thr Phe Arg Pro Arg Pro Asp Gly Ser 115  
 105 110  
 acc ttt gca gag ctg gtc act gtt gcc cac gat tcc gga att ctc atc 499  
 Thr Phe Ala Glu Leu Val Thr Val Ala His Asp Ser Gly Ile Leu Ile 130  
 120 125  
 atg gcg gac tgc gca act ccc gaa gaa gtt ctc agt gcg cat aag gct 547  
 Met Ala Asp Cys Ala Thr Pro Glu Glu Val Leu Ser Ala His Lys Ala 145  
 135 140  
 ggc gcg gat ttt gtg tcc acc acg ctt gct gga tac acc gaa cac cgc 595  
 Gly Ala Asp Phe Val Ser Thr Thr Leu Ala Gly Tyr Thr Glu His Arg 165  
 150 155 160

gag aaa aca gtc ggt cca gat ttc gat tgc ctc cgc gaa gca cgt gag 643  
 Glu Lys Thr Val Gly Pro Asp Phe Asp Cys Leu Arg Glu Ala Arg Glu  
 170 175 180  
  
 tta gtt ccc gat gcg ttc ctc att ggc gaa ggt cgc ttc tcc aac cct 691  
 Leu Val Pro Asp Ala Phe Leu Ile Gly Glu Gly Arg Phe Ser Asn Pro  
 185 190 195  
  
 gcg gat gtg gcg cac ggt cgt ctc att ggt gcc aac gcg atc atc gtg 739  
 Ala Asp Val Ala His Gly Arg Leu Ile Gly Ala Asn Ala Ile Ile Val  
 200 205 210  
  
 ggc acc gca atc act gac cct ggt ttc atc act gga cag ttc gcg tca 787  
 Gly Thr Ala Ile Thr Asp Pro Gly Phe Ile Thr Gly Gln Phe Ala Ser  
 215 220 225  
  
 ctg ttg cac tagcacttag tccagcgctg cac 819  
 Leu Leu His  
 230

<210> 514  
 <211> 232  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 514  
 Met Asp Leu Asn Thr Gln Arg Ser Lys Leu Tyr Ala Gln Leu Gln Gly  
 1 5 10 15  
  
 Gln Leu Ile Val Ser Val Gln Ala Pro Asp Gly His Ala Met Arg Asp  
 20 25 30  
  
 Thr His Thr Leu Thr His Val Ala Ala Ala Cys Val Asp Gly Gly Ala  
 35 40 45  
  
 Pro Ala Ile Arg Cys Gly Gly Tyr Gly Gly Leu Glu Asp Ile Arg Ser  
 50 55 60  
  
 Ile Ser Asn Arg Val Asp Val Pro Val Phe Gly Leu Thr Lys Glu Gly  
 65 70 75 80  
  
 Ser Glu Gly Val Tyr Ile Thr Pro Thr Arg Asp Ser Val Arg Ala Val  
 85 90 95  
  
 Ala Glu Ser Gly Ala Thr Val Val Cys Ala Asp Ala Thr Phe Arg Pro  
 100 105 110  
  
 Arg Pro Asp Gly Ser Thr Phe Ala Glu Leu Val Thr Val Ala His Asp  
 115 120 125  
  
 Ser Gly Ile Leu Ile Met Ala Asp Cys Ala Thr Pro Glu Glu Val Leu  
 130 135 140  
  
 Ser Ala His Lys Ala Gly Ala Asp Phe Val Ser Thr Thr Leu Ala Gly  
 145 150 155 160  
  
 Tyr Thr Glu His Arg Glu Lys Thr Val Gly Pro Asp Phe Asp Cys Leu  
 165 170 175

Arg Glu Ala Arg Glu Leu Val Pro Asp Ala Phe Leu Ile Gly Glu Gly  
 180 185 190

Arg Phe Ser Asn Pro Ala Asp Val Ala His Gly Arg Leu Ile Gly Ala  
 195 200 205

Asn Ala Ile Ile Val Gly Thr Ala Ile Thr Asp Pro Gly Phe Ile Thr  
 210 215 220

Gly Gln Phe Ala Ser Leu Leu His  
 225 230

&lt;210&gt; 515

&lt;211&gt; 819

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(796)

&lt;223&gt; FRXA00046

&lt;400&gt; 515

tggtgcccac gcagccgtca tcgcagcagc aaaatatgcc cgcgataacg ccttttaagc 60

acctaaaaacg ctgttctcaa cacaggagtt tccttaaata atg gac tta aat act 115  
 Met Asp Leu Asn Thr  
 1 5

caa cgc tca aag ctc tac gca cag ctt caa ggc cag ctc att gtt tcc 163  
 Gln Arg Ser Lys Leu Tyr Ala Gln Leu Gln Gly Gln Leu Ile Val Ser  
 10 15 20

gtg caa gct ccc gac ggc cat gcc atg cga gat acc cat acg ctc acc 211  
 Val Gln Ala Pro Asp Gly His Ala Met Arg Asp Thr His Thr Leu Thr  
 25 30 35

cat gtg gcc gca gcc tgt gtc gat ggc ggt gct cct gcc att cgc tgt 259  
 His Val Ala Ala Ala Cys Val Asp Gly Gly Ala Pro Ala Ile Arg Cys  
 40 45 50

ggc ggt tac ggc ggt ttg gaa gat atc cgt tca atc tcc aac cgt gtc 307  
 Gly Gly Tyr Gly Gly Leu Glu Asp Ile Arg Ser Ile Ser Asn Arg Val  
 55 60 65

gac gtt ccc gtt ttc gga ctc acc aaa gaa ggc tcc gaa gga gtt tac 355  
 Asp Val Pro Val Phe Gly Leu Thr Lys Glu Gly Ser Glu Gly Val Tyr  
 70 75 80 85

atc acc cca acc agg gat tcc gtt cga gca gtg gca gaa tcc ggc gcc 403  
 Ile Thr Pro Thr Arg Asp Ser Val Arg Ala Val Ala Glu Ser Gly Ala  
 90 95 100

act gta gtc tgc gcg gat gca act ttc cga cct agg cct gac ggc tcc 451  
 Thr Val Val Cys Ala Asp Ala Thr Phe Arg Pro Arg Pro Asp Gly Ser  
 105 110 115

acc ttt gca gag ctg gtc act gtt gcc cac gat tcc gga att ctc atc 499  
 Thr Phe Ala Glu Leu Val Thr Val Ala His Asp Ser Gly Ile Leu Ile  
 120 125 130

atg gcg gac tgc gca act ccc gaa gaa gtt ctc agt gcg cat aag gct 547  
 Met Ala Asp Cys Ala Thr Pro Glu Glu Val Leu Ser Ala His Lys Ala  
 135 140 145  
  
 ggc gcg gat ttt gtg tcc acc acg ctt gct gga tac acc gaa cac cgc 595  
 Gly Ala Asp Phe Val Ser Thr Thr Leu Ala Gly Tyr Thr Glu His Arg  
 150 155 160 165  
  
 gag aaa aca gtc ggt cca gat ttc gat tgc ctc cgc gaa gca cgt gag 643  
 Glu Lys Thr Val Gly Pro Asp Phe Asp Cys Leu Arg Glu Ala Arg Glu  
 170 175 180  
  
 tta gtt ccc gat gcg ttc ctc att ggc gaa ggt cgc ttc tcc aac cct 691  
 Leu Val Pro Asp Ala Phe Leu Ile Gly Glu Gly Arg Phe Ser Asn Pro  
 185 190 195  
  
 gcg gat gtg gcg cac ggt cgt ctc att ggt gcc aac gcg atc atc gtg 739  
 Ala Asp Val Ala His Gly Arg Leu Ile Gly Ala Asn Ala Ile Ile Val  
 200 205 210  
  
 ggc acc gga atc act gac cct ggt ttc atc act gga cag ttc gcg tca 787  
 Gly Thr Gly Ile Thr Asp Pro Gly Phe Ile Thr Gly Gln Phe Ala Ser  
 215 220 225  
  
 ctg ttg cac taacacttag tccaacgctg cac 819  
 Leu Leu His  
 230

&lt;210&gt; 516

&lt;211&gt; 232

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 516

Met Asp Leu Asn Thr Gln Arg Ser Lys Leu Tyr Ala Gln Leu Gln Gly  
 1 5 10 15  
  
 Gln Leu Ile Val Ser Val Gln Ala Pro Asp Gly His Ala Met Arg Asp  
 20 25 30  
  
 Thr His Thr Leu Thr His Val Ala Ala Ala Cys Val Asp Gly Gly Ala  
 35 40 45  
  
 Pro Ala Ile Arg Cys Gly Gly Tyr Gly Gly Leu Glu Asp Ile Arg Ser  
 50 55 60  
  
 Ile Ser Asn Arg Val Asp Val Pro Val Phe Gly Leu Thr Lys Glu Gly  
 65 70 75 80  
  
 Ser Glu Gly Val Tyr Ile Thr Pro Thr Arg Asp Ser Val Arg Ala Val  
 85 90 95  
  
 Ala Glu Ser Gly Ala Thr Val Val Cys Ala Asp Ala Thr Phe Arg Pro  
 100 105 110  
  
 Arg Pro Asp Gly Ser Thr Phe Ala Glu Leu Val Thr Val Ala His Asp  
 115 120 125  
  
 Ser Gly Ile Leu Ile Met Ala Asp Cys Ala Thr Pro Glu Glu Val Leu

130	135	140
Ser Ala His Lys Ala Gly	Ala Asp Phe Val Ser Thr Thr Leu Ala Gly	
145	150	155 160
Tyr Thr Glu His Arg Glu Lys Thr Val Gly Pro Asp Phe Asp Cys Leu		
	165	170 175
Arg Glu Ala Arg Glu Leu Val Pro Asp Ala Phe Leu Ile Gly Glu Gly		
	180	185 190
Arg Phe Ser Asn Pro Ala Asp Val Ala His Gly Arg Leu Ile Gly Ala		
	195	200 205
Asn Ala Ile Ile Val Gly Thr Gly Ile Thr Asp Pro Gly Phe Ile Thr		
	210	215 220
Gly Gln Phe Ala Ser Leu Leu His		
225	230	

<210> 517  
 <211> 1445  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(1422)  
 <223> RXA00753

<400> 517	
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Val Val Asp Gly Val Gly Gly Tyr Thr Glu Gln Glu Val Ala Glu Ile	
1 5 10 15	
cat gag gct atc cgt caa gcc caa gac tct ggt gca cct aat gat gaa	96
His Glu Ala Ile Arg Gln Ala Gln Asp Ser Gly Ala Pro Asn Asp Glu	
20 25 30	
ctt att cct ggt gag atg tgg tca gat aag gtc gag tta ccc tca acg	144
Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val Glu Leu Pro Ser Thr	
35 40 45	
att gat aaa gca gct gct gat gaa gct gag ata gct att gca cag caa	192
Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile Ala Ile Ala Gln Gln	
50 55 60	
cag tcc caa ccc cag gcg aga gga cta gcc gct gct gca gcg tgt cag	240
Gln Ser Gln Pro Gln Ala Arg Gly Leu Ala Ala Ala Ala Ala Cys Gln	
65 70 75 80	
aca ttt tgg ccg tca cct tat caa gtt tgt ggt gct atc tta gag cgc	288
Thr Phe Trp Pro Ser Pro Tyr Gln Val Cys Gly Ala Ile Leu Glu Arg	
85 90 95	
tat atc cag cag ggt gcc cag ttt ggg tgg atg ttg ttg ctt act gaa	336
Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met Leu Leu Leu Thr Glu	
100 105 110	
ggc caa gcg ctt aac cct gat ggt cag gga tat cgt cag cgg ttt atg	384

Gly	Gln	Ala	Leu	Asn	Pro	Asp	Gly	Gln	Gly	Tyr	Arg	Gln	Arg	Phe	Met	
		115					120					125				
aat	ggg	ttt	atc	tat	tgg	cat	cct	tct	act	ggg	gcg	cac	gcg	gtt	aat	432
Asn	Gly	Phe	Ile	Tyr	Trp	His	Pro	Ser	Thr	Gly	Ala	His	Ala	Val	Asn	
	130					135					140					
aat	tac	agt	gca	caa	gtc	tgg	gag	cgt	aac	ggg	tgg	gag	tct	ggg	tgg	480
Asn	Tyr	Ser	Ala	Gln	Val	Trp	Glu	Arg	Asn	Gly	Trp	Glu	Ser	Gly	Trp	
	145				150					155					160	
atg	ggg	tat	ccc	act	ggg	ggg	gaa	gtc	cct	gtg	tct	ggg	tct	aat	ccg	528
Met	Gly	Tyr	Pro	Thr	Gly	Gly	Glu	Val	Pro	Val	Ser	Gly	Ser	Asn	Pro	
				165					170					175		
att	gat	ggg	gag	ttg	agt	ggg	tgg	gtg	caa	acc	ttc	caa	ggg	ggg	cga	576
Ile	Asp	Gly	Glu	Leu	Ser	Gly	Trp	Val	Gln	Thr	Phe	Gln	Gly	Gly	Arg	
			180					185					190			
gtg	tat	cgc	agt	ccg	gta	ttg	gac	ggg	ttc	cag	gtg	gcc	agt	att	aat	624
Val	Tyr	Arg	Ser	Pro	Val	Leu	Asp	Gly	Phe	Gln	Val	Ala	Ser	Ile	Asn	
		195					200					205				
ggg	ctg	atc	ttg	gat	aaa	tgg	ctt	gaa	ttg	ggg	ggg	cct	gat	agt	gac	672
Gly	Leu	Ile	Leu	Asp	Lys	Trp	Leu	Glu	Leu	Gly	Gly	Pro	Asp	Ser	Asp	
	210					215					220					
ctt	ggg	ttt	ccc	att	gcg	gat	gag	gct	gtg	aca	gct	gac	ggg	gtg	ggg	720
Leu	Gly	Phe	Pro	Ile	Ala	Asp	Glu	Ala	Val	Thr	Ala	Asp	Gly	Val	Gly	
	225				230				235					240		
aga	ttt	tct	gtt	ttc	cag	aac	gga	gtt	gtc	tac	tgg	cat	ccg	caa	cac	768
Arg	Phe	Ser	Val	Phe	Gln	Asn	Gly	Val	Val	Tyr	Trp	His	Pro	Gln	His	
				245					250					255		
gga	gct	cac	cct	ata	tta	ggg	aat	ata	tac	agt	atc	tgg	aga	gaa	gaa	816
Gly	Ala	His	Pro	Ile	Leu	Gly	Asn	Ile	Tyr	Ser	Ile	Trp	Arg	Glu	Glu	
			260					265					270			
gga	gct	gag	agt	ggg	gaa	ttc	ggg	tac	cct	atc	ggc	gat	cca	gaa	aag	864
Gly	Ala	Glu	Ser	Gly	Glu	Phe	Gly	Tyr	Pro	Ile	Gly	Asp	Pro	Glu	Lys	
		275					280					285				
tat	aca	gaa	aac	atg	gct	aat	cag	gta	ttc	gaa	aaa	ggc	gaa	ctt	gca	912
Tyr	Thr	Glu	Asn	Met	Ala	Asn	Gln	Val	Phe	Glu	Lys	Gly	Glu	Leu	Ala	
	290					295					300					
gct	aac	cta	tac	ccc	aat	cct	ctt	gag	gct	ttt	att	gag	ttt	tta	ccc	960
Ala	Asn	Leu	Tyr	Pro	Asn	Pro	Leu	Glu	Ala	Phe	Ile	Glu	Phe	Leu	Pro	
	305				310					315					320	
ttt	gct	aat	ctt	gag	gaa	gca	ata	gag	tat	ttt	gag	aac	gga	ttg	tca	1008
Phe	Ala	Asn	Leu	Glu	Glu	Ala	Ile	Glu	Tyr	Phe	Glu	Asn	Gly	Leu	Ser	
				325					330					335		
aat	tct	cgt	gta	gag	gcg	aat	tca	ctt	aac	gcc	aag	aaa	gat	tcg	att	1056
Asn	Ser	Arg	Val	Glu	Ala	Asn	Ser	Leu	Asn	Ala	Lys	Lys	Asp	Ser	Ile	
			340					345					350			
caa	tgt	caa	tcg	caa	tcc	gct	aac	att	cat	gtg	aga	acg	aag	agt	gac	1104
Gln	Cys	Gln	Ser	Gln	Ser	Ala	Asn	Ile	His	Val	Arg	Thr	Lys	Ser	Asp	

355	360	365	
gga gtc ggg att agg gtt cca aag att ggg ttt aag gct agg atg gat			1152
Gly Val Gly Ile Arg Val Pro Lys Ile Gly Phe Lys Ala Arg Met Asp			
370	375	380	
tgc gac ctt cct gga act gtc tca gat gta gtg ggg tat gga tgg att			1200
Cys Asp Leu Pro Gly Thr Val Ser Asp Val Val Gly Tyr Gly Trp Ile			
385	390	395	400
tac tac gac tat tgg gga cga tgg gct caa gca gca tat gca caa caa			1248
Tyr Tyr Asp Tyr Trp Gly Arg Trp Ala Gln Ala Ala Tyr Ala Gln Gln			
405	410	415	
ttc ttc ggt aat agg aat tct gtt gtg caa acc aat tta gag gcg ggt			1296
Phe Phe Gly Asn Arg Asn Ser Val Val Gln Thr Asn Leu Glu Ala Gly			
420	425	430	
tgc agc ggg gag aag aat aca tta ttt tgg ggt act tca tat ttt cag			1344
Cys Ser Gly Glu Lys Asn Thr Leu Phe Trp Gly Thr Ser Tyr Phe Gln			
435	440	445	
gtg act tat gaa ggt cag ccg tat ttc ggt cag tca gca act aac tac			1392
Val Thr Tyr Glu Gly Gln Pro Tyr Phe Gly Gln Ser Ala Thr Asn Tyr			
450	455	460	
gct tat ctt ccg tgt acg ata gac cgt agt taacataagg aatggaatag gag			1445
Ala Tyr Leu Pro Cys Thr Ile Asp Arg Ser			
465	470		

&lt;210&gt; 518

&lt;211&gt; 474

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 518

Val Val Asp Gly Val Gly Gly Tyr Thr Glu Gln Glu Val Ala Glu Ile	
1	15
His Glu Ala Ile Arg Gln Ala Gln Asp Ser Gly Ala Pro Asn Asp Glu	
20	30
Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val Glu Leu Pro Ser Thr	
35	45
Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile Ala Ile Ala Gln Gln	
50	60
Gln Ser Gln Pro Gln Ala Arg Gly Leu Ala Ala Ala Ala Cys Gln	
65	80
Thr Phe Trp Pro Ser Pro Tyr Gln Val Cys Gly Ala Ile Leu Glu Arg	
85	95
Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met Leu Leu Leu Thr Glu	
100	110
Gly Gln Ala Leu Asn Pro Asp Gly Gln Gly Tyr Arg Gln Arg Phe Met	
115	125

Asn Gly Phe Ile Tyr Trp His Pro Ser Thr Gly Ala His Ala Val Asn  
 130 135 140  
 Asn Tyr Ser Ala Gln Val Trp Glu Arg Asn Gly Trp Glu Ser Gly Trp  
 145 150 155 160  
 Met Gly Tyr Pro Thr Gly Gly Glu Val Pro Val Ser Gly Ser Asn Pro  
 165 170 175  
 Ile Asp Gly Glu Leu Ser Gly Trp Val Gln Thr Phe Gln Gly Gly Arg  
 180 185 190  
 Val Tyr Arg Ser Pro Val Leu Asp Gly Phe Gln Val Ala Ser Ile Asn  
 195 200 205  
 Gly Leu Ile Leu Asp Lys Trp Leu Glu Leu Gly Gly Pro Asp Ser Asp  
 210 215 220  
 Leu Gly Phe Pro Ile Ala Asp Glu Ala Val Thr Ala Asp Gly Val Gly  
 225 230 235 240  
 Arg Phe Ser Val Phe Gln Asn Gly Val Val Tyr Trp His Pro Gln His  
 245 250 255  
 Gly Ala His Pro Ile Leu Gly Asn Ile Tyr Ser Ile Trp Arg Glu Glu  
 260 265 270  
 Gly Ala Glu Ser Gly Glu Phe Gly Tyr Pro Ile Gly Asp Pro Glu Lys  
 275 280 285  
 Tyr Thr Glu Asn Met Ala Asn Gln Val Phe Glu Lys Gly Glu Leu Ala  
 290 295 300  
 Ala Asn Leu Tyr Pro Asn Pro Leu Glu Ala Phe Ile Glu Phe Leu Pro  
 305 310 315 320  
 Phe Ala Asn Leu Glu Glu Ala Ile Glu Tyr Phe Glu Asn Gly Leu Ser  
 325 330 335  
 Asn Ser Arg Val Glu Ala Asn Ser Leu Asn Ala Lys Lys Asp Ser Ile  
 340 345 350  
 Gln Cys Gln Ser Gln Ser Ala Asn Ile His Val Arg Thr Lys Ser Asp  
 355 360 365  
 Gly Val Gly Ile Arg Val Pro Lys Ile Gly Phe Lys Ala Arg Met Asp  
 370 375 380  
 Cys Asp Leu Pro Gly Thr Val Ser Asp Val Val Gly Tyr Gly Trp Ile  
 385 390 395 400  
 Tyr Tyr Asp Tyr Trp Gly Arg Trp Ala Gln Ala Ala Tyr Ala Gln Gln  
 405 410 415  
 Phe Phe Gly Asn Arg Asn Ser Val Val Gln Thr Asn Leu Glu Ala Gly  
 420 425 430  
 Cys Ser Gly Glu Lys Asn Thr Leu Phe Trp Gly Thr Ser Tyr Phe Gln  
 435 440 445  
 Val Thr Tyr Glu Gly Gln Pro Tyr Phe Gly Gln Ser Ala Thr Asn Tyr

450

455

460

Ala Tyr Leu Pro Cys Thr Ile Asp Arg Ser  
465 470

&lt;210&gt; 519

&lt;211&gt; 826

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(826)

&lt;223&gt; RXN03038

&lt;400&gt; 519

gcgcggaataa caccaagtaa gccttacagt ccgacagcct catagcggat gggataagtt 60

ccaaacacgt tcaaatccgt taaagtgcct gtttaaaact atg cat tca aag gaa 115  
Met His Ser Lys Glu  
1 5

gag tta aca gtg cgt aaa gga att tcc cgc gtc ctc tcg gta gcg gtt 163  
Glu Leu Thr Val Arg Lys Gly Ile Ser Arg Val Leu Ser Val Ala Val  
10 15 20

gct agt tca atc gga ttc gga act gta ctg aca ggc acc ggc atc gca 211  
Ala Ser Ser Ile Gly Phe Gly Thr Val Leu Thr Gly Thr Gly Ile Ala  
25 30 35

gca gct caa gac tct gca ttt gac tac ggt atg gat cca aac atg aac 259  
Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly Met Asp Pro Asn Met Asn  
40 45 50

tac aac ccg atc gat gac atc aag gat cgt ccc gaa gga ttg tcc aat 307  
Tyr Asn Pro Ile Asp Asp Ile Lys Asp Arg Pro Glu Gly Leu Ser Asn  
55 60 65

ctt ccc tac ttc gga agt aaa ttg acc agc tgg ggc tca tca tat gcc 355  
Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser Trp Gly Ser Ser Tyr Ala  
70 75 80 85

acc gcc tca tcc ggc gtc gtg acc tcc gcg ctc ccg cag tac acc gat 403  
Thr Ala Ser Ser Gly Val Val Thr Ser Ala Leu Pro Gln Tyr Thr Asp  
90 95 100

ccg cgc tac ccc ctc ggc aaa gac gac ctg ccc aag gca acc atc gac 451  
Pro Arg Tyr Pro Leu Gly Lys Asp Asp Leu Pro Lys Ala Thr Ile Asp  
105 110 115

atg gag cca gaa gtt ctt gcg cgc ctt gag cga ttc gtc ggc gtt gac 499  
Met Glu Pro Glu Val Leu Ala Arg Leu Glu Arg Phe Val Gly Val Asp  
120 125 130

ggt gat cgc atc cgc caa atc aac gcg tac tcg cca tca atg gga cgc 547  
Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser Pro Ser Met Gly Arg  
135 140 145

acc att cct cta gtc tgg gtt gtt cca gaa gac aac acc gtg cct ggc 595  
Thr Ile Pro Leu Val Trp Val Val Pro Glu Asp Asn Thr Val Pro Gly

150	155	160	165	
cca acg gtc tac gca ctc gga ggc ggt gac ggt gga caa ggc ggc cag				643
Pro Thr Val Tyr Ala Leu Gly Gly Gly Asp Gly Gly Gln Gly Gly Gln				
	170	175	180	
aac tgg gtc acc cgc acc gac ctt gag gaa tta acc agt gac aac aac				691
Asn Trp Val Thr Arg Thr Asp Leu Glu Glu Leu Thr Ser Asp Asn Asn				
	185	190	195	
atc aac ctc atc atg ccg atg ctc gga tct ttt agt ttc tac tct gac				739
Ile Asn Leu Ile Met Pro Met Leu Gly Ser Phe Ser Phe Tyr Ser Asp				
	200	205	210	
tgg gca cgc gaa agc caa tcc atg ggt tgt gcg caa cag tgg gaa aca				787
Trp Ala Arg Glu Ser Gln Ser Met Gly Cys Ala Gln Gln Trp Glu Thr				
	215	220	225	
ttg ctc atg cac gaa ctg cct gag ccg ctt gta gcg gcc				826
Leu Leu Met His Glu Leu Pro Glu Pro Leu Val Ala Ala				
	230	235	240	
<210> 520				
<211> 242				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 520				
Met His Ser Lys Glu Glu Leu Thr Val Arg Lys Gly Ile Ser Arg Val				
1	5	10	15	
Leu Ser Val Ala Val Ala Ser Ser Ile Gly Phe Gly Thr Val Leu Thr				
	20	25	30	
Gly Thr Gly Ile Ala Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly Met				
	35	40	45	
Asp Pro Asn Met Asn Tyr Asn Pro Ile Asp Asp Ile Lys Asp Arg Pro				
	50	55	60	
Glu Gly Leu Ser Asn Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser Trp				
	65	70	75	80
Gly Ser Ser Tyr Ala Thr Ala Ser Ser Gly Val Val Thr Ser Ala Leu				
	85	90	95	
Pro Gln Tyr Thr Asp Pro Arg Tyr Pro Leu Gly Lys Asp Asp Leu Pro				
	100	105	110	
Lys Ala Thr Ile Asp Met Glu Pro Glu Val Leu Ala Arg Leu Glu Arg				
	115	120	125	
Phe Val Gly Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser				
	130	135	140	
Pro Ser Met Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro Glu Asp				
	145	150	155	160
Asn Thr Val Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly Asp Gly				
	165	170	175	

Gly Gln Gly Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Glu Glu Leu  
 180 185 190

Thr Ser Asp Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly Ser Phe  
 195 200 205

Ser Phe Tyr Ser Asp Trp Ala Arg Glu Ser Gln Ser Met Gly Cys Ala  
 210 215 220

Gln Gln Trp Glu Thr Leu Leu Met His Glu Leu Pro Glu Pro Leu Val  
 225 230 235 240

Ala Ala

<210> 521  
 <211> 613  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(613)  
 <223> FRXA01179

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ccaaacacgt tcaaatccgt taaagtgcct gtttaaaact atg cat tca aag gaa 115  
 Met His Ser Lys Glu  
 1 5

gag tta aca gtg cgt aaa gga att tcc cgc gtc ctc tcg gta gcg gtt 163  
 Glu Leu Thr Val Arg Lys Gly Ile Ser Arg Val Leu Ser Val Ala Val  
 10 15 20

gct agt tca atc gga ttc gga act gta ctg aca ggc acc ggc atc gca 211  
 Ala Ser Ser Ile Gly Phe Gly Thr Val Leu Thr Gly Thr Gly Ile Ala  
 25 30 35

gca gct caa gac tct gca ttt gac tac ggt atg gat cca aac atg aac 259  
 Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly Met Asp Pro Asn Met Asn  
 40 45 50

tac aac ccg atc gat gac atc aag gat cgt ccc gaa gga ttg tcc aat 307  
 Tyr Asn Pro Ile Asp Asp Ile Lys Asp Arg Pro Glu Gly Leu Ser Asn  
 55 60 65

ctt ccc tac ttc gga agt aaa ttg acc agc tgg ggc tca tca tat gcc 355  
 Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser Trp Gly Ser Ser Tyr Ala  
 70 75 80 85

acc gcc tca tcc ggc gtc gtg acc tcc gcg ctc ccg cag tac acc gat 403  
 Thr Ala Ser Ser Gly Val Val Thr Ser Ala Leu Pro Gln Tyr Thr Asp  
 90 95 100

ccg cgc tac ccc ctc ggc aaa gac gac ctg ccc aag gca acc atc gac 451  
 Pro Arg Tyr Pro Leu Gly Lys Asp Asp Leu Pro Lys Ala Thr Ile Asp  
 105 110 115

atg gag cca gaa gtt ctt gcg cgc ctt gag cga ttc gtc ggc gtt gac 499  
 Met Glu Pro Glu Val Leu Ala Arg Leu Glu Arg Phe Val Gly Val Asp  
           120                          125                          130

ggt gat cgc atc cgc caa atc aac gcg tac tcg cca tca atg gga cgc 547  
 Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser Pro Ser Met Gly Arg  
           135                          140                          145

acc att cct cta gtc tgg gtt gtt cca aaa gac aac acc gtg cct tgc 595  
 Thr Ile Pro Leu Val Trp Val Val Pro Lys Asp Asn Thr Val Pro Cys  
           150                          155                          160                          165

cca acg gtc tac gca cta 613  
 Pro Thr Val Tyr Ala Leu  
                           170

<210> 522

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 522

Met His Ser Lys Glu Glu Leu Thr Val Arg Lys Gly Ile Ser Arg Val  
           1                          5                          10                          15

Leu Ser Val Ala Val Ala Ser Ser Ile Gly Phe Gly Thr Val Leu Thr  
                           20                          25                          30

Gly Thr Gly Ile Ala Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly Met  
           35                          40                          45

Asp Pro Asn Met Asn Tyr Asn Pro Ile Asp Asp Ile Lys Asp Arg Pro  
           50                          55                          60

Glu Gly Leu Ser Asn Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser Trp  
           65                          70                          75                          80

Gly Ser Ser Tyr Ala Thr Ala Ser Ser Gly Val Val Thr Ser Ala Leu  
                           85                          90                          95

Pro Gln Tyr Thr Asp Pro Arg Tyr Pro Leu Gly Lys Asp Asp Leu Pro  
           100                          105                          110

Lys Ala Thr Ile Asp Met Glu Pro Glu Val Leu Ala Arg Leu Glu Arg  
           115                          120                          125

Phe Val Gly Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser  
           130                          135                          140

Pro Ser Met Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro Lys Asp  
           145                          150                          155                          160

Asn Thr Val Pro Cys Pro Thr Val Tyr Ala Leu  
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<210> 523

<211> 1218

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1195)

<223> RXA01274

<400> 523

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                                         Met Lys Leu Leu Arg
                                         1 5

cgc atc gct gca cca gcc atc gcg ctg gga att gcg atg tcc acc att 163
Arg Ile Ala Ala Pro Ala Ile Ala Leu Gly Ile Ala Met Ser Thr Ile
                        10 15 20

gtc acg cca tcc acc gca ggc gct gcc gaa gta acc cca gca gac gtt 211
Val Thr Pro Ser Thr Ala Gly Ala Ala Glu Val Thr Pro Ala Asp Val
                        25 30 35

gct ggc gat act gca cta tcc acc atc tcc gat agt gct cct gca gat 259
Ala Gly Asp Thr Ala Leu Ser Thr Ile Ser Asp Ser Ala Pro Ala Asp
                        40 45 50

gaa gcc tct gca cct cgc tgg cgc gca cac gtc aac gca gca gac gag 307
Glu Ala Ser Ala Pro Arg Trp Arg Ala His Val Asn Ala Ala Asp Glu
                        55 60 65

cgc gtc aaa gaa atg tgg gca tac tcc cct tcc atg gac cgc aat gtg 355
Arg Val Lys Glu Met Trp Ala Tyr Ser Pro Ser Met Asp Arg Asn Val
                        70 75 80 85

cca ctg gta gtt ata act gcc gat gag tcc gca ggt cct cgt cct gtg 403
Pro Leu Val Val Ile Thr Ala Asp Glu Ser Ala Gly Pro Arg Pro Val
                        90 95 100

att tac ctt ctt aac ggt ggc gac ggt ggc gaa ggt gcc gct aac tgg 451
Ile Tyr Leu Leu Asn Gly Gly Asp Gly Gly Glu Gly Ala Ala Asn Trp
                        105 110 115

gtt atg cag act gac gtt ctg gat ttc tac cta gaa aag aac gtt aac 499
Val Met Gln Thr Asp Val Leu Asp Phe Tyr Leu Glu Lys Asn Val Asn
                        120 125 130

gtt gtt att cca atg gaa ggc aag ttt tcc tac tac acc gac tgg gta 547
Val Val Ile Pro Met Glu Gly Lys Phe Ser Tyr Tyr Thr Asp Trp Val
                        135 140 145

gaa gag aat gcg tcc ctc ggt ggc aag caa atg tgg gaa acc ttc ctg 595
Glu Glu Asn Ala Ser Leu Gly Gly Lys Gln Met Trp Glu Thr Phe Leu
                        150 155 160 165

gtg aag gaa ctt cca gga cca ttg gaa gaa aag ctc aac act gac ggt 643
Val Lys Glu Leu Pro Gly Pro Leu Glu Glu Lys Leu Asn Thr Asp Gly
                        170 175 180

cag cgt gca att gct ggc atg tcc atg tcc gca act act tcc cta ctc 691
Gln Arg Ala Ile Ala Gly Met Ser Met Ser Ala Thr Thr Ser Leu Leu
                        185 190 195

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ttc cca caa cac ttc cca ggc ttc tac gac gca gca gca tcc ttc tca 739  
 Phe Pro Gln His Phe Pro Gly Phe Tyr Asp Ala Ala Ala Ser Phe Ser  
 200 205 210  
  
 gga tgc gca gca acc tca agc ctg ctc cca tgg gaa tac ctc aaa ctc 787  
 Gly Cys Ala Ala Thr Ser Ser Leu Leu Pro Trp Glu Tyr Leu Lys Leu  
 215 220 225  
  
 acc ctt gac cgc ggc aac gca acc cca gaa caa atg tgg gga cca cgt 835  
 Thr Leu Asp Arg Gly Asn Ala Thr Pro Glu Gln Met Trp Gly Pro Arg  
 230 235 240 245  
  
 ggt ggc gaa tac aac atc tac aac gac gca ctg atc aac tcc gac aaa 883  
 Gly Gly Glu Tyr Asn Ile Tyr Asn Asp Ala Leu Ile Asn Ser Asp Lys  
 250 255 260  
  
 cta cgc gga acc gaa cta tac gtc tcc aac gca tcc ggc ctt gct ggt 931  
 Leu Arg Gly Thr Glu Leu Tyr Val Ser Asn Ala Ser Gly Leu Ala Gly  
 265 270 275  
  
 gaa tgg gaa tcc gtc gac agc cca cgc ttc gaa gga ctc aac caa caa 979  
 Glu Trp Glu Ser Val Asp Ser Pro Arg Phe Glu Gly Leu Asn Gln Gln  
 280 285 290  
  
 gtt cag tcc atc gca atg gca gaa act gtg gta acc ggc ggc atc atc 1027  
 Val Gln Ser Ile Ala Met Ala Glu Thr Val Val Thr Gly Gly Ile Ile  
 295 300 305  
  
 gaa gct gca acc aac aag tgc acc cac gac ctc aag gca aaa ctt gac 1075  
 Glu Ala Ala Thr Asn Lys Cys Thr His Asp Leu Lys Ala Lys Leu Asp  
 310 315 320 325  
  
 tcc gcc ggc atc cca gcc gac tgg aac ctc cgc cca acc ggc acc cac 1123  
 Ser Ala Gly Ile Pro Ala Asp Trp Asn Leu Arg Pro Thr Gly Thr His  
 330 335 340  
  
 tca tgg ggc tgg tgg caa gat gac ctc cgc gga tct tgg acc acc ttc 1171  
 Ser Trp Gly Trp Trp Gln Asp Asp Leu Arg Gly Ser Trp Thr Thr Phe  
 345 350 355  
  
 gct cgt gcg ttt gag cta gag gcc tagaaacaga tttaacattg aaa 1218  
 Ala Arg Ala Phe Glu Leu Glu Ala  
 360 365

&lt;210&gt; 524

&lt;211&gt; 365

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 524

Met Lys Leu Leu Arg Arg Ile Ala Ala Pro Ala Ile Ala Leu Gly Ile  
 1 5 10 15

Ala Met Ser Thr Ile Val Thr Pro Ser Thr Ala Gly Ala Ala Glu Val  
 20 25 30

Thr Pro Ala Asp Val Ala Gly Asp Thr Ala Leu Ser Thr Ile Ser Asp  
 35 40 45

Ser Ala Pro Ala Asp Glu Ala Ser Ala Pro Arg Trp Arg Ala His Val  
 50 55 60  
 Asn Ala Ala Asp Glu Arg Val Lys Glu Met Trp Ala Tyr Ser Pro Ser  
 65 70 75 80  
 Met Asp Arg Asn Val Pro Leu Val Val Ile Thr Ala Asp Glu Ser Ala  
 85 90 95  
 Gly Pro Arg Pro Val Ile Tyr Leu Leu Asn Gly Gly Asp Gly Gly Glu  
 100 105 110  
 Gly Ala Ala Asn Trp Val Met Gln Thr Asp Val Leu Asp Phe Tyr Leu  
 115 120 125  
 Glu Lys Asn Val Asn Val Val Ile Pro Met Glu Gly Lys Phe Ser Tyr  
 130 135 140  
 Tyr Thr Asp Trp Val Glu Glu Asn Ala Ser Leu Gly Gly Lys Gln Met  
 145 150 155 160  
 Trp Glu Thr Phe Leu Val Lys Glu Leu Pro Gly Pro Leu Glu Glu Lys  
 165 170 175  
 Leu Asn Thr Asp Gly Gln Arg Ala Ile Ala Gly Met Ser Met Ser Ala  
 180 185 190  
 Thr Thr Ser Leu Leu Phe Pro Gln His Phe Pro Gly Phe Tyr Asp Ala  
 195 200 205  
 Ala Ala Ser Phe Ser Gly Cys Ala Ala Thr Ser Ser Leu Leu Pro Trp  
 210 215 220  
 Glu Tyr Leu Lys Leu Thr Leu Asp Arg Gly Asn Ala Thr Pro Glu Gln  
 225 230 235 240  
 Met Trp Gly Pro Arg Gly Gly Glu Tyr Asn Ile Tyr Asn Asp Ala Leu  
 245 250 255  
 Ile Asn Ser Asp Lys Leu Arg Gly Thr Glu Leu Tyr Val Ser Asn Ala  
 260 265 270  
 Ser Gly Leu Ala Gly Glu Trp Glu Ser Val Asp Ser Pro Arg Phe Glu  
 275 280 285  
 Gly Leu Asn Gln Gln Val Gln Ser Ile Ala Met Ala Glu Thr Val Val  
 290 295 300  
 Thr Gly Gly Ile Ile Glu Ala Ala Thr Asn Lys Cys Thr His Asp Leu  
 305 310 315 320  
 Lys Ala Lys Leu Asp Ser Ala Gly Ile Pro Ala Asp Trp Asn Leu Arg  
 325 330 335  
 Pro Thr Gly Thr His Ser Trp Gly Trp Trp Gln Asp Asp Leu Arg Gly  
 340 345 350  
 Ser Trp Thr Thr Phe Ala Arg Ala Phe Glu Leu Glu Ala  
 355 360 365

<210> 525  
 <211> 1141  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1141)  
 <223> RXA01449

<400> 525  
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 Leu Lys Leu Phe Ile  
 1 5  
 tcc cgc gca ctc atc gcc ggt act gtt tct ttg act ctt ttc tct tca 163  
 Ser Arg Ala Leu Ile Ala Gly Thr Val Ser Leu Thr Leu Phe Ser Ser  
 10 15 20  
 ccg ctc gct tcc gca cag agc tcg gga ctc agt tca gta cta agt tcc 211  
 Pro Leu Ala Ser Ala Gln Ser Ser Gly Leu Ser Ser Val Leu Ser Ser  
 25 30 35  
 gaa gac agc tca gca act aat tca gag cag gac ttt gag aaa agc tcc 259  
 Glu Asp Ser Ser Ala Thr Asn Ser Glu Gln Asp Phe Glu Lys Ser Ser  
 40 45 50  
 gaa tcc gga tct tcc gcc cag gat ttc atc gcg ctt tct act gcc aac 307  
 Glu Ser Gly Ser Ser Ala Gln Asp Phe Ile Ala Leu Ser Thr Ala Asn  
 55 60 65  
 cca gat ctc act ggc ggt tct gtt gaa ggc ttg ctg agt tcg atg tcg 355  
 Pro Asp Leu Thr Gly Gly Ser Val Glu Gly Leu Leu Ser Ser Met Ser  
 70 75 80 85  
 ctg att ggt tcg tcc cag ttg cct ctt gga ggc ccg ctc ttg agt agt 403  
 Leu Ile Gly Ser Ser Gln Leu Pro Leu Gly Gly Pro Leu Leu Ser Ser  
 90 95 100  
 gat tcc aac tat ccg ctc gag aca gac ccc tcg att act gag gca aga 451  
 Asp Ser Asn Tyr Pro Leu Glu Thr Asp Pro Ser Ile Thr Glu Ala Arg  
 105 110 115  
 atc gtc gaa aag cgt gtt tta aat ggt ctt cga ctg gaa aaa tgg tct 499  
 Ile Val Glu Lys Arg Val Leu Asn Gly Leu Arg Leu Glu Lys Trp Ser  
 120 125 130  
 gtt gcg tcg cct tcg atg cag cgc aat gtg gat gtg cag atc atg aag 547  
 Val Ala Ser Pro Ser Met Gln Arg Asn Val Asp Val Gln Ile Met Lys  
 135 140 145  
 tcc gcg gag gcg gac tcc cct gct ccg atg ctg tac atg ctt gat gga 595  
 Ser Ala Glu Ala Asp Ser Pro Ala Pro Met Leu Tyr Met Leu Asp Gly  
 150 155 160 165  
 atc ggc gga aat aag aat tct tct ggt tgg atc aat ggt ggc gag ggt 643  
 Ile Gly Gly Asn Lys Asn Ser Ser Gly Trp Ile Asn Gly Gly Glu Gly  
 170 175 180

ccg aag gtt ttc gcg gat gaa aat gtg act gta gta atg ccg ttg ggt 691  
 Pro Lys Val Phe Ala Asp Glu Asn Val Thr Val Val Met Pro Leu Gly  
 185 190 195

gct gct tca tcc atg tac tcg gat tgg ttg gaa gag gac cct gcg cta 739  
 Ala Ala Ser Ser Met Tyr Ser Asp Trp Leu Glu Glu Asp Pro Ala Leu  
 200 205 210

ggg cgc atc aag tgg gaa act ttt atc gtc gag gag ctc gcg ccc ctg 787  
 Gly Arg Ile Lys Trp Glu Thr Phe Ile Val Glu Glu Leu Ala Pro Leu  
 215 220 225

ctt gag gct gag gaa gag ctg aac ttc aat ggt cac cgt ggc atc ggc 835  
 Leu Glu Ala Glu Glu Glu Leu Asn Phe Asn Gly His Arg Gly Ile Gly  
 230 235 240 245

gga tta tcc atg ggt gct act ggt gcg gtt cat tta gct aac tcg aac 883  
 Gly Leu Ser Met Gly Ala Thr Gly Ala Val His Leu Ala Asn Ser Asn  
 250 255 260

cct gat ctc ttt gat gga gtc att ggc atc tct ggt tgc tac tcc acg 931  
 Pro Asp Leu Phe Asp Gly Val Ile Gly Ile Ser Gly Cys Tyr Ser Thr  
 265 270 275

ctt gat ccc att gga caa acc acg gtg tca cta att gtt aat tct cgc 979  
 Leu Asp Pro Ile Gly Gln Thr Thr Val Ser Leu Ile Val Asn Ser Arg  
 280 285 290

ggt ggc aat gta gaa aat atg tgg ggt ccc act ggt tct gaa act tgg 1027  
 Gly Gly Asn Val Glu Asn Met Trp Gly Pro Thr Gly Ser Glu Thr Trp  
 295 300 305

aaa gct cac gat gtc aca tca aat cct gag ggg ctg cgc gac atg gct 1075  
 Lys Ala His Asp Val Thr Ser Asn Pro Glu Gly Leu Arg Asp Met Ala  
 310 315 320 325

gtc tat ttg tca gct gcg aac gga gtt gta gat gac atc gat ttg gcg 1123  
 Val Tyr Leu Ser Ala Ala Asn Gly Val Val Asp Asp Ile Asp Leu Ala  
 330 335 340

gat tcc gag aaa gag cct 1141  
 Asp Ser Glu Lys Glu Pro  
 345

&lt;210&gt; 526

&lt;211&gt; 347

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 526

Leu Lys Leu Phe Ile Ser Arg Ala Leu Ile Ala Gly Thr Val Ser Leu  
 1 5 10 15

Thr Leu Phe Ser Ser Pro Leu Ala Ser Ala Gln Ser Ser Gly Leu Ser  
 20 25 30

Ser Val Leu Ser Ser Glu Asp Ser Ser Ala Thr Asn Ser Glu Gln Asp  
 35 40 45

Phe Glu Lys Ser Ser Glu Ser Gly Ser Ser Ala Gln Asp Phe Ile Ala

50	55	60
Leu Ser Thr Ala Asn Pro Asp Leu Thr Gly Gly Ser Val Glu Gly Leu 65 70 75 80		
Leu Ser Ser Met Ser Leu Ile Gly Ser Ser Gln Leu Pro Leu Gly Gly 85 90 95		
Pro Leu Leu Ser Ser Asp Ser Asn Tyr Pro Leu Glu Thr Asp Pro Ser 100 105 110		
Ile Thr Glu Ala Arg Ile Val Glu Lys Arg Val Leu Asn Gly Leu Arg 115 120 125		
Leu Glu Lys Trp Ser Val Ala Ser Pro Ser Met Gln Arg Asn Val Asp 130 135 140		
Val Gln Ile Met Lys Ser Ala Glu Ala Asp Ser Pro Ala Pro Met Leu 145 150 155 160		
Tyr Met Leu Asp Gly Ile Gly Gly Asn Lys Asn Ser Ser Gly Trp Ile 165 170 175		
Asn Gly Gly Glu Gly Pro Lys Val Phe Ala Asp Glu Asn Val Thr Val 180 185 190		
Val Met Pro Leu Gly Ala Ala Ser Ser Met Tyr Ser Asp Trp Leu Glu 195 200 205		
Glu Asp Pro Ala Leu Gly Arg Ile Lys Trp Glu Thr Phe Ile Val Glu 210 215 220		
Glu Leu Ala Pro Leu Leu Glu Ala Glu Glu Glu Leu Asn Phe Asn Gly 225 230 235 240		
His Arg Gly Ile Gly Gly Leu Ser Met Gly Ala Thr Gly Ala Val His 245 250 255		
Leu Ala Asn Ser Asn Pro Asp Leu Phe Asp Gly Val Ile Gly Ile Ser 260 265 270		
Gly Cys Tyr Ser Thr Leu Asp Pro Ile Gly Gln Thr Thr Val Ser Leu 275 280 285		
Ile Val Asn Ser Arg Gly Gly Asn Val Glu Asn Met Trp Gly Pro Thr 290 295 300		
Gly Ser Glu Thr Trp Lys Ala His Asp Val Thr Ser Asn Pro Glu Gly 305 310 315 320		
Leu Arg Asp Met Ala Val Tyr Leu Ser Ala Ala Asn Gly Val Val Asp 325 330 335		
Asp Ile Asp Leu Ala Asp Ser Glu Lys Glu Pro 340 345		

&lt;210&gt; 527

&lt;211&gt; 373

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(373)

&lt;223&gt; RXA01798

&lt;400&gt; 527

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                                         Met His Arg Lys Lys
                                         1 5

gaa gag tta aca atg cgt aaa gga att tcc cgc atc ctc tcg gta gcg 163
Glu Glu Leu Thr Met Arg Lys Gly Ile Ser Arg Ile Leu Ser Val Ala
                        10 15 20

gtt gct agt tct att gga ttc ggt tcg gtg ttg tct gga acc ggc atc 211
Val Ala Ser Ser Ile Gly Phe Gly Ser Val Leu Ser Gly Thr Gly Ile
                        25 30 35

gca gca gct caa gac tct gca ttt gac tac ggt atg gat cct agc atg 259
Ala Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly Met Asp Pro Ser Met
                        40 45 50

aac tac aac ccg atc gac gac atg aag gat cgt ccc caa ggg tta tcc 307
Asn Tyr Asn Pro Ile Asp Asp Met Lys Asp Arg Pro Gln Gly Leu Ser
                        55 60 65

aac ctt ccc tac ttc gga agc aaa cta acc agc tgg ggc tca tca gat 355
Asn Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser Trp Gly Ser Ser Asp
                        70 75 80 85

gcc acc gcc tca tcc ggc 373
Ala Thr Ala Ser Ser Gly
                        90

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&lt;210&gt; 528

&lt;211&gt; 91

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 528

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Met His Arg Lys Lys Glu Glu Leu Thr Met Arg Lys Gly Ile Ser Arg
  1 5 10 15

Ile Leu Ser Val Ala Val Ala Ser Ser Ile Gly Phe Gly Ser Val Leu
  20 25 30

Ser Gly Thr Gly Ile Ala Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly
  35 40 45

Met Asp Pro Ser Met Asn Tyr Asn Pro Ile Asp Asp Met Lys Asp Arg
  50 55 60

Pro Gln Gly Leu Ser Asn Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser
  65 70 75 80

Trp Gly Ser Ser Asp Ala Thr Ala Ser Ser Gly
  85 90

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<400> 529															
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Met Gly Tyr Pro Ile 5															
ggg ggt gaa gtc cct gtt tgc ggg tgc aat ctc att gac ggt gag atc 163															
Gly Gly Glu Val Pro Val Ser Gly Ser Asn Leu Ile Asp Gly Glu Ile 20															
aat ggt tgg gtg caa acg ttc caa ggt ggg cgg gtc tat cgt acc ccg 211															
Asn Gly Trp Val Gln Thr Phe Gln Gly Gly Arg Val Tyr Arg Thr Pro 35															
atg ctt gag ggg ttc cag att gcc agt att aac ggc atg att tta aat 259															
Met Leu Glu Gly Phe Gln Ile Ala Ser Ile Asn Gly Met Ile Leu Asn 50															
aga tgg ttg gct att ggc ggg ccg gat agc gct ctt ggt ttt ccc att 307															
Arg Trp Leu Ala Ile Gly Gly Pro Asp Ser Ala Leu Gly Phe Pro Ile 65															
gcc gat gaa gct gtt gca tcc gat ggt gtg ggt cga ttt agt gtt ttc 355															
Ala Asp Glu Ala Val Ala Ser Asp Gly Val Gly Arg Phe Ser Val Phe 85															
cag aat ggt gta ctt tac tgg cac cct aat cac gga gca tgg gaa atg 403															
Gln Asn Gly Val Leu Tyr Trp His Pro Asn His Gly Ala Trp Glu Met 100															
acc gga ttt att gaa gaa gta tgg aaa atg cga ggt ggc ttg gat tct 451															
Thr Gly Phe Ile Glu Glu Val Trp Lys Met Arg Gly Gly Leu Asp Ser 115															
caa tgg ggt tat ccc aca tcc gcc ccg gtg tta gat tca gat gcc cca 499															
Gln Trp Gly Tyr Pro Thr Ser Ala Pro Val Leu Asp Ser Asp Ala Pro 130															
gtg gaa att gcc caa aac ttt tct gga ggc gtt ttc gac cta gca acc 547															
Val Glu Ile Ala Gln Asn Phe Ser Gly Gly Val Phe Asp Leu Ala Thr 145															
gag atc gag gat gct ggt ttt agt ccg atc gag gat aag gag atg agc 595															
Glu Ile Glu Asp Ala Gly Phe Ser Pro Ile Glu Asp Lys Glu Met Ser 165															
aac ttg ata ctt gaa tat ttt ggt tat tta gga ttc gat ttc cct gga 643															
Asn Leu Ile Leu Glu Tyr Phe Gly Tyr Leu Gly Phe Asp Phe Pro Gly															

170										175										180										
agc	tct	tct	cga	gag	ttg	gtg	caa	gac	cat	tct	aaa	tca	gac	ttg	atg	691														
Ser	Ser	Ser	Arg	Glu	Leu	Val	Gln	Asp	His	Ser	Lys	Ser	Asp	Leu	Met															
			185					190					195																	
act	ctt	agg	gct	agt	aga	tgt	gcg	ctc	aag	gat	tct	tct	cag	gca	agt	739														
Thr	Leu	Arg	Ala	Ser	Arg	Cys	Ala	Leu	Lys	Asp	Ser	Ser	Gln	Ala	Ser															
		200					205					210																		
ttc	ggg	ggg	gtg	acg	att	cct	agc	cac	tat	gac	tac	tgg	gga	tgt	ctt	787														
Phe	Gly	Gly	Val	Thr	Ile	Pro	Ser	His	Tyr	Asp	Tyr	Trp	Gly	Cys	Leu															
	215					220				225																				
gac	aag	tcc	gac	cga	ccc	gac	cct	gat	gct	tat	ggg	cgc	cat	gac	tac	835														
Asp	Lys	Ser	Asp	Arg	Pro	Asp	Pro	Asp	Ala	Tyr	Gly	Arg	His	Asp	Tyr															
230					235				240					245																
tgc	act	ctt	tcg	cct	gat	tcg	tat	ggg	ccc	cta	ggg	aag	aag	gct	gag	883														
Cys	Thr	Leu	Ser	Pro	Asp	Ser	Tyr	Gly	Pro	Leu	Gly	Lys	Lys	Ala	Glu															
				250				255						260																
ttt	agt	ggg	gct	tgt	gca	aga	cac	gat	ctg	tgt	atg	gat	gcc	gtt	gat	931														
Phe	Ser	Gly	Ala	Cys	Ala	Arg	His	Asp	Leu	Cys	Met	Asp	Ala	Val	Asp															
			265					270				275																		
gcg	aat	ggc	acg	ggg	tat	gct	ccg	tgc	cac	ccg	gct	ttt	tat	acg	tgg	979														
Ala	Asn	Gly	Thr	Gly	Tyr	Ala	Pro	Cys	His	Pro	Ala	Phe	Tyr	Thr	Trp															
		280					285					290																		
atg	agc	aca	gtt	tgt	act	acc	aac	tat	gct	gag	gat	gct	aat	ttc	aag	1027														
Met	Ser	Thr	Val	Cys	Thr	Thr	Asn	Tyr	Ala	Glu	Asp	Ala	Asn	Phe	Lys															
		295				300				305																				
aag	ggc	tgt	gtg	aat	acc	gcg	aag	gcc	tac	tat	aag	gca	gtc	caa	tta	1075														
Lys	Gly	Cys	Val	Asn	Thr	Ala	Lys	Ala	Tyr	Tyr	Lys	Ala	Val	Gln	Leu															
310					315				320					325																
aag	aac	ccg	aat	tagaa	atatg	cgtg	attata	cga								1110														
Lys	Asn	Pro	Asn																											

&lt;210&gt; 530

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 530

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1				5					10					15	
Ile	Asp	Gly	Glu	Ile	Asn	Gly	Trp	Val	Gln	Thr	Phe	Gln	Gly	Gly	Arg
			20					25					30		
Val	Tyr	Arg	Thr	Pro	Met	Leu	Glu	Gly	Phe	Gln	Ile	Ala	Ser	Ile	Asn
		35					40					45			
Gly	Met	Ile	Leu	Asn	Arg	Trp	Leu	Ala	Ile	Gly	Gly	Pro	Asp	Ser	Ala
	50					55					60				

Leu Gly Phe Pro Ile Ala Asp Glu Ala Val Ala Ser Asp Gly Val Gly  
 65 70 75 80  
 Arg Phe Ser Val Phe Gln Asn Gly Val Leu Tyr Trp His Pro Asn His  
 85 90 95  
 Gly Ala Trp Glu Met Thr Gly Phe Ile Glu Glu Val Trp Lys Met Arg  
 100 105 110  
 Gly Gly Leu Asp Ser Gln Trp Gly Tyr Pro Thr Ser Ala Pro Val Leu  
 115 120 125  
 Asp Ser Asp Ala Pro Val Glu Ile Ala Gln Asn Phe Ser Gly Gly Val  
 130 135 140  
 Phe Asp Leu Ala Thr Glu Ile Glu Asp Ala Gly Phe Ser Pro Ile Glu  
 145 150 155 160  
 Asp Lys Glu Met Ser Asn Leu Ile Leu Glu Tyr Phe Gly Tyr Leu Gly  
 165 170 175  
 Phe Asp Phe Pro Gly Ser Ser Ser Arg Glu Leu Val Gln Asp His Ser  
 180 185 190  
 Lys Ser Asp Leu Met Thr Leu Arg Ala Ser Arg Cys Ala Leu Lys Asp  
 195 200 205  
 Ser Ser Gln Ala Ser Phe Gly Gly Val Thr Ile Pro Ser His Tyr Asp  
 210 215 220  
 Tyr Trp Gly Cys Leu Asp Lys Ser Asp Arg Pro Asp Pro Asp Ala Tyr  
 225 230 235 240  
 Gly Arg His Asp Tyr Cys Thr Leu Ser Pro Asp Ser Tyr Gly Pro Leu  
 245 250 255  
 Gly Lys Lys Ala Glu Phe Ser Gly Ala Cys Ala Arg His Asp Leu Cys  
 260 265 270  
 Met Asp Ala Val Asp Ala Asn Gly Thr Gly Tyr Ala Pro Cys His Pro  
 275 280 285  
 Ala Phe Tyr Thr Trp Met Ser Thr Val Cys Thr Thr Asn Tyr Ala Glu  
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 Asp Ala Asn Phe Lys Lys Gly Cys Val Asn Thr Ala Lys Ala Tyr Tyr  
 305 310 315 320  
 Lys Ala Val Gln Leu Lys Asn Pro Asn  
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<210> 531

<211> 342

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(319)

<223> RXA02607

&lt;400&gt; 531

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gtgcgcagta tccaaaaatc aaaatgagaa ggaaaacttc atg cgc gac acc gca 115  
Met Arg Asp Thr Ala  
1 5

ttt cgt tcc atc aag gct aaa gct cag gct aag cgc cgt tcc ctc tgg 163  
Phe Arg Ser Ile Lys Ala Lys Ala Gln Ala Lys Arg Arg Ser Leu Trp  
10 15 20

att gca gca ggc gct gtc cca acc gca att gcg ttg act atg tcc ctg 211  
Ile Ala Ala Gly Ala Val Pro Thr Ala Ile Ala Leu Thr Met Ser Leu  
25 30 35

gca cct atg gct tcg gct cag tcc agc aac ctt tcc tct gat gcc gtt 259  
Ala Pro Met Ala Ser Ala Gln Ser Ser Asn Leu Ser Ser Asp Ala Val  
40 45 50

att ggc agc atc gcg cag ggc gtc acc gat ggc ctg act gac tac ctg 307  
Ile Gly Ser Ile Ala Gln Gly Val Thr Asp Gly Leu Thr Asp Tyr Leu  
55 60 65

aag cct cgc gtc tgaagagctt cctgctggtg aag 342  
Lys Pro Arg Val  
70

&lt;210&gt; 532

&lt;211&gt; 73

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 532

Met Arg Asp Thr Ala Phe Arg Ser Ile Lys Ala Lys Ala Gln Ala Lys  
1 5 10 15

Arg Arg Ser Leu Trp Ile Ala Ala Gly Ala Val Pro Thr Ala Ile Ala  
20 25 30

Leu Thr Met Ser Leu Ala Pro Met Ala Ser Ala Gln Ser Ser Asn Leu  
35 40 45

Ser Ser Asp Ala Val Ile Gly Ser Ile Ala Gln Gly Val Thr Asp Gly  
50 55 60

Leu Thr Asp Tyr Leu Lys Pro Arg Val  
65 70

&lt;210&gt; 533

&lt;211&gt; 1818

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1795)

&lt;223&gt; RXA02608

&lt;400&gt; 533

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tgaagtcacc tacccagaga tcgccgggct gcctgatggg 115
                               Val Arg Val Ile Ser
                               1           5

gct gag tgg gca acc tcc aag cat gtc att ttg act att cag tct gca 163
Ala Glu Trp Ala Thr Ser Lys His Val Ile Leu Thr Ile Gln Ser Ala
                10                15                20

gca atg cca gag cgc cca atc aag gtg cag ctg ctg ctt ccg cgt gac 211
Ala Met Pro Glu Arg Pro Ile Lys Val Gln Leu Leu Leu Pro Arg Asp
                25                30                35

tgg tac tct tcc ccg aac cgt gag ttc cct gaa atc tgg gca ctt gac 259
Trp Tyr Ser Ser Pro Asn Arg Glu Phe Pro Glu Ile Trp Ala Leu Asp
                40                45                50

ggg ctg cgc gcg att gaa gag cag agt ggt tgg acc att gag acc aac 307
Gly Leu Arg Ala Ile Glu Glu Gln Ser Gly Trp Thr Ile Glu Thr Asn
                55                60                65

att gag cag tac tac gcc gat aag aac gcc att gtt gtg ctc cct gtc 355
Ile Glu Gln Tyr Tyr Ala Asp Lys Asn Ala Ile Val Val Leu Pro Val
                70                75                80                85

ggg ggc gag agc tcc ttc tac tct gac tgg gaa ggg cca aac aac ggc 403
Gly Gly Glu Ser Ser Phe Tyr Ser Asp Trp Glu Gly Pro Asn Asn Gly
                90                95                100

aag aac tac cag tgg gag acc ttc ctg act cag gag ctc gca ccg atc 451
Lys Asn Tyr Gln Trp Glu Thr Phe Leu Thr Gln Glu Leu Ala Pro Ile
                105                110                115

ctg gac aag ggt ttc cgt tct aac acc gat cgc gcc atc acc ggt atc 499
Leu Asp Lys Gly Phe Arg Ser Asn Thr Asp Arg Ala Ile Thr Gly Ile
                120                125                130

tcc atg ggc ggt acc gct gcg gtt aac atc gca acc cac cac cca gac 547
Ser Met Gly Gly Thr Ala Ala Val Asn Ile Ala Thr His His Pro Asp
                135                140                145

atg ttt aag ttc gtc ggt tcc ttc tcc ggc tat ctg gac acc acc tcc 595
Met Phe Lys Phe Val Gly Ser Phe Ser Gly Tyr Leu Asp Thr Thr Ser
                150                155                160                165

gct ggc atg cca atc gct att tcc gca gcc ctg gca gac gcc ggc gga 643
Ala Gly Met Pro Ile Ala Ile Ser Ala Ala Leu Ala Asp Ala Gly Gly
                170                175                180

tac gat gcc aac gca atg tgg gga cca gtc ggt tct gag cgc tgg cag 691
Tyr Asp Ala Asn Ala Met Trp Gly Pro Val Gly Ser Glu Arg Trp Gln
                185                190                195

gaa aac gat cca aag agc aac gta gac aag ctc aag ggc aag acc atc 739
Glu Asn Asp Pro Lys Ser Asn Val Asp Lys Leu Lys Gly Lys Thr Ile
                200                205                210

tac gtt tcc tct ggt aac ggt gca gat gac ttc ggt aag gaa ggc tct 787
Tyr Val Ser Ser Gly Asn Gly Ala Asp Asp Phe Gly Lys Glu Gly Ser

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215	220	225	
gta gct att gga cct gca aac gca gca ggt gtc ggt ctg gaa gtt atc			835
Val Ala Ile Gly Pro Ala Asn Ala Ala Gly Val Gly Leu Glu Val Ile			
230	235	240	245
tcc cgt atg act tcc cag acc ttc gtc gat cgt gca agc cag gct ggc			883
Ser Arg Met Thr Ser Gln Thr Phe Val Asp Arg Ala Ser Gln Ala Gly			
	250	255	260
gtg gaa gtt gtt gct agc ttc cgt cca tcc ggc gtg cac tca tgg gaa			931
Val Glu Val Val Ala Ser Phe Arg Pro Ser Gly Val His Ser Trp Glu			
	265	270	275
tac tgg cag ttc gag atg act cag gcg ttc cct cac atc gct aac gct			979
Tyr Trp Gln Phe Glu Met Thr Gln Ala Phe Pro His Ile Ala Asn Ala			
	280	285	290
ctt ggc atg tcc act gag gac cgt ggc gtt gag tgt gca cct gtc ggc			1027
Leu Gly Met Ser Thr Glu Asp Arg Gly Val Glu Cys Ala Pro Val Gly			
	295	300	305
gca atc gct gac gct gtt gcg gat ggc gcg atg ggc acc tgc ctg acc			1075
Ala Ile Ala Asp Ala Val Ala Asp Gly Ala Met Gly Thr Cys Leu Thr			
310	315	320	325
aac gaa tac gat gtt acc ggc ggt aag gcc cag gac ttc gct aac ggt			1123
Asn Glu Tyr Asp Val Thr Gly Gly Lys Ala Gln Asp Phe Ala Asn Gly			
	330	335	340
cgc gca tac tgg tct gca aac act ggc gct ttc ggc ctg gtt gga cgc			1171
Arg Ala Tyr Trp Ser Ala Asn Thr Gly Ala Phe Gly Leu Val Gly Arg			
	345	350	355
atc aac gct cgt tac tct gag ctg ggt gga cct gcc tcc tgg ttg ggc			1219
Ile Asn Ala Arg Tyr Ser Glu Leu Gly Gly Pro Ala Ser Trp Leu Gly			
	360	365	370
tac cca acc tct tct gag ttg aag aca cca gac gga cgt ggc cgc ttc			1267
Tyr Pro Thr Ser Ser Glu Leu Lys Thr Pro Asp Gly Arg Gly Arg Phe			
	375	380	385
gtc acc ttc gag cac ggc tcc atc tac tgg acc gcc acc act ggt cct			1315
Val Thr Phe Glu His Gly Ser Ile Tyr Trp Thr Ala Thr Thr Gly Pro			
390	395	400	405
tgg gaa atc cca ggc gat atg ctc gcc gca tgg ggc acc cag gac tat			1363
Trp Glu Ile Pro Gly Asp Met Leu Ala Ala Trp Gly Thr Gln Asp Tyr			
	410	415	420
gag aag ggc agc ctc ggc tac cca acc ggc gct gca gtt gaa tac aac			1411
Glu Lys Gly Ser Leu Gly Tyr Pro Thr Gly Ala Ala Val Glu Tyr Asn			
	425	430	435
ggg ggc ctg cgc cag cag ttc gaa ggt ggc tac gta ttc cgt acc tcc			1459
Gly Gly Leu Arg Gln Gln Phe Glu Gly Gly Tyr Val Phe Arg Thr Ser			
	440	445	450
aat aac cag tct tac tgg gtt cgc gga gaa atc tcc aag aag tac gcc			1507
Asn Asn Gln Ser Tyr Trp Val Arg Gly Glu Ile Ser Lys Lys Tyr Ala			
	455	460	465

gaa gac gga atc ttc gct cag ctt ggt ttc cca acc ggc aat gag aag 1555  
 Glu Asp Gly Ile Phe Ala Gln Leu Gly Phe Pro Thr Gly Asn Glu Lys  
 470 475 480 485  
  
 ttg atc aac ggt ggc gct ttc cag gaa ttc gaa aag ggc aac atc tac 1603  
 Leu Ile Asn Gly Gly Ala Phe Gln Glu Phe Glu Lys Gly Asn Ile Tyr  
 490 495 500  
  
 tgg tcc gca tcc act ggc gcg cac gtg att ctg cac ggc gac atc ttc 1651  
 Trp Ser Ala Ser Thr Gly Ala His Val Ile Leu His Gly Asp Ile Phe  
 505 510 515  
  
 gac gca tgg ggt gct aag ggc tgg gag cag ggc gaa tac ggc ttc cca 1699  
 Asp Ala Trp Gly Ala Lys Gly Trp Glu Gln Gly Glu Tyr Gly Phe Pro  
 520 525 530  
  
 acc tct gac cag acc gca atc acc gcg ggt gga cag acc att gat ttc 1747  
 Thr Ser Asp Gln Thr Ala Ile Thr Ala Gly Gly Gln Thr Ile Asp Phe  
 535 540 545  
  
 cag aac ggc acc atc cgt cag gtc aat ggc cga att gag gag tct cgc 1795  
 Gln Asn Gly Thr Ile Arg Gln Val Asn Gly Arg Ile Glu Glu Ser Arg  
 550 555 560 565  
  
 taatagtga ggcgcacatctac gca 1818

&lt;210&gt; 534

&lt;211&gt; 565

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 534

Val Arg Val Ile Ser Ala Glu Trp Ala Thr Ser Lys His Val Ile Leu  
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 Thr Ile Gln Ser Ala Ala Met Pro Glu Arg Pro Ile Lys Val Gln Leu  
 20 25 30  
  
 Leu Leu Pro Arg Asp Trp Tyr Ser Ser Pro Asn Arg Glu Phe Pro Glu  
 35 40 45  
  
 Ile Trp Ala Leu Asp Gly Leu Arg Ala Ile Glu Glu Gln Ser Gly Trp  
 50 55 60  
  
 Thr Ile Glu Thr Asn Ile Glu Gln Tyr Tyr Ala Asp Lys Asn Ala Ile  
 65 70 75 80  
  
 Val Val Leu Pro Val Gly Gly Glu Ser Ser Phe Tyr Ser Asp Trp Glu  
 85 90 95  
  
 Gly Pro Asn Asn Gly Lys Asn Tyr Gln Trp Glu Thr Phe Leu Thr Gln  
 100 105 110  
  
 Glu Leu Ala Pro Ile Leu Asp Lys Gly Phe Arg Ser Asn Thr Asp Arg  
 115 120 125  
  
 Ala Ile Thr Gly Ile Ser Met Gly Gly Thr Ala Ala Val Asn Ile Ala  
 130 135 140

Thr	His	His	Pro	Asp	Met	Phe	Lys	Phe	Val	Gly	Ser	Phe	Ser	Gly	Tyr	145	150	155	160
Leu	Asp	Thr	Thr	Ser	Ala	Gly	Met	Pro	Ile	Ala	Ile	Ser	Ala	Ala	Leu	165	170	175	
Ala	Asp	Ala	Gly	Gly	Tyr	Asp	Ala	Asn	Ala	Met	Trp	Gly	Pro	Val	Gly	180	185	190	
Ser	Glu	Arg	Trp	Gln	Glu	Asn	Asp	Pro	Lys	Ser	Asn	Val	Asp	Lys	Leu	195	200	205	
Lys	Gly	Lys	Thr	Ile	Tyr	Val	Ser	Ser	Gly	Asn	Gly	Ala	Asp	Asp	Phe	210	215	220	
Gly	Lys	Glu	Gly	Ser	Val	Ala	Ile	Gly	Pro	Ala	Asn	Ala	Ala	Gly	Val	225	230	235	240
Gly	Leu	Glu	Val	Ile	Ser	Arg	Met	Thr	Ser	Gln	Thr	Phe	Val	Asp	Arg	245	250	255	
Ala	Ser	Gln	Ala	Gly	Val	Glu	Val	Val	Ala	Ser	Phe	Arg	Pro	Ser	Gly	260	265	270	
Val	His	Ser	Trp	Glu	Tyr	Trp	Gln	Phe	Glu	Met	Thr	Gln	Ala	Phe	Pro	275	280	285	
His	Ile	Ala	Asn	Ala	Leu	Gly	Met	Ser	Thr	Glu	Asp	Arg	Gly	Val	Glu	290	295	300	
Cys	Ala	Pro	Val	Gly	Ala	Ile	Ala	Asp	Ala	Val	Ala	Asp	Gly	Ala	Met	305	310	315	320
Gly	Thr	Cys	Leu	Thr	Asn	Glu	Tyr	Asp	Val	Thr	Gly	Gly	Lys	Ala	Gln	325	330	335	
Asp	Phe	Ala	Asn	Gly	Arg	Ala	Tyr	Trp	Ser	Ala	Asn	Thr	Gly	Ala	Phe	340	345	350	
Gly	Leu	Val	Gly	Arg	Ile	Asn	Ala	Arg	Tyr	Ser	Glu	Leu	Gly	Gly	Pro	355	360	365	
Ala	Ser	Trp	Leu	Gly	Tyr	Pro	Thr	Ser	Ser	Glu	Leu	Lys	Thr	Pro	Asp	370	375	380	
Gly	Arg	Gly	Arg	Phe	Val	Thr	Phe	Glu	His	Gly	Ser	Ile	Tyr	Trp	Thr	385	390	395	400
Ala	Thr	Thr	Gly	Pro	Trp	Glu	Ile	Pro	Gly	Asp	Met	Leu	Ala	Ala	Trp	405	410	415	
Gly	Thr	Gln	Asp	Tyr	Glu	Lys	Gly	Ser	Leu	Gly	Tyr	Pro	Thr	Gly	Ala	420	425	430	
Ala	Val	Glu	Tyr	Asn	Gly	Gly	Leu	Arg	Gln	Gln	Phe	Glu	Gly	Gly	Tyr	435	440	445	
Val	Phe	Arg	Thr	Ser	Asn	Asn	Gln	Ser	Tyr	Trp	Val	Arg	Gly	Glu	Ile	450	455	460	
Ser	Lys	Lys	Tyr	Ala	Glu	Asp	Gly	Ile	Phe	Ala	Gln	Leu	Gly	Phe	Pro				

465		470		475		480
Thr Gly Asn Glu Lys Leu Ile Asn Gly Gly Ala Phe Gln Glu Phe Glu						
		485		490		495
Lys Gly Asn Ile Tyr Trp Ser Ala Ser Thr Gly Ala His Val Ile Leu						
		500		505		510
His Gly Asp Ile Phe Asp Ala Trp Gly Ala Lys Gly Trp Glu Gln Gly						
		515		520		525
Glu Tyr Gly Phe Pro Thr Ser Asp Gln Thr Ala Ile Thr Ala Gly Gly						
		530		535		540
Gln Thr Ile Asp Phe Gln Asn Gly Thr Ile Arg Gln Val Asn Gly Arg						
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						560
Ile Glu Glu Ser Arg						
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<210> 535  
 <211> 1704  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(1681)  
 <223> RXN03054

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 Met Lys Leu Phe Ser  
 1 5  
 aag gct gca ggc gtc att gct gca gca ctt ctt gtt gca ggt ggt ata 163  
 Lys Ala Ala Gly Val Ile Ala Ala Ala Leu Leu Val Ala Gly Gly Ile  
 10 15 20  
 gca cct gtg gca cag ggg caa gct agt cag gtg gtc aca cct gaa gac 211  
 Ala Pro Val Ala Gln Gly Gln Ala Ser Gln Val Val Thr Pro Glu Asp  
 25 30 35  
 caa gat gcg tat gtt caa cag ttc cac cac gaa ggg aat acc cca cct 259  
 Gln Asp Ala Tyr Val Gln Gln Phe His His Glu Gly Asn Thr Pro Pro  
 40 45 50  
 gtg gta gac ggg gtg ggt ggc tac act gag caa gaa atc gcc gag atc 307  
 Val Val Asp Gly Val Gly Gly Tyr Thr Glu Gln Glu Ile Ala Glu Ile  
 55 60 65  
 cac gag gct atc cga caa gcc caa gaa tct ggc gca cct aat gaa gag 355  
 His Glu Ala Ile Arg Gln Ala Gln Glu Ser Gly Ala Pro Asn Glu Glu  
 70 75 80 85  
 ctc att ccg ggt gag atg tgg tca gat aag gtg gag ctg cca gta act 403  
 Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val Glu Leu Pro Val Thr  
 90 95 100

att gat aaa gca gcc gct gat gag gca gag ata gct att gca cag caa	451
Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile Ala Ile Ala Gln Gln	
105 110 115	
caa tct cag cca cag acg cga ggc ctt gct gcg gct gcg gcg tgt cag	499
Gln Ser Gln Pro Gln Thr Arg Gly Leu Ala Ala Ala Ala Cys Gln	
120 125 130	
acg ttt tgg ccg tca cct cat cag gtt tgt ggt gct att tta gag cgc	547
Thr Phe Trp Pro Ser Pro His Gln Val Cys Gly Ala Ile Leu Glu Arg	
135 140 145	
tat att cag cag ggt gcc cag ttt ggg tgg atg ttg ttt ccg agt gaa	595
Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met Leu Phe Pro Ser Glu	
150 155 160 165	
ggc caa acg tta aat cct gat ggt cag ggg tat cgt cag ccg ttt atg	643
Gly Gln Thr Leu Asn Pro Asp Gly Gln Gly Tyr Arg Gln Arg Phe Met	
170 175 180	
aat ggg ttt gtt tat tgg cat ccg aca act ggt gcg cat gct gtt aat	691
Asn Gly Phe Val Tyr Trp His Pro Thr Thr Gly Ala His Ala Val Asn	
185 190 195	
aat tac agt gcg cag gtg tgg gag cgt aat ggg tgg gag tct ggg tgg	739
Asn Tyr Ser Ala Gln Val Trp Glu Arg Asn Gly Trp Glu Ser Gly Trp	
200 205 210	
atg ggt tat ccc act ggt ggt gaa gtc cct gtg aat ggt tcc aat ccg	787
Met Gly Tyr Pro Thr Gly Gly Glu Val Pro Val Asn Gly Ser Asn Pro	
215 220 225	
att gat ggt gag ttg agt ggg tgg gtg caa act ttc caa ggt ggg cga	835
Ile Asp Gly Glu Leu Ser Gly Trp Val Gln Thr Phe Gln Gly Gly Arg	
230 235 240 245	
gtg tat cgc agt ccg gta ttg gac ggt ttc cag gtg gcc agt att aat	883
Val Tyr Arg Ser Pro Val Leu Asp Gly Phe Gln Val Ala Ser Ile Asn	
250 255 260	
ggg ctg atc ttg gat aaa tgg ctt gaa ttg ggt ggt cct gat agt gac	931
Gly Leu Ile Leu Asp Lys Trp Leu Glu Leu Gly Gly Pro Asp Ser Asp	
265 270 275	
ctt ggt ttt ccc att gcg gat gag gct gtg aca gct gac ggt gtg ggt	979
Leu Gly Phe Pro Ile Ala Asp Glu Ala Val Thr Ala Asp Gly Val Gly	
280 285 290	
aga ttt tct gtt ttc cag aac gga gtt gtc tac tgg cat ccg caa cac	1027
Arg Phe Ser Val Phe Gln Asn Gly Val Val Tyr Trp His Pro Gln His	
295 300 305	
gga gct cac cct ata tta ggg aat ata tac agt atc tgg aga gaa gaa	1075
Gly Ala His Pro Ile Leu Gly Asn Ile Tyr Ser Ile Trp Arg Glu Glu	
310 315 320 325	
gga gct gag agt ggg gaa ttc ggt tac cct atc ggc gat cca gaa aag	1123
Gly Ala Glu Ser Gly Glu Phe Gly Tyr Pro Ile Gly Asp Pro Glu Lys	
330 335 340	

tat aca gaa aac atg gct aat cag gta ttc gaa aaa ggc gaa ctt gca 1171  
 Tyr Thr Glu Asn Met Ala Asn Gln Val Phe Glu Lys Gly Glu Leu Ala  
 345 350 355  
  
 gct aac cta tac ccc aat cct ctt gag gct ttt att gag ttt tta ccc 1219  
 Ala Asn Leu Tyr Pro Asn Pro Leu Glu Ala Phe Ile Glu Phe Leu Pro  
 360 365 370  
  
 ttt gct aat ctt gag gaa gca ata gag tat ttt gag aac gga ttg tca 1267  
 Phe Ala Asn Leu Glu Glu Ala Ile Glu Tyr Phe Glu Asn Gly Leu Ser  
 375 380 385  
  
 aat tct cgt gta gag gcg aat tca ctt aac gcc aag aaa gat tcg att 1315  
 Asn Ser Arg Val Glu Ala Asn Ser Leu Asn Ala Lys Lys Asp Ser Ile  
 390 395 400 405  
  
 caa tgt caa tcg caa tcc gct aac att cat gtg aga acg aag agt gac 1363  
 Gln Cys Gln Ser Gln Ser Ala Asn Ile His Val Arg Thr Lys Ser Asp  
 410 415 420  
  
 gga gtc ggg att agg gtt cca aag att ggg ttt aag gct agg atg gat 1411  
 Gly Val Gly Ile Arg Val Pro Lys Ile Gly Phe Lys Ala Arg Met Asp  
 425 430 435  
  
 tgc gac ctt cct gga act gtc tca gat gta gtg ggg tat gga tgg att 1459  
 Cys Asp Leu Pro Gly Thr Val Ser Asp Val Val Gly Tyr Gly Trp Ile  
 440 445 450  
  
 tac tac gac tat tgg gga cga tgg gct caa gca gca tat gca caa caa 1507  
 Tyr Tyr Asp Tyr Trp Gly Arg Trp Ala Gln Ala Ala Tyr Ala Gln Gln  
 455 460 465  
  
 ttc ttc ggt aat agg aat tct gtt gtg caa acc aat tta gag gcg ggt 1555  
 Phe Phe Gly Asn Arg Asn Ser Val Val Gln Thr Asn Leu Glu Ala Gly  
 470 475 480 485  
  
 tgc agc ggg gag aag aat aca tta ttt tgg ggt act tca tat ttt cag 1603  
 Cys Ser Gly Glu Lys Asn Thr Leu Phe Trp Gly Thr Ser Tyr Phe Gln  
 490 495 500  
  
 gtg act tat gaa ggt cag ccg tat ttc ggt cag tca gca act aat tac 1651  
 Val Thr Tyr Glu Gly Gln Pro Tyr Phe Gly Gln Ser Ala Thr Asn Tyr  
 505 510 515  
  
 gct tat ctt ccg tgt acg ata gac cgt agt taacataagg aatggaatag gag 1704  
 Ala Tyr Leu Pro Cys Thr Ile Asp Arg Ser  
 520 525

&lt;210&gt; 536

&lt;211&gt; 527

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 536

Met Lys Leu Phe Ser Lys Ala Ala Gly Val Ile Ala Ala Ala Leu Leu  
 1 5 10 15

Val Ala Gly Gly Ile Ala Pro Val Ala Gln Gly Gln Ala Ser Gln Val  
 20 25 30

Val Thr Pro Glu Asp Gln Asp Ala Tyr Val Gln Gln Phe His His Glu  
                   35                                  40                                  45  
 Gly Asn Thr Pro Pro Val Val Asp Gly Val Gly Gly Tyr Thr Glu Gln  
                   50                                  55                                  60  
 Glu Ile Ala Glu Ile His Glu Ala Ile Arg Gln Ala Gln Glu Ser Gly  
   65                                  70                                  75                                  80  
 Ala Pro Asn Glu Glu Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val  
                                   85                                  90                                  95  
 Glu Leu Pro Val Thr Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile  
                                   100                                  105                                  110  
 Ala Ile Ala Gln Gln Gln Ser Gln Pro Gln Thr Arg Gly Leu Ala Ala  
                                   115                                  120                                  125  
 Ala Ala Ala Cys Gln Thr Phe Trp Pro Ser Pro His Gln Val Cys Gly  
                                   130                                  135                                  140  
 Ala Ile Leu Glu Arg Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met  
   145                                  150                                  155                                  160  
 Leu Phe Pro Ser Glu Gly Gln Thr Leu Asn Pro Asp Gly Gln Gly Tyr  
                                   165                                  170                                  175  
 Arg Gln Arg Phe Met Asn Gly Phe Val Tyr Trp His Pro Thr Thr Gly  
                                   180                                  185                                  190  
 Ala His Ala Val Asn Asn Tyr Ser Ala Gln Val Trp Glu Arg Asn Gly  
                                   195                                  200                                  205  
 Trp Glu Ser Gly Trp Met Gly Tyr Pro Thr Gly Gly Glu Val Pro Val  
   210                                  215                                  220  
 Asn Gly Ser Asn Pro Ile Asp Gly Glu Leu Ser Gly Trp Val Gln Thr  
   225                                  230                                  235                                  240  
 Phe Gln Gly Gly Arg Val Tyr Arg Ser Pro Val Leu Asp Gly Phe Gln  
                                   245                                  250                                  255  
 Val Ala Ser Ile Asn Gly Leu Ile Leu Asp Lys Trp Leu Glu Leu Gly  
                                   260                                  265                                  270  
 Gly Pro Asp Ser Asp Leu Gly Phe Pro Ile Ala Asp Glu Ala Val Thr  
                                   275                                  280                                  285  
 Ala Asp Gly Val Gly Arg Phe Ser Val Phe Gln Asn Gly Val Val Tyr  
                                   290                                  295                                  300  
 Trp His Pro Gln His Gly Ala His Pro Ile Leu Gly Asn Ile Tyr Ser  
   305                                  310                                  315                                  320  
 Ile Trp Arg Glu Glu Gly Ala Glu Ser Gly Glu Phe Gly Tyr Pro Ile  
                                   325                                  330                                  335  
 Gly Asp Pro Glu Lys Tyr Thr Glu Asn Met Ala Asn Gln Val Phe Glu  
                                   340                                  345                                  350  
 Lys Gly Glu Leu Ala Ala Asn Leu Tyr Pro Asn Pro Leu Glu Ala Phe

355	360	365
Ile Glu Phe Leu Pro Phe Ala Asn Leu Glu Glu Ala Ile Glu Tyr Phe 370 375 380		
Glu Asn Gly Leu Ser Asn Ser Arg Val Glu Ala Asn Ser Leu Asn Ala 385 390 395 400		
Lys Lys Asp Ser Ile Gln Cys Gln Ser Gln Ser Ala Asn Ile His Val 405 410 415		
Arg Thr Lys Ser Asp Gly Val Gly Ile Arg Val Pro Lys Ile Gly Phe 420 425 430		
Lys Ala Arg Met Asp Cys Asp Leu Pro Gly Thr Val Ser Asp Val Val 435 440 445		
Gly Tyr Gly Trp Ile Tyr Tyr Asp Tyr Trp Gly Arg Trp Ala Gln Ala 450 455 460		
Ala Tyr Ala Gln Gln Phe Phe Gly Asn Arg Asn Ser Val Val Gln Thr 465 470 475 480		
Asn Leu Glu Ala Gly Cys Ser Gly Glu Lys Asn Thr Leu Phe Trp Gly 485 490 495		
Thr Ser Tyr Phe Gln Val Thr Tyr Glu Gly Gln Pro Tyr Phe Gly Gln 500 505 510		
Ser Ala Thr Asn Tyr Ala Tyr Leu Pro Cys Thr Ile Asp Arg Ser 515 520 525		

&lt;210&gt; 537

&lt;211&gt; 931

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(931)

&lt;223&gt; FRXA02886

&lt;400&gt; 537

gggtgaaata cgcgcacaaac aattttatttc acagaactta tgatttttttc gggttagggt 60

cagtttggttc acatcaacta gtaacgaaag gatcatgtga	atg aaa ctg ttt tcc	115
	Met Lys Leu Phe Ser	
	1 5	

aag gct gca ggc gtc att gct gca gca ctt ctt gtt gca ggt ggt ata	163
Lys Ala Ala Gly Val Ile Ala Ala Ala Leu Leu Val Ala Gly Gly Ile	
10 15 20	

gca cct gtg gca cag ggg caa gct agt cag gtg gtc aca cct gaa gac	211
Ala Pro Val Ala Gln Gly Gln Ala Ser Gln Val Val Thr Pro Glu Asp	
25 30 35	

caa gat gcg tat gtt caa cag ttc cac cac gaa ggg aat acc cca cct	259
Gln Asp Ala Tyr Val Gln Gln Phe His His Glu Gly Asn Thr Pro Pro	
40 45 50	

gtg gta gac ggg gtg ggt ggc tac act gag caa gaa atc gcc gag atc 307  
 Val Val Asp Gly Val Gly Gly Tyr Thr Glu Gln Glu Ile Ala Glu Ile  
 55 60 65  
 cac gag gct atc cga caa gcc caa gaa tct ggc gca cct aat gaa gag 355  
 His Glu Ala Ile Arg Gln Ala Gln Glu Ser Gly Ala Pro Asn Glu Glu  
 70 75 80 85  
 ctc att ccg ggt gag atg tgg tca gat aag gtg gag ctg cca gta act 403  
 Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val Glu Leu Pro Val Thr  
 90 95 100  
 att gat aaa gca gcc gct gat gag gca gag ata gct att gca cag caa 451  
 Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile Ala Ile Ala Gln Gln  
 105 110 115  
 caa tct cag cca cag acg cga ggc ctt gct gcg gct gcg gcg tgt cag 499  
 Gln Ser Gln Pro Gln Thr Arg Gly Leu Ala Ala Ala Ala Ala Cys Gln  
 120 125 130  
 acg ttt tgg ccg tca cct cat cag gtt tgt ggt gct att tta gag cgc 547  
 Thr Phe Trp Pro Ser Pro His Gln Val Cys Gly Ala Ile Leu Glu Arg  
 135 140 145  
 tat att cag cag ggt gcc cag ttt ggg tgg atg ttg ttt ccg agt gaa 595  
 Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met Leu Phe Pro Ser Glu  
 150 155 160 165  
 ggc caa acg tta aat cct gat ggt cag ggg tat cgt cag cgg ttt atg 643  
 Gly Gln Thr Leu Asn Pro Asp Gly Gln Gly Tyr Arg Gln Arg Phe Met  
 170 175 180  
 aat ggg ttt gtt tat tgg cat ccg aca act ggt gcg cat gct gtt aat 691  
 Asn Gly Phe Val Tyr Trp His Pro Thr Thr Gly Ala His Ala Val Asn  
 185 190 195  
 aat tac agt gcg cag gtg tgg gag cgt aat ggg tgg gag tct ggg tgg 739  
 Asn Tyr Ser Ala Gln Val Trp Glu Arg Asn Gly Trp Glu Ser Gly Trp  
 200 205 210  
 atg ggt tat ccc act ggt ggt gaa gtc cct gtg aat ggt tcc aat ccg 787  
 Met Gly Tyr Pro Thr Gly Gly Glu Val Pro Val Asn Gly Ser Asn Pro  
 215 220 225  
 att gat ggt gag ttg agt ggg tgg gtg caa act ttc caa ggt ggg cga 835  
 Ile Asp Gly Glu Leu Ser Gly Trp Val Gln Thr Phe Gln Gly Gly Arg  
 230 235 240 245  
 gtg tat cgc agt ccg gta ttg gac ggt ttc cag gtg gcc agt att aat 883  
 Val Tyr Arg Ser Pro Val Leu Asp Gly Phe Gln Val Ala Ser Ile Asn  
 250 255 260  
 ggg ctg atc ttg gat aaa tgg ctt gaa ttg ggt ggt cct gat agt gac 931  
 Gly Leu Ile Leu Asp Lys Trp Leu Glu Leu Gly Gly Pro Asp Ser Asp  
 265 270 275

&lt;210&gt; 538

&lt;211&gt; 277

&lt;212&gt; PRT

<213> Corynebacterium glutamicum

<400> 538

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Met Lys Leu Phe Ser Lys Ala Ala Gly Val Ile Ala Ala Ala Leu Leu
 1             5             10             15

Val Ala Gly Gly Ile Ala Pro Val Ala Gln Gly Gln Ala Ser Gln Val
          20             25             30

Val Thr Pro Glu Asp Gln Asp Ala Tyr Val Gln Gln Phe His His Glu
          35             40             45

Gly Asn Thr Pro Pro Val Val Asp Gly Val Gly Gly Tyr Thr Glu Gln
          50             55             60

Glu Ile Ala Glu Ile His Glu Ala Ile Arg Gln Ala Gln Glu Ser Gly
          65             70             75             80

Ala Pro Asn Glu Glu Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val
          85             90             95

Glu Leu Pro Val Thr Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile
          100            105            110

Ala Ile Ala Gln Gln Gln Ser Gln Pro Gln Thr Arg Gly Leu Ala Ala
          115            120            125

Ala Ala Ala Cys Gln Thr Phe Trp Pro Ser Pro His Gln Val Cys Gly
          130            135            140

Ala Ile Leu Glu Arg Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met
          145            150            155            160

Leu Phe Pro Ser Glu Gly Gln Thr Leu Asn Pro Asp Gly Gln Gly Tyr
          165            170            175

Arg Gln Arg Phe Met Asn Gly Phe Val Tyr Trp His Pro Thr Thr Gly
          180            185            190

Ala His Ala Val Asn Asn Tyr Ser Ala Gln Val Trp Glu Arg Asn Gly
          195            200            205

Trp Glu Ser Gly Trp Met Gly Tyr Pro Thr Gly Gly Glu Val Pro Val
          210            215            220

Asn Gly Ser Asn Pro Ile Asp Gly Glu Leu Ser Gly Trp Val Gln Thr
          225            230            235            240

Phe Gln Gly Gly Arg Val Tyr Arg Ser Pro Val Leu Asp Gly Phe Gln
          245            250            255

Val Ala Ser Ile Asn Gly Leu Ile Leu Asp Lys Trp Leu Glu Leu Gly
          260            265            270

Gly Pro Asp Ser Asp
          275

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<210> 539

<211> 653

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(630)

<223> RXN03039

<220>

<223> All occurrences of Xaa = any amino acid

<400> 539

gca ctc ccg caa tac acc gac cca cgc tac ccc ctc ggc aaa gac gac	48
Ala Leu Pro Gln Tyr Thr Asp Pro Arg Tyr Pro Leu Gly Lys Asp Asp	
1 5 10 15	
ctg ccc aaa gca acc atc gac atg gag cca gaa gct ctt gcg cgc ctt	96
Leu Pro Lys Ala Thr Ile Asp Met Glu Pro Glu Ala Leu Ala Arg Leu	
20 25 30	
gag cga ttc gtc ggc gtt gac ggt gat cgc atc cgc caa atc aac gcg	144
Glu Arg Phe Val Gly Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala	
35 40 45	
tac tcg cca tca atg gga cgc acc att cct cta gtc tgg gtc gtg cca	192
Tyr Ser Pro Ser Met Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro	
50 55 60	
gaa gac aac acc gtg cct ggc cca acg gtc tac gca ctc ggc ggc ggc	240
Glu Asp Asn Thr Val Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly	
65 70 75 80	
gac ggt ggc caa ggc ggc caa aac tgg gtc acc cgc acc gac ctt gat	288
Asp Gly Gly Gln Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Asp	
85 90 95	
gag ttg acc agt gaa aac aac atc aac ctc atc atg ccc atg ctc gga	336
Glu Leu Thr Ser Glu Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly	
100 105 110	
tct ttt agt ttc tac gct gac tgg gca ggc gaa agc gaa tcc atg ggt	384
Ser Phe Ser Phe Tyr Ala Asp Trp Ala Gly Glu Ser Glu Ser Met Gly	
115 120 125	
ggt gcg caa cag tgg gaa aca ttc ctc atg cac gaa ctr ccm gag ccg	432
Gly Ala Gln Gln Trp Glu Thr Phe Leu Met His Glu Xaa Xaa Glu Pro	
130 135 140	
cta gaa gcg gcc atc ggc gca gac ggg caa cgc agc atc gtc ggc atg	480
Leu Glu Ala Ala Ile Gly Ala Asp Gly Gln Arg Ser Ile Val Gly Met	
145 150 155 160	
tcc atg tcc ggg gga tcr gtg ctg aac ttt gcg acg cat gac ccc aac	528
Ser Met Ser Gly Gly Xaa Val Leu Asn Phe Ala Thr His Asp Pro Asn	
165 170 175	
ttt tay tcc tck gtc ggc tca ttt tct gga tgt gcc gaa acc aac tcc	576
Phe Xaa Ser Xaa Val Gly Ser Phe Ser Gly Cys Ala Glu Thr Asn Ser	
180 185 190	
tgg atg ggr cgc cgn tgg cat cgc agc cac tgc cta caa cgg caa tgt	624
Trp Met Xaa Arg Arg Trp His Arg Ser His Cys Leu Gln Arg Gln Cys	

195

200

205

cgt gcc tgagcaaatc tttggtgaag tag  
 Arg Ala  
 210

653

&lt;210&gt; 540

&lt;211&gt; 210

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;223&gt; All occurrences of Xaa = any amino acid

&lt;400&gt; 540

Ala Leu Pro Gln Tyr Thr Asp Pro Arg Tyr Pro Leu Gly Lys Asp Asp  
 1 5 10 15

Leu Pro Lys Ala Thr Ile Asp Met Glu Pro Glu Ala Leu Ala Arg Leu  
 20 25 30

Glu Arg Phe Val Gly Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala  
 35 40 45

Tyr Ser Pro Ser Met Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro  
 50 55 60

Glu Asp Asn Thr Val Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly  
 65 70 75 80

Asp Gly Gly Gln Gly Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Asp  
 85 90 95

Glu Leu Thr Ser Glu Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly  
 100 105 110

Ser Phe Ser Phe Tyr Ala Asp Trp Ala Gly Glu Ser Glu Ser Met Gly  
 115 120 125

Gly Ala Gln Gln Trp Glu Thr Phe Leu Met His Glu Xaa Xaa Glu Pro  
 130 135 140

Leu Glu Ala Ala Ile Gly Ala Asp Gly Gln Arg Ser Ile Val Gly Met  
 145 150 155 160

Ser Met Ser Gly Gly Xaa Val Leu Asn Phe Ala Thr His Asp Pro Asn  
 165 170 175

Phe Xaa Ser Xaa Val Gly Ser Phe Ser Gly Cys Ala Glu Thr Asn Ser  
 180 185 190

Trp Met Xaa Arg Arg Trp His Arg Ser His Cys Leu Gln Arg Gln Cys  
 195 200 205

Arg Ala  
 210

&lt;210&gt; 541

&lt;211&gt; 809

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(786)

&lt;223&gt; FRXA02894

&lt;400&gt; 541

ttc ctc atg cac gaa ctg cca gag ccg cta gaa gcg gcc atc ggc gca	48
Phe Leu Met His Glu Leu Pro Glu Pro Leu Glu Ala Ala Ile Gly Ala	
1 5 10 15	
gac ggg caa cgc agc atc gtc ggc atg tcc atg tcc ggg gga tca gtg	96
Asp Gly Gln Arg Ser Ile Val Gly Met Ser Met Ser Gly Gly Ser Val	
20 25 30	
ctg aac ttt gcg acg cat gac ccc aac ttt tac tcc tcg gtc ggc tca	144
Leu Asn Phe Ala Thr His Asp Pro Asn Phe Tyr Ser Ser Val Gly Ser	
35 40 45	
ttt tct gga tgt gcc gaa acc aac tcc tgg atg gga cgc cgt ggc atc	192
Phe Ser Gly Cys Ala Glu Thr Asn Ser Trp Met Gly Arg Arg Gly Ile	
50 55 60	
gca gcc acc gcc tac aac ggc aat gtc gtg cct gag caa atc ttt ggt	240
Ala Ala Thr Ala Tyr Asn Gly Asn Val Val Pro Glu Gln Ile Phe Gly	
65 70 75 80	
gaa gta gac agt gat tac tcc cgc tat aac gat cct ttg ctc aac gct	288
Glu Val Asp Ser Asp Tyr Ser Arg Tyr Asn Asp Pro Leu Leu Asn Ala	
85 90 95	
gcg aag ctc gaa gaa caa gac aac ctc tac atc ttc gcc ggt tcc ggt	336
Ala Lys Leu Glu Glu Gln Asp Asn Leu Tyr Ile Phe Ala Gly Ser Gly	
100 105 110	
gtg ttc tct gaa cta gat gtc att ggt gac aac gca ccg att gat gag	384
Val Phe Ser Glu Leu Asp Val Ile Gly Asp Asn Ala Pro Ile Asp Glu	
115 120 125	
gat gcg ttt aaa aac cgc gtt ctg gtc gga ttt gaa atc gaa gct atg	432
Asp Ala Phe Lys Asn Arg Val Leu Val Gly Phe Glu Ile Glu Ala Met	
130 135 140	
tcc aac acc tgc acc cat aat ctt aag gct gcg act gat caa atg ggc	480
Ser Asn Thr Cys Thr His Asn Leu Lys Ala Ala Thr Asp Gln Met Gly	
145 150 155 160	
att gac aac att aac tat gat ttc cga cca acc ggt act cat gct tgg	528
Ile Asp Asn Ile Asn Tyr Asp Phe Arg Pro Thr Gly Thr His Ala Trp	
165 170 175	
gac tat tgg aat gag gca ctg cac cgt ttc ttc ccg ttg atg atg cag	576
Asp Tyr Trp Asn Glu Ala Leu His Arg Phe Phe Pro Leu Met Met Gln	
180 185 190	
ggc ttc ggg ctt gat ggt ggt ccg atc ccg gtt tat aac cct aac ggt	624
Gly Phe Gly Leu Asp Gly Gly Pro Ile Pro Val Tyr Asn Pro Asn Gly	
195 200 205	

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gtg tcc tct agt gag tct tct tct gag ctg tcg tct gat gtg agt ctt 672
Val Ser Ser Ser Glu Ser Ser Ser Glu Leu Ser Ser Ser Asp Val Ser Leu
210 215 220

ggc acc gtg atc ggt agt gtg gcg gga agc tcc gga tca agt gaa ggc 720
Gly Thr Val Ile Gly Ser Val Ala Gly Ser Ser Gly Ser Ser Glu Gly
225 230 235 240

agc agc gtc cga gag ttc ctt gca gga agt tcc gga tca agc caa tca 768
Ser Ser Val Arg Glu Phe Leu Ala Gly Ser Ser Gly Ser Ser Gln Ser
245 250 255

aca gga agc ttc tac gaa tagctagggc tgcgcaagat tcc 809
Thr Gly Ser Phe Tyr Glu
260

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&lt;210&gt; 542

&lt;211&gt; 262

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 542

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Phe Leu Met His Glu Leu Pro Glu Pro Leu Glu Ala Ala Ile Gly Ala
1 5 10 15

Asp Gly Gln Arg Ser Ile Val Gly Met Ser Met Ser Gly Gly Ser Val
20 25 30

Leu Asn Phe Ala Thr His Asp Pro Asn Phe Tyr Ser Ser Val Gly Ser
35 40 45

Phe Ser Gly Cys Ala Glu Thr Asn Ser Trp Met Gly Arg Arg Gly Ile
50 55 60

Ala Ala Thr Ala Tyr Asn Gly Asn Val Val Pro Glu Gln Ile Phe Gly
65 70 75 80

Glu Val Asp Ser Asp Tyr Ser Arg Tyr Asn Asp Pro Leu Leu Asn Ala
85 90 95

Ala Lys Leu Glu Glu Gln Asp Asn Leu Tyr Ile Phe Ala Gly Ser Gly
100 105 110

Val Phe Ser Glu Leu Asp Val Ile Gly Asp Asn Ala Pro Ile Asp Glu
115 120 125

Asp Ala Phe Lys Asn Arg Val Leu Val Gly Phe Glu Ile Glu Ala Met
130 135 140

Ser Asn Thr Cys Thr His Asn Leu Lys Ala Ala Thr Asp Gln Met Gly
145 150 155 160

Ile Asp Asn Ile Asn Tyr Asp Phe Arg Pro Thr Gly Thr His Ala Trp
165 170 175

Asp Tyr Trp Asn Glu Ala Leu His Arg Phe Phe Pro Leu Met Met Gln
180 185 190

Gly Phe Gly Leu Asp Gly Gly Pro Ile Pro Val Tyr Asn Pro Asn Gly
195 200 205

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Val Ser Ser Ser Glu Ser Ser Ser Glu Leu Ser Ser Asp Val Ser Leu  
 210 215 220

Gly Thr Val Ile Gly Ser Val Ala Gly Ser Ser Gly Ser Ser Glu Gly  
 225 230 235 240

Ser Ser Val Arg Glu Phe Leu Ala Gly Ser Ser Gly Ser Ser Gln Ser  
 245 250 255

Thr Gly Ser Phe Tyr Glu  
 260

<210> 543  
 <211> 686  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(675)  
 <223> FRXA02904

<400> 543  
 acc gac cca cgc tac ccc ctc ggc aaa gac gac ctg ccc aaa gca acc 48  
 Thr Asp Pro Arg Tyr Pro Leu Gly Lys Asp Asp Leu Pro Lys Ala Thr  
 1 5 10 15

atc gac atg gag cca gaa gct ctt gcg cgc ctt gag cga ttc gtc ggc 96  
 Ile Asp Met Glu Pro Glu Ala Leu Ala Arg Leu Glu Arg Phe Val Gly  
 20 25 30

gtt gac ggt gat cgc atc cgc caa atc aac gcg tac tcg cca tca atg 144  
 Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser Pro Ser Met  
 35 40 45

gga cgc acc att cct cta gtc tgg gtc gtg cca gaa gac aac acc gtg 192  
 Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro Glu Asp Asn Thr Val  
 50 55 60

cct ggc cca acg gtc tac gca ctc ggc ggc ggc gac ggt ggc caa ggc 240  
 Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly Asp Gly Gly Gln Gly  
 65 70 75 80

ggc caa aac tgg gtc acc cgc acc gac ctt gat gag ttg acc agt gaa 288  
 Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Asp Glu Leu Thr Ser Glu  
 85 90 95

aac aac atc aac ctc atc atg ccc atg ctc gga tct ttt agt ttc tac 336  
 Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly Ser Phe Ser Phe Tyr  
 100 105 110

gct gac tgg gca ggc gaa agc gaa tcc atg ggt ggt gcg caa cag tgg 384  
 Ala Asp Trp Ala Gly Glu Ser Glu Ser Met Gly Gly Ala Gln Gln Trp  
 115 120 125

gaa aca ttc ctc atg cac gaa cta ccc gag ccg cta gaa gcg gcc atc 432  
 Glu Thr Phe Leu Met His Glu Leu Pro Glu Pro Leu Glu Ala Ala Ile  
 130 135 140

ggc gca gac ggg caa cgc agc atc gtc ggc atg tcc atg tcc ggg gga 480  
 Gly Ala Asp Gly Gln Arg Ser Ile Val Gly Met Ser Met Ser Gly Gly  
 145 150 155 160

tcg gtg ctg aac ttt gcg acg cat gac ccc aac ttt tat tcc tct gtc 528  
 Ser Val Leu Asn Phe Ala Thr His Asp Pro Asn Phe Tyr Ser Ser Val  
 165 170 175

ggc tca ttt tct gga tgt gcc gaa acc aac tcc tgg atg ggg cgc cgt 576  
 Gly Ser Phe Ser Gly Cys Ala Glu Thr Asn Ser Trp Met Gly Arg Arg  
 180 185 190

ggc atc gca gcc act gcc tac aac ggc aat gtc gtg cct gag caa atc 624  
 Gly Ile Ala Ala Thr Ala Tyr Asn Gly Asn Val Val Pro Glu Gln Ile  
 195 200 205

ttt ggt gaa gta gac agt gat tac tct cgc tat aac gat cct agt att 672  
 Phe Gly Glu Val Asp Ser Asp Tyr Ser Arg Tyr Asn Asp Pro Ser Ile  
 210 215 220

cta tagtgtcacc t 686  
 Leu  
 225

<210> 544

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 544

Thr Asp Pro Arg Tyr Pro Leu Gly Lys Asp Asp Leu Pro Lys Ala Thr  
 1 5 10 15

Ile Asp Met Glu Pro Glu Ala Leu Ala Arg Leu Glu Arg Phe Val Gly  
 20 25 30

Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser Pro Ser Met  
 35 40 45

Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro Glu Asp Asn Thr Val  
 50 55 60

Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly Asp Gly Gly Gln Gly  
 65 70 75 80

Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Asp Glu Leu Thr Ser Glu  
 85 90 95

Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly Ser Phe Ser Phe Tyr  
 100 105 110

Ala Asp Trp Ala Gly Glu Ser Glu Ser Met Gly Gly Ala Gln Gln Trp  
 115 120 125

Glu Thr Phe Leu Met His Glu Leu Pro Glu Pro Leu Glu Ala Ala Ile  
 130 135 140

Gly Ala Asp Gly Gln Arg Ser Ile Val Gly Met Ser Met Ser Gly Gly  
 145 150 155 160

Leu  
225

gag gtt gtt tac gat cct tcg aag att tcc ctc gag cag ctt gtt gcc 451  
Glu Val Val Tyr Asp Pro Ser Lys Ile Ser Leu Glu Gln Leu Val Ala  
105 110 115

cgc ggc ctg gaa gca cac gat ccg act cag ggt ttc cgc cag ggt aac 499  
 Arg Gly Leu Glu Ala His Asp Pro Thr Gln Gly Phe Arg Gln Gly Asn  
 120 125 130  
  
 gat gtg gga acg cag tac cgc tct gct tat tac acc gag aac gaa gag 547  
 Asp Val Gly Thr Gln Tyr Arg Ser Ala Tyr Tyr Thr Glu Asn Glu Glu  
 135 140 145  
  
 gac gct gcg cgc gta aaa gcc gtg gtc gat gcc tat ggt gag acg ctg 595  
 Asp Ala Ala Arg Val Lys Ala Val Val Asp Ala Tyr Gly Glu Thr Leu  
 150 155 160 165  
  
 aag cag cac ggt ttt ggt gaa atc acc acg gaa atc ggt gtc att agc 643  
 Lys Gln His Gly Phe Gly Glu Ile Thr Thr Glu Ile Gly Val Ile Ser  
 170 175 180  
  
 ccg tct gac tac ttc ctc gcc gag gat tac cac cag caa tac ctg gac 691  
 Pro Ser Asp Tyr Phe Leu Ala Glu Asp Tyr His Gln Gln Tyr Leu Asp  
 185 190 195  
  
 aag aat ccc gat ggc tac tgc cct cat cac tcc acg ggc atc ccg tgc 739  
 Lys Asn Pro Asp Gly Tyr Cys Pro His His Ser Thr Gly Ile Pro Cys  
 200 205 210  
  
 ggg gta gaa gct taaaagattt ttgcttttcg acg 774  
 Gly Val Glu Ala  
 215

&lt;210&gt; 546

&lt;211&gt; 217

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 546

Met Ala Trp Phe Phe Ala Pro Glu Pro Val Met Val Thr Ala Asp Glu  
 1 5 10 15  
  
 Ala Leu Lys Gly Gly Arg His Pro Val Leu Glu Asn Pro Ala Pro His  
 20 25 30  
  
 Thr Val Leu Gly Thr Pro Val Thr Gly Pro Trp Lys Glu Gly Gln Gln  
 35 40 45  
  
 Arg Ile Trp Ile Gly Leu Gly Cys Phe Trp Gly Val Glu Gln Met Tyr  
 50 55 60  
  
 Trp Gln Met Asp Gly Val Glu Gly Thr Ser Val Gly Tyr Ala Gly Gly  
 65 70 75 80  
  
 Phe Thr Pro Asn Pro Thr Tyr Arg Glu Val Cys Ser Gly Arg Thr Gly  
 85 90 95  
  
 His Thr Glu Ile Val Glu Val Val Tyr Asp Pro Ser Lys Ile Ser Leu  
 100 105 110  
  
 Glu Gln Leu Val Ala Arg Gly Leu Glu Ala His Asp Pro Thr Gln Gly  
 115 120 125  
  
 Phe Arg Gln Gly Asn Asp Val Gly Thr Gln Tyr Arg Ser Ala Tyr Tyr  
 130 135 140

Thr Glu Asn Glu Glu Asp Ala Ala Arg Val Lys Ala Val Val Asp Ala  
 145 150 155 160  
 Tyr Gly Glu Thr Leu Lys Gln His Gly Phe Gly Glu Ile Thr Thr Glu  
 165 170 175  
 Ile Gly Val Ile Ser Pro Ser Asp Tyr Phe Leu Ala Glu Asp Tyr His  
 180 185 190  
 Gln Gln Tyr Leu Asp Lys Asn Pro Asp Gly Tyr Cys Pro His His Ser  
 195 200 205  
 Thr Gly Ile Pro Cys Gly Val Glu Ala  
 210 215

<210> 547  
 <211> 444  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <223> RXA01431

<400> 547  
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 attccccagg agtcccg tca ttgttaattt aggagaaaacc atg agc aat gtt gtt 115  
 Met Ser Asn Val Val  
 1 5  
 gca gta acc gag cag acc ttc aag tcc acc gtc atc gat tcc gac aag 163  
 Ala Val Thr Glu Gln Thr Phe Lys Ser Thr Val Ile Asp Ser Asp Lys  
 10 15 20  
 cca gtc atc gtt gac ttc tgg gca gaa tgg tgt ggc ccc tgc aag aag 211  
 Pro Val Ile Val Asp Phe Trp Ala Glu Trp Cys Gly Pro Cys Lys Lys  
 25 30 35  
 ctc agc ccc atc att gag gaa atc gca ggc gag tac ggc gac aag gca 259  
 Leu Ser Pro Ile Ile Glu Glu Ile Ala Gly Glu Tyr Gly Asp Lys Ala  
 40 45 50  
 gtc gtt gcc agc gtc gac gtc gat gca gag cgt acc ttg ggt gcc atg 307  
 Val Val Ala Ser Val Asp Val Asp Ala Glu Arg Thr Leu Gly Ala Met  
 55 60 65  
 ttc cag att atg tcg att cct tct gtt ctc att ttc aaa aat ggt gca 355  
 Phe Gln Ile Met Ser Ile Pro Ser Val Leu Ile Phe Lys Asn Gly Ala  
 70 75 80 85  
 aaa gtc gag gaa ttt gtc ggt ctg cgc ccc aag aac gaa att gtg gaa 403  
 Lys Val Glu Glu Phe Val Gly Leu Arg Pro Lys Asn Glu Ile Val Glu  
 90 95 100  
 aaa cta gag aag cac ctc tagctggtat tcttactgca gtc 444  
 Lys Leu Glu Lys His Leu  
 105

<210> 548  
 <211> 107  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 548  
 Met Ser Asn Val Val Ala Val Thr Glu Gln Thr Phe Lys Ser Thr Val  
     1                    5                    10                    15  
 Ile Asp Ser Asp Lys Pro Val Ile Val Asp Phe Trp Ala Glu Trp Cys  
                     20                    25                    30  
 Gly Pro Cys Lys Lys Leu Ser Pro Ile Ile Glu Glu Ile Ala Gly Glu  
                     35                    40                    45  
 Tyr Gly Asp Lys Ala Val Val Ala Ser Val Asp Val Asp Ala Glu Arg  
             50                    55                    60  
 Thr Leu Gly Ala Met Phe Gln Ile Met Ser Ile Pro Ser Val Leu Ile  
     65                    70                    75                    80  
 Phe Lys Asn Gly Ala Lys Val Glu Glu Phe Val Gly Leu Arg Pro Lys  
                     85                    90                    95  
 Asn Glu Ile Val Glu Lys Leu Glu Lys His Leu  
                     100                    105

<210> 549  
 <211> 1074  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
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 <222> (101)..(1051)  
 <223> RXA01432

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 gtgatgctgc actttttacgt ttactacttt gagggaaaca atg tct gaa gaa caa 115  
   Met Ser Glu Glu Gln  
   1                    5  
 tct gcc gta gca cca aag att cat gat gtc gcc atc atc ggc tcc ggt 163  
 Ser Ala Val Ala Pro Lys Ile His Asp Val Ala Ile Ile Gly Ser Gly  
                     10                    15                    20  
 cca gct ggc tat acc gca gca gta tat gca gcc cgc gct gac ctc aac 211  
 Pro Ala Gly Tyr Thr Ala Ala Val Tyr Ala Ala Arg Ala Asp Leu Asn  
                     25                    30                    35  
 ccc atc atg ttc gag ggc tat gaa tac ggt gga tct ttg atg acc act 259  
 Pro Ile Met Phe Glu Gly Tyr Glu Tyr Gly Gly Ser Leu Met Thr Thr  
                     40                    45                    50  
 act gac gtg gaa aac ttc cca ggc ttt gaa aag gga atc ctg ggc cca 307  
 Thr Asp Val Glu Asn Phe Pro Gly Phe Glu Lys Gly Ile Leu Gly Pro

55	60	65	
gag ctc atg gaa aac atg cgc gct cag gcc gag cgt ttc ggc acc gac			355
Glu Leu Met Glu Asn Met Arg Ala Gln Ala Glu Arg Phe Gly Thr Asp			
70	75	80	85
atg cac atg gag ctt gtc gac cgc gtt gat ctc acc ggc gac atc aag			403
Met His Met Glu Leu Val Asp Arg Val Asp Leu Thr Gly Asp Ile Lys			
	90	95	100
aag ctg tgg gtc ggc gac gat gag tac cac gcg cgt gct gtc atc ttg			451
Lys Leu Trp Val Gly Asp Asp Glu Tyr His Ala Arg Ala Val Ile Leu			
	105	110	115
tcc atg ggt tct gca cct cgc tac ttg ggt gtg aag ggc gag cag gaa			499
Ser Met Gly Ser Ala Pro Arg Tyr Leu Gly Val Lys Gly Glu Gln Glu			
	120	125	130
ctg ctc ggc cgc ggc gtt tct gca tgt gca acc tgc gat ggt ttc ttc			547
Leu Leu Gly Arg Gly Val Ser Ala Cys Ala Thr Cys Asp Gly Phe Phe			
	135	140	145
ttc cgc gat cag gac atc gcc gtg atc ggt ggt ggc gac tcc gcg atg			595
Phe Arg Asp Gln Asp Ile Ala Val Ile Gly Gly Gly Asp Ser Ala Met			
150	155	160	165
gag gaa gca acc ttc ctc acc aag ttc gct cgc agt gtc acc atc gtg			643
Glu Glu Ala Thr Phe Leu Thr Lys Phe Ala Arg Ser Val Thr Ile Val			
	170	175	180
cac cgc cgc gaa gag ttc cgc gcc agc gcc atc atg ctg gag cgt gct			691
His Arg Arg Glu Glu Phe Arg Ala Ser Ala Ile Met Leu Glu Arg Ala			
	185	190	195
cag aag aac gag aag att cgc ttc gtc acc aac aag act gtc gaa gag			739
Gln Lys Asn Glu Lys Ile Arg Phe Val Thr Asn Lys Thr Val Glu Glu			
	200	205	210
gtc atc gag gca gac ggc aag gtc agc ggt ctg aag ctc aac gac acc			787
Val Ile Glu Ala Asp Gly Lys Val Ser Gly Leu Lys Leu Asn Asp Thr			
	215	220	225
gtc act ggt gaa gat tcc gtc ttg gat gtc acc gcc atg ttc gtt gcc			835
Val Thr Gly Glu Asp Ser Val Leu Asp Val Thr Ala Met Phe Val Ala			
230	235	240	245
atc ggc cat gat cca cgc tct gaa atc ctc gca ggt cag gtc gag gtt			883
Ile Gly His Asp Pro Arg Ser Glu Ile Leu Ala Gly Gln Val Glu Val			
	250	255	260
gat cct tcc aac tac gtt ttg gtt cag gag cct tcc acc cgc acc aac			931
Asp Pro Ser Asn Tyr Val Leu Val Gln Glu Pro Ser Thr Arg Thr Asn			
	265	270	275
ctt gat ggt gtt ttc gct gct ggc gac ctg gtg gac agc cac tac cag			979
Leu Asp Gly Val Phe Ala Ala Gly Asp Leu Val Asp Ser His Tyr Gln			
	280	285	290
cag gcc atc acc gca gct ggt tcc ggt tgc cgc gca gcg atc gat gca			1027
Gln Ala Ile Thr Ala Ala Gly Ser Gly Cys Arg Ala Ala Ile Asp Ala			
295	300	305	

gag cat tac cta gct tct ctg gcc taattcacag ttagccttaa acc  
 Glu His Tyr Leu Ala Ser Leu Ala  
 310 315

1074

&lt;210&gt; 550

&lt;211&gt; 317

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 550

Met Ser Glu Glu Gln Ser Ala Val Ala Pro Lys Ile His Asp Val Ala  
 1 5 10 15

Ile Ile Gly Ser Gly Pro Ala Gly Tyr Thr Ala Ala Val Tyr Ala Ala  
 20 25 30

Arg Ala Asp Leu Asn Pro Ile Met Phe Glu Gly Tyr Glu Tyr Gly Gly  
 35 40 45

Ser Leu Met Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Glu Lys  
 50 55 60

Gly Ile Leu Gly Pro Glu Leu Met Glu Asn Met Arg Ala Gln Ala Glu  
 65 70 75 80

Arg Phe Gly Thr Asp Met His Met Glu Leu Val Asp Arg Val Asp Leu  
 85 90 95

Thr Gly Asp Ile Lys Lys Leu Trp Val Gly Asp Asp Glu Tyr His Ala  
 100 105 110

Arg Ala Val Ile Leu Ser Met Gly Ser Ala Pro Arg Tyr Leu Gly Val  
 115 120 125

Lys Gly Glu Gln Glu Leu Leu Gly Arg Gly Val Ser Ala Cys Ala Thr  
 130 135 140

Cys Asp Gly Phe Phe Phe Arg Asp Gln Asp Ile Ala Val Ile Gly Gly  
 145 150 155 160

Gly Asp Ser Ala Met Glu Glu Ala Thr Phe Leu Thr Lys Phe Ala Arg  
 165 170 175

Ser Val Thr Ile Val His Arg Arg Glu Glu Phe Arg Ala Ser Ala Ile  
 180 185 190

Met Leu Glu Arg Ala Gln Lys Asn Glu Lys Ile Arg Phe Val Thr Asn  
 195 200 205

Lys Thr Val Glu Glu Val Ile Glu Ala Asp Gly Lys Val Ser Gly Leu  
 210 215 220

Lys Leu Asn Asp Thr Val Thr Gly Glu Asp Ser Val Leu Asp Val Thr  
 225 230 235 240

Ala Met Phe Val Ala Ile Gly His Asp Pro Arg Ser Glu Ile Leu Ala  
 245 250 255

Gly Gln Val Glu Val Asp Pro Ser Asn Tyr Val Leu Val Gln Glu Pro

<400> 551																
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tctatatata gaccttaciaa atcttgaacg gagattctta											atg gca acc atc gat	115				
											Met Ala Thr Ile Asp	5				
											1					
gta acc gaa gaa aca ttt gag agc aca gtt acc ggc gac gga att gtc																163
Val Thr Glu Glu Thr Phe Glu Ser Thr Val Thr Gly Asp Gly Ile Val																
10 15 20																
ctc gta gac gca tgg gca tcc tgg tgc gga cct tgc cgc cag ttc gcc																211
Leu Val Asp Ala Trp Ala Ser Trp Cys Gly Pro Cys Arg Gln Phe Ala																
25 30 35																
cca acc tac gag aag gtt tcc gaa acc cac acc gac gca acc ttc gcc																259
Pro Thr Tyr Glu Lys Val Ser Glu Thr His Thr Asp Ala Thr Phe Ala																
40 45 50																
aag ctt gat acc gaa gca aac cag ggc ctg gct gca gca ctg cag atc																307
Lys Leu Asp Thr Glu Ala Asn Gln Gly Leu Ala Ala Leu Gln Ile																
55 60 65																
cag tcc atc cca act ctg atg gtt ttc cgc gac ggc atc atg gtc tac																355
Gln Ser Ile Pro Thr Leu Met Val Phe Arg Asp Gly Ile Met Val Tyr																
70 75 80 85																
cgc gaa gcc ggc acc atg cca gct cct gca ctg gat gat ctg gtc aac																403
Arg Glu Ala Gly Thr Met Pro Ala Pro Ala Leu Asp Asp Leu Val Asn																
90 95 100																
cag gtt aag gca ctc gac atg gat gac gtt cgt cgc cag gtc gca gag																451
Gln Val Lys Ala Leu Asp Met Asp Asp Val Arg Arg Gln Val Ala Glu																
105 110 115																
cag cag ggt tct gca gag gca taagcttcca attgtgtttt ggt																495
Gln Gln Gly Ser Ala Glu Ala																
120																

<210> 552  
 <211> 124  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 552  
 Met Ala Thr Ile Asp Val Thr Glu Glu Thr Phe Glu Ser Thr Val Thr  
     1                    5                    10                    15  
 Gly Asp Gly Ile Val Leu Val Asp Ala Trp Ala Ser Trp Cys Gly Pro  
                     20                    25                    30  
 Cys Arg Gln Phe Ala Pro Thr Tyr Glu Lys Val Ser Glu Thr His Thr  
             35                    40                    45  
 Asp Ala Thr Phe Ala Lys Leu Asp Thr Glu Ala Asn Gln Gly Leu Ala  
         50                    55                    60  
 Ala Ala Leu Gln Ile Gln Ser Ile Pro Thr Leu Met Val Phe Arg Asp  
     65                    70                    75                    80  
 Gly Ile Met Val Tyr Arg Glu Ala Gly Thr Met Pro Ala Pro Ala Leu  
                     85                    90                    95  
 Asp Asp Leu Val Asn Gln Val Lys Ala Leu Asp Met Asp Asp Val Arg  
             100                    105                    110  
 Arg Gln Val Ala Glu Gln Gln Gly Ser Ala Glu Ala  
         115                    120

<210> 553  
 <211> 146  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (1)..(123)  
 <223> FRXA00937

<400> 553  
 gtc tac cgc gaa gcc ggc acc atg cca gct cct gca ctg gat gat ctg 48  
 Val Tyr Arg Glu Ala Gly Thr Met Pro Ala Pro Ala Leu Asp Asp Leu  
     1                    5                    10                    15  
 gtc aac cag gtt aag gca ctc gac atg gat gac gtt cgt cgc cag gtc 96  
 Val Asn Gln Val Lys Ala Leu Asp Met Asp Asp Val Arg Arg Gln Val  
                     20                    25                    30  
 gca gag cag cag ggt tct gca gag gca taagcttcca attgtgtttt ggt 146  
 Ala Glu Gln Gln Gly Ser Ala Glu Ala  
         35                    40

<210> 554  
 <211> 41  
 <212> PRT  
 <213> Corynebacterium glutamicum

&lt;400&gt; 554

Val Tyr Arg Glu Ala Gly Thr Met Pro Ala Pro Ala Leu Asp Asp Leu  
 1 5 10 15

Val Asn Gln Val Lys Ala Leu Asp Met Asp Asp Val Arg Arg Gln Val  
 20 25 30

Ala Glu Gln Gln Gly Ser Ala Glu Ala  
 35 40

&lt;210&gt; 555

&lt;211&gt; 871

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(871)

&lt;223&gt; RXA01199

&lt;400&gt; 555

ctagctaggg attagctttg tacttaaact tggtgttttt aagtggattt ccacaaagtg 60

ttagaaaaag tcattcgaga agaaggcgtg agttttaatc gtg acg tcc ccg cat 115  
 Val Thr Ser Pro His  
 1 5

aat ttt gtc agt ggt gct att gat ctg ggt gag gtg aaa gcg cgt gcg 163  
 Asn Phe Val Ser Gly Ala Ile Asp Leu Gly Glu Val Lys Ala Arg Ala  
 10 15 20

gat gcg cgc cag aag gcc cat gag cag ggg ccg gta act cag ggc att 211  
 Asp Ala Arg Gln Lys Ala His Glu Gln Gly Pro Val Thr Gln Gly Ile  
 25 30 35

gct agt tcc ctt gat gtg acc atg gag aac ctg gag aat gag gtg ctg 259  
 Ala Ser Ser Leu Asp Val Thr Met Glu Asn Leu Glu Asn Glu Val Leu  
 40 45 50

cgt cgt tcc acg cag gtt ccg gtg att gtt ctc gtg ggt acc ccg cgc 307  
 Arg Arg Ser Thr Gln Val Pro Val Ile Val Leu Val Gly Thr Pro Arg  
 55 60 65

agc cct gat tcg gag cag ttg aag tcg gat ctg acc acg ctt gct gct 355  
 Ser Pro Asp Ser Glu Gln Leu Lys Ser Asp Leu Thr Thr Leu Ala Ala  
 70 75 80 85

gaa agt ggc agg aag ttc att ttc ggt tat gtc aat gct gat acc gat 403  
 Glu Ser Gly Arg Lys Phe Ile Phe Gly Tyr Val Asn Ala Asp Thr Asp  
 90 95 100

gct gat gtg gcc cag gtg ttt ggg gtg cag ggc ttg ccg tcg gtg att 451  
 Ala Asp Val Ala Gln Val Phe Gly Val Gln Gly Leu Pro Ser Val Ile  
 105 110 115

gct gtg gca gcg gga cgc cct ctg gct gat ttc cag ggc gga cag cca 499  
 Ala Val Ala Ala Gly Arg Pro Leu Ala Asp Phe Gln Gly Gly Gln Pro  
 120 125 130

gcg gat gca cta aag cag tgg act gat cag gtg gtt cag gct gtg ggt 547

Ala	Asp	Ala	Leu	Lys	Gln	Trp	Thr	Asp	Gln	Val	Val	Gln	Ala	Val	Gly		
135						140					145						
gga	cag	ctg	gaa	gga	ctg	cca	gag	gag	gcc	aca	gac	ggc	gaa	caa	gaa	595	
Gly	Gln	Leu	Glu	Gly	Leu	Pro	Glu	Glu	Ala	Thr	Asp	Gly	Glu	Gln	Glu		
150					155				160						165		
gac	gct	cct	gtg	gaa	gac	ccc	cgc	ttc	gat	gct	gcc	act	gat	gct	cta	643	
Asp	Ala	Pro	Val	Glu	Asp	Pro	Arg	Phe	Asp	Ala	Ala	Thr	Asp	Ala	Leu		
				170					175					180			
aac	cgt	ggc	gct	ttc	gat	gag	gcg	att	gcg	gtt	tat	gag	tcc	att	ttg	691	
Asn	Arg	Gly	Ala	Phe	Asp	Glu	Ala	Ile	Ala	Val	Tyr	Glu	Ser	Ile	Leu		
			185					190					195				
gcg	cag	gag	cca	aac	aac	gct	gat	gcg	aag	caa	gca	ccg	cga	tac	cgc	739	
Ala	Gln	Glu	Pro	Asn	Asn	Ala	Asp	Ala	Lys	Gln	Ala	Pro	Arg	Tyr	Arg		
		200					205					210					
aaa	gct	gtt	ggg	ccg	gct	tgc	cac	cgg	tgg	atc	ctt	cgg	tgg	atg	ttg	787	
Lys	Ala	Val	Gly	Pro	Ala	Cys	His	Arg	Trp	Ile	Leu	Arg	Trp	Met	Leu		
	215					220					225						
tcg	ctg	ctg	cag	atg	ctg	atc	caa	caa	acg	ttg	atc	tgg	cct	aca	caa	835	
Ser	Leu	Leu	Gln	Met	Leu	Ile	Gln	Gln	Thr	Leu	Ile	Trp	Pro	Thr	Gln		
230					235					240					245		
gca	act	gac	gcg	gct	gtt	gtt	gcg	ggt	gat	cct	gag					871	
Ala	Thr	Asp	Ala	Ala	Val	Val	Ala	Gly	Asp	Pro	Glu						
				250					255								

<210> 556  
 <211> 257  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 556																	
Val	Thr	Ser	Pro	His	Asn	Phe	Val	Ser	Gly	Ala	Ile	Asp	Leu	Gly	Glu		
1				5					10					15			
Val	Lys	Ala	Arg	Ala	Asp	Ala	Arg	Gln	Lys	Ala	His	Glu	Gln	Gly	Pro		
			20					25					30				
Val	Thr	Gln	Gly	Ile	Ala	Ser	Ser	Leu	Asp	Val	Thr	Met	Glu	Asn	Leu		
		35					40					45					
Glu	Asn	Glu	Val	Leu	Arg	Arg	Ser	Thr	Gln	Val	Pro	Val	Ile	Val	Leu		
	50					55					60						
Val	Gly	Thr	Pro	Arg	Ser	Pro	Asp	Ser	Glu	Gln	Leu	Lys	Ser	Asp	Leu		
65					70					75					80		
Thr	Thr	Leu	Ala	Ala	Glu	Ser	Gly	Arg	Lys	Phe	Ile	Phe	Gly	Tyr	Val		
				85				90						95			
Asn	Ala	Asp	Thr	Asp	Ala	Asp	Val	Ala	Gln	Val	Phe	Gly	Val	Gln	Gly		
			100					105					110				
Leu	Pro	Ser	Val	Ile	Ala	Val	Ala	Ala	Gly	Arg	Pro	Leu	Ala	Asp	Phe		
		115					120					125					

Gln Gly Gly Gln Pro Ala Asp Ala Leu Lys Gln Trp Thr Asp Gln Val  
 130 135 140  
 Val Gln Ala Val Gly Gly Gln Leu Glu Gly Leu Pro Glu Glu Ala Thr  
 145 150 155 160  
 Asp Gly Glu Gln Glu Asp Ala Pro Val Glu Asp Pro Arg Phe Asp Ala  
 165 170 175  
 Ala Thr Asp Ala Leu Asn Arg Gly Ala Phe Asp Glu Ala Ile Ala Val  
 180 185 190  
 Tyr Glu Ser Ile Leu Ala Gln Glu Pro Asn Asn Ala Asp Ala Lys Gln  
 195 200 205  
 Ala Pro Arg Tyr Arg Lys Ala Val Gly Pro Ala Cys His Arg Trp Ile  
 210 215 220  
 Leu Arg Trp Met Leu Ser Leu Leu Gln Met Leu Ile Gln Gln Thr Leu  
 225 230 235 240  
 Ile Trp Pro Thr Gln Ala Thr Asp Ala Ala Val Val Ala Gly Asp Pro  
 245 250 255  
 Glu

<210> 557  
 <211> 681  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(658)  
 <223> RXA00824

<400> 557  
 tttggtttgg aggggccgtc agatccattt gaggcgcaaa aactcattaa aagtgatgat 60  
 agggagcacc tgctgaaaat ggcaggaatg tagaaaacaa atg aca agc agt gca 115  
 Met Thr Ser Ser Ala  
 1 5  
 aag tgg tcc atc gtt gga gtt gtc gcc atc ctg gct gtg atc gtt gcg 163  
 Lys Trp Ser Ile Val Gly Val Val Ala Ile Leu Ala Val Ile Val Ala  
 10 15 20  
 tta atc ccg cag ctt gtg ggt gga gaa agc gca gag gaa gcg cag ggg 211  
 Leu Ile Pro Gln Leu Val Gly Gly Glu Ser Ala Glu Glu Ala Gln Gly  
 25 30 35  
 gag acg tcg aca agc aaa att acg acg cgt cct gac tgc gtg gcc tct 259  
 Glu Thr Ser Thr Ser Lys Ile Thr Thr Arg Pro Asp Cys Val Ala Ser  
 40 45 50  
 ggc gcg gcg ggt gtg gat ctg ccc tgc ttg ggc ggc gcc aac ggc gtc 307  
 Gly Ala Ala Gly Val Asp Leu Pro Cys Leu Gly Gly Ala Asn Gly Val  
 55 60 65

ggc aac gag ctg gcc acc gtg gtg aat ctg tgg gcg tgg tgg tgc gaa 355  
 Gly Asn Glu Leu Ala Thr Val Val Asn Leu Trp Ala Trp Trp Cys Glu  
 70 75 80 85  
  
 ccg tgc cgc gcg gag ctg ccg att ttt gat gaa ttc gcc acc acc cac 403  
 Pro Cys Arg Ala Glu Leu Pro Ile Phe Asp Glu Phe Ala Thr Thr His  
 90 95 100  
  
 ccc gaa ctc aac gtc att ggc gtg cat gca gac caa aac gca gcc aac 451  
 Pro Glu Leu Asn Val Ile Gly Val His Ala Asp Gln Asn Ala Ala Asn  
 105 110 115  
  
 ggc gcc gca ctc ctt gag gat ctg ggc gtg aat ctt gca agc tac caa 499  
 Gly Ala Ala Leu Leu Glu Asp Leu Gly Val Asn Leu Ala Ser Tyr Gln  
 120 125 130  
  
 gac gat tcc aac ctg ttc gca ggc acc ctt ggg ctg ccg ggc gtc gtg 547  
 Asp Asp Ser Asn Leu Phe Ala Gly Thr Leu Gly Leu Pro Gly Val Val  
 135 140 145  
  
 ccg atc acc atc gtg gtt tct cca gac ggc aat gta gtg gac acc ttc 595  
 Pro Ile Thr Ile Val Val Ser Pro Asp Gly Asn Val Val Asp Thr Phe  
 150 155 160 165  
  
 ccg cag cct ttc gaa acc atc gat gac ctc gaa acc gct gtg gca ggg 643  
 Pro Gln Pro Phe Glu Thr Ile Asp Asp Leu Glu Thr Ala Val Ala Gly  
 170 175 180  
  
 gcg ctg cag aat gcg taactaccct gatttaccgc atg 681  
 Ala Leu Gln Asn Ala  
 185

&lt;210&gt; 558

&lt;211&gt; 186

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 558

Met Thr Ser Ser Ala Lys Trp Ser Ile Val Gly Val Val Ala Ile Leu  
 1 5 10 15  
  
 Ala Val Ile Val Ala Leu Ile Pro Gln Leu Val Gly Gly Glu Ser Ala  
 20 25 30  
  
 Glu Glu Ala Gln Gly Glu Thr Ser Thr Ser Lys Ile Thr Thr Arg Pro  
 35 40 45  
  
 Asp Cys Val Ala Ser Gly Ala Ala Gly Val Asp Leu Pro Cys Leu Gly  
 50 55 60  
  
 Gly Ala Asn Gly Val Gly Asn Glu Leu Ala Thr Val Val Asn Leu Trp  
 65 70 75 80  
  
 Ala Trp Trp Cys Glu Pro Cys Arg Ala Glu Leu Pro Ile Phe Asp Glu  
 85 90 95  
  
 Phe Ala Thr Thr His Pro Glu Leu Asn Val Ile Gly Val His Ala Asp  
 100 105 110

Gln Asn Ala Ala Asn Gly Ala Ala Leu Leu Glu Asp Leu Gly Val Asn  
 115 120 125

Leu Ala Ser Tyr Gln Asp Asp Ser Asn Leu Phe Ala Gly Thr Leu Gly  
 130 135 140

Leu Pro Gly Val Val Pro Ile Thr Ile Val Val Ser Pro Asp Gly Asn  
 145 150 155 160

Val Val Asp Thr Phe Pro Gln Pro Phe Glu Thr Ile Asp Asp Leu Glu  
 165 170 175

Thr Ala Val Ala Gly Ala Leu Gln Asn Ala  
 180 185

&lt;210&gt; 559

&lt;211&gt; 486

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(463)

&lt;223&gt; RXA01841

&lt;400&gt; 559

tcgggggggca ccttcagtt ccactcacca gaaggccaac cgagattatc tacgcaaagg 60

aggaacgtgc cccgctgcgg acttctccgg cccgtcgctg atg gag gag ggt gag 115  
 Met Glu Glu Gly Glu  
 1 5

gag atc agc ctg tct gat ttt gaa ggc gag gtc gtc gtc ctc aac gct 163  
 Glu Ile Ser Leu Ser Asp Phe Glu Gly Glu Val Val Val Leu Asn Ala  
 10 15 20

tgg ggc cag tgg tgt gca ccg tgt cgg gcg gaa gtc gat gac ctg cag 211  
 Trp Gly Gln Trp Cys Ala Pro Cys Arg Ala Glu Val Asp Asp Leu Gln  
 25 30 35

ctt gtc cag gag act ctc gac ccc ctc ggt ggc acg gtg ctg ggc atc 259  
 Leu Val Gln Glu Thr Leu Asp Pro Leu Gly Gly Thr Val Leu Gly Ile  
 40 45 50

aac gtc cgt gac tac aac cag acc atc gcc cag gac ttc aaa ctc gac 307  
 Asn Val Arg Asp Tyr Asn Gln Thr Ile Ala Gln Asp Phe Lys Leu Asp  
 55 60 65

aac gcg gtg acc tat ccc tcg atc tac gac ccg ccg ttt cgt atc gct 355  
 Asn Ala Val Thr Tyr Pro Ser Ile Tyr Asp Pro Pro Phe Arg Ile Ala  
 70 75 80 85

gcg gcc ctg ggt ggg gtg ccg acc tcg gtc atc ccg acc acc att gtc 403  
 Ala Ala Leu Gly Gly Val Pro Thr Ser Val Ile Pro Thr Thr Ile Val  
 90 95 100

ctg gac cga agc cac cgc ccg gcc gcg gtg ttc ctg agg gag gtc acc 451  
 Leu Asp Arg Ser His Arg Pro Ala Ala Val Phe Leu Arg Glu Val Thr  
 105 110 115

gcg ttg tct ggt tagtcctggg aggtgatgag ctc  
 Ala Leu Ser Gly  
 120

486

<210> 560  
 <211> 121  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 560  
 Met Glu Glu Gly Glu Glu Ile Ser Leu Ser Asp Phe Glu Gly Glu Val  
 1 5 10 15  
 Val Val Leu Asn Ala Trp Gly Gln Trp Cys Ala Pro Cys Arg Ala Glu  
 20 25 30  
 Val Asp Asp Leu Gln Leu Val Gln Glu Thr Leu Asp Pro Leu Gly Gly  
 35 40 45  
 Thr Val Leu Gly Ile Asn Val Arg Asp Tyr Asn Gln Thr Ile Ala Gln  
 50 55 60  
 Asp Phe Lys Leu Asp Asn Ala Val Thr Tyr Pro Ser Ile Tyr Asp Pro  
 65 70 75 80  
 Pro Phe Arg Ile Ala Ala Ala Leu Gly Gly Val Pro Thr Ser Val Ile  
 85 90 95  
 Pro Thr Thr Ile Val Leu Asp Arg Ser His Arg Pro Ala Ala Val Phe  
 100 105 110  
 Leu Arg Glu Val Thr Ala Leu Ser Gly  
 115 120

<210> 561  
 <211> 1219  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (48)..(1196)  
 <223> RXN01863

<400> 561  
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 Met Asn Ser  
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 gtc aaa ttg aag caa cct gtt agc att tac aat gat cca tgg gaa tca 104  
 Val Lys Leu Lys Gln Pro Val Ser Ile Tyr Asn Asp Pro Trp Glu Ser  
 5 10 15  
 tat aac gat gtt aaa gaa cat ggc caa tta act tta agt aac atc gaa 152  
 Tyr Asn Asp Val Lys Glu His Gly Gln Leu Thr Leu Ser Asn Ile Glu  
 20 25 30 35  
 ttt aca act aca aat ctt tgt aat atg cgt tgt agc cac tgt gca gtt 200  
 Phe Thr Thr Thr Asn Leu Cys Asn Met Arg Cys Ser His Cys Ala Val

40										45					50					
ggt	tat	act	tta	caa	act	gtc	gac	ccc	gag	cct	tta	gat	atg	gac	tta	248				
Gly	Tyr	Thr	Leu	Gln	Thr	Val	Asp	Pro	Glu	Pro	Leu	Asp	Met	Asp	Leu					
			55					60					65							
att	tat	cgt	aga	ctt	gat	gaa	att	cca	aat	ctg	cga	acg	atg	tca	att	296				
Ile	Tyr	Arg	Arg	Leu	Asp	Glu	Ile	Pro	Asn	Leu	Arg	Thr	Met	Ser	Ile					
		70					75					80								
aca	ggt	ggc	gaa	cca	atg	ttt	tct	aaa	aag	tct	att	aga	aat	ggt	ggt	344				
Thr	Gly	Gly	Glu	Pro	Met	Phe	Ser	Lys	Lys	Ser	Ile	Arg	Asn	Val	Val					
	85					90					95									
aaa	cct	cta	tta	aag	tat	gca	cat	cat	cga	ggt	ata	tat	aca	caa	atg	392				
Lys	Pro	Leu	Leu	Lys	Tyr	Ala	His	His	Arg	Gly	Ile	Tyr	Thr	Gln	Met					
100				105					110						115					
aat	tca	aac	cta	aca	ttg	cct	caa	gat	cgt	tat	tta	gat	att	gct	gaa	440				
Asn	Ser	Asn	Leu	Thr	Leu	Pro	Gln	Asp	Arg	Tyr	Leu	Asp	Ile	Ala	Glu					
			120					125						130						
tat	atc	gat	ggt	atg	cat	atc	tca	cat	aac	tgg	gga	aca	act	gat	gaa	488				
Tyr	Ile	Asp	Val	Met	His	Ile	Ser	His	Asn	Trp	Gly	Thr	Thr	Asp	Glu					
			135					140					145							
ttc	gca	aat	ggt	ggc	ttt	ggc	gca	atg	aag	aag	caa	cca	ccg	tta	aaa	536				
Phe	Ala	Asn	Val	Gly	Phe	Gly	Ala	Met	Lys	Lys	Gln	Pro	Pro	Leu	Lys					
		150					155					160								
gct	aag	tta	aaa	tta	tat	gaa	caa	atg	att	tcg	aat	gca	cgt	aca	tta	584				
Ala	Lys	Leu	Lys	Leu	Tyr	Glu	Gln	Met	Ile	Ser	Asn	Ala	Arg	Thr	Leu					
	165					170				175										
tca	gaa	caa	gga	atg	ttt	gta	tct	gcg	gaa	aca	atg	ctc	aat	caa	agt	632				
Ser	Glu	Gln	Gly	Met	Phe	Val	Ser	Ala	Glu	Thr	Met	Leu	Asn	Gln	Ser					
180				185						190					195					
acg	cta	cca	cat	tta	cga	aaa	ata	cat	caa	gaa	gtc	ggt	cat	gat	atg	680				
Thr	Leu	Pro	His	Leu	Arg	Lys	Ile	His	Gln	Glu	Val	Val	His	Asp	Met					
			200						205					210						
aaa	tgt	agc	aga	cac	gag	att	cac	cct	atg	tat	cca	gct	gac	ttt	gca	728				
Lys	Cys	Ser	Arg	His	Glu	Ile	His	Pro	Met	Tyr	Pro	Ala	Asp	Phe	Ala					
			215					220					225							
agt	caa	tta	aat	gtg	tta	act	cta	gcg	gaa	atg	aaa	aag	aca	att	cat	776				
Ser	Gln	Leu	Asn	Val	Leu	Thr	Leu	Ala	Glu	Met	Lys	Lys	Thr	Ile	His					
		230					235					240								
gat	ata	ttg	gat	ttc	aga	gat	gaa	gat	att	tgg	atg	tta	ttt	ggt	act	824				
Asp	Ile	Leu	Asp	Phe	Arg	Asp	Glu	Asp	Ile	Trp	Met	Leu	Phe	Gly	Thr					
	245					250					255									
ttg	cct	gtg	ttt	cca	tgc	tta	aag	gat	gat	gaa	gat	caa	aag	tta	cta	872				
Leu	Pro	Val	Phe	Pro	Cys	Leu	Lys	Asp	Asp	Glu	Asp	Gln	Lys	Leu	Leu					
260					265					270					275					
tca	cgt	tta	aga	aat	gct	aac	aat	gta	acg	act	aga	aat	gac	ccg	gat	920				
Ser	Arg	Leu	Arg	Asn	Ala	Asn	Asn	Val	Thr	Thr	Arg	Asn	Asp	Pro	Asp					
				280					285					290						

ggc cgt agt cgt tta aat gtc aat gta ttt aca ggt aat gta atc gta 968  
 Gly Arg Ser Arg Leu Asn Val Asn Val Phe Thr Gly Asn Val Ile Val  
 295 300 305  
  
 act gat ttc gga gat gaa aca ggt aca att tcg aat ata caa aaa gat 1016  
 Thr Asp Phe Gly Asp Glu Thr Gly Thr Ile Ser Asn Ile Gln Lys Asp  
 310 315 320  
  
 aaa tta aca gat gta ttt gat aaa tgg tta tcc tct gat ctt gct aaa 1064  
 Lys Leu Thr Asp Val Phe Asp Lys Trp Leu Ser Ser Asp Leu Ala Lys  
 325 330 335  
  
 tca tta aat tgt cat tgt tcc gag ttt agt tgt tta gga cca aat gtt 1112  
 Ser Leu Asn Cys His Cys Ser Glu Phe Ser Cys Leu Gly Pro Asn Val  
 340 345 350 355  
  
 ctt gtt aaa aat atg tac tat ccg aat atg gat ttt aaa gat aat gag 1160  
 Leu Val Lys Asn Met Tyr Tyr Pro Asn Met Asp Phe Lys Asp Asn Glu  
 360 365 370  
  
 cgt cat atg cac aaa caa cca caa att ata caa ttt taaaaactct 1206  
 Arg His Met His Lys Gln Pro Gln Ile Ile Gln Phe  
 375 380  
  
 taattatgcg gag 1219

&lt;210&gt; 562

&lt;211&gt; 383

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 562

Met Asn Ser Val Lys Leu Lys Gln Pro Val Ser Ile Tyr Asn Asp Pro  
 1 5 10 15  
  
 Trp Glu Ser Tyr Asn Asp Val Lys Glu His Gly Gln Leu Thr Leu Ser  
 20 25 30  
  
 Asn Ile Glu Phe Thr Thr Thr Asn Leu Cys Asn Met Arg Cys Ser His  
 35 40 45  
  
 Cys Ala Val Gly Tyr Thr Leu Gln Thr Val Asp Pro Glu Pro Leu Asp  
 50 55 60  
  
 Met Asp Leu Ile Tyr Arg Arg Leu Asp Glu Ile Pro Asn Leu Arg Thr  
 65 70 75 80  
  
 Met Ser Ile Thr Gly Gly Glu Pro Met Phe Ser Lys Lys Ser Ile Arg  
 85 90 95  
  
 Asn Val Val Lys Pro Leu Leu Lys Tyr Ala His His Arg Gly Ile Tyr  
 100 105 110  
  
 Thr Gln Met Asn Ser Asn Leu Thr Leu Pro Gln Asp Arg Tyr Leu Asp  
 115 120 125  
  
 Ile Ala Glu Tyr Ile Asp Val Met His Ile Ser His Asn Trp Gly Thr  
 130 135 140

Thr Asp Glu Phe Ala Asn Val Gly Phe Gly Ala Met Lys Lys Gln Pro  
 145 150 155 160  
 Pro Leu Lys Ala Lys Leu Lys Leu Tyr Glu Gln Met Ile Ser Asn Ala  
 165 170 175  
 Arg Thr Leu Ser Glu Gln Gly Met Phe Val Ser Ala Glu Thr Met Leu  
 180 185 190  
 Asn Gln Ser Thr Leu Pro His Leu Arg Lys Ile His Gln Glu Val Val  
 195 200 205  
 His Asp Met Lys Cys Ser Arg His Glu Ile His Pro Met Tyr Pro Ala  
 210 215 220  
 Asp Phe Ala Ser Gln Leu Asn Val Leu Thr Leu Ala Glu Met Lys Lys  
 225 230 235 240  
 Thr Ile His Asp Ile Leu Asp Phe Arg Asp Glu Asp Ile Trp Met Leu  
 245 250 255  
 Phe Gly Thr Leu Pro Val Phe Pro Cys Leu Lys Asp Asp Glu Asp Gln  
 260 265 270  
 Lys Leu Leu Ser Arg Leu Arg Asn Ala Asn Asn Val Thr Thr Arg Asn  
 275 280 285  
 Asp Pro Asp Gly Arg Ser Arg Leu Asn Val Asn Val Phe Thr Gly Asn  
 290 295 300  
 Val Ile Val Thr Asp Phe Gly Asp Glu Thr Gly Thr Ile Ser Asn Ile  
 305 310 315 320  
 Gln Lys Asp Lys Leu Thr Asp Val Phe Asp Lys Trp Leu Ser Ser Asp  
 325 330 335  
 Leu Ala Lys Ser Leu Asn Cys His Cys Ser Glu Phe Ser Cys Leu Gly  
 340 345 350  
 Pro Asn Val Leu Val Lys Asn Met Tyr Tyr Pro Asn Met Asp Phe Lys  
 355 360 365  
 Asp Asn Glu Arg His Met His Lys Gln Pro Gln Ile Ile Gln Phe  
 370 375 380

&lt;210&gt; 563

&lt;211&gt; 888

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (59) .. (865)

&lt;223&gt; FRXA01863

&lt;400&gt; 563

ttagaaatgt tgtaaactc tattaaagta tgcacatcat cgaggtatat atacacaa atg 61  
 Met

1

aat tca aac cta aca ttg cct caa gat cgt tat tta gat att gct gaa	109
Asn Ser Asn Leu Thr Leu Pro Gln Asp Arg Tyr Leu Asp Ile Ala Glu	
5 10 15	
tat atc gat gtt atg cat atc tca cat aac tgg gga aca act gat gaa	157
Tyr Ile Asp Val Met His Ile Ser His Asn Trp Gly Thr Asp Glu	
20 25 30	
ttc gca aat gtt ggc ttt ggc gca atg aag aag caa cca ccg tta aaa	205
Phe Ala Asn Val Gly Phe Gly Ala Met Lys Lys Gln Pro Pro Leu Lys	
35 40 45	
gct aag tta aaa tta tat gaa caa atg att tcg aat gca cgt aca tta	253
Ala Lys Leu Lys Leu Tyr Glu Gln Met Ile Ser Asn Ala Arg Thr Leu	
50 55 60 65	
tca gaa caa gga atg ttt gta tct gcg gaa aca atg ctc aat caa agt	301
Ser Glu Gln Gly Met Phe Val Ser Ala Glu Thr Met Leu Asn Gln Ser	
70 75 80	
acg cta cca cat tta cga aaa ata cat caa gaa gtc gtt cat gat atg	349
Thr Leu Pro His Leu Arg Lys Ile His Gln Glu Val Val His Asp Met	
85 90 95	
aaa tgt agc aga cac gag att cac cct atg tat cca gct gac ttt gca	397
Lys Cys Ser Arg His Glu Ile His Pro Met Tyr Pro Ala Asp Phe Ala	
100 105 110	
agt caa tta aat gtg tta act cta gcg gaa atg aaa aag aca att cat	445
Ser Gln Leu Asn Val Leu Thr Leu Ala Glu Met Lys Lys Thr Ile His	
115 120 125	
gat ata ttg gat ttc aga gat gaa gat att tgg atg tta ttt ggt act	493
Asp Ile Leu Asp Phe Arg Asp Glu Asp Ile Trp Met Leu Phe Gly Thr	
130 135 140 145	
ttg cct gtg ttt cca tgc tta aag gat gat gaa gat caa aag tta cta	541
Leu Pro Val Phe Pro Cys Leu Lys Asp Asp Glu Asp Gln Lys Leu Leu	
150 155 160	
tca cgt tta aga aat gct aac aat gta acg act aga aat gac ccg gat	589
Ser Arg Leu Arg Asn Ala Asn Asn Val Thr Thr Arg Asn Asp Pro Asp	
165 170 175	
ggc cgt agt cgt tta aat gtc aat gta ttt aca ggt aat gta atc gta	637
Gly Arg Ser Arg Leu Asn Val Asn Val Phe Thr Gly Asn Val Ile Val	
180 185 190	
act gat ttc gga gat gaa aca ggt aca att tcg aat ata caa aaa gat	685
Thr Asp Phe Gly Asp Glu Thr Gly Thr Ile Ser Asn Ile Gln Lys Asp	
195 200 205	
aaa tta aca gat gta ttt gat aaa tgg tta tcc tct gat ctt gct aaa	733
Lys Leu Thr Asp Val Phe Asp Lys Trp Leu Ser Ser Asp Leu Ala Lys	
210 215 220 225	
tca tta aat tgt cat tgt tcc gag ttt agt tgt tta gga cca aat gtt	781
Ser Leu Asn Cys His Cys Ser Glu Phe Ser Cys Leu Gly Pro Asn Val	
230 235 240	
ctt gtt aaa aat atg tac tat ccg aat atg gat ttt aaa gat aat gag	829

Leu Val Lys Asn Met Tyr Tyr Pro Asn Met Asp Phe Lys Asp Asn Glu  
 245 250 255

cgt cat atg cac aaa caa cca caa att ata caa ttt taaaaactct 875  
 Arg His Met His Lys Gln Pro Gln Ile Ile Gln Phe  
 260 265

taattatgcg gag 888

<210> 564

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 564

Met Asn Ser Asn Leu Thr Leu Pro Gln Asp Arg Tyr Leu Asp Ile Ala  
 1 5 10 15

Glu Tyr Ile Asp Val Met His Ile Ser His Asn Trp Gly Thr Thr Asp  
 20 25 30

Glu Phe Ala Asn Val Gly Phe Gly Ala Met Lys Lys Gln Pro Pro Leu  
 35 40 45

Lys Ala Lys Leu Lys Leu Tyr Glu Gln Met Ile Ser Asn Ala Arg Thr  
 50 55 60

Leu Ser Glu Gln Gly Met Phe Val Ser Ala Glu Thr Met Leu Asn Gln  
 65 70 75 80

Ser Thr Leu Pro His Leu Arg Lys Ile His Gln Glu Val Val His Asp  
 85 90 95

Met Lys Cys Ser Arg His Glu Ile His Pro Met Tyr Pro Ala Asp Phe  
 100 105 110

Ala Ser Gln Leu Asn Val Leu Thr Leu Ala Glu Met Lys Lys Thr Ile  
 115 120 125

His Asp Ile Leu Asp Phe Arg Asp Glu Asp Ile Trp Met Leu Phe Gly  
 130 135 140

Thr Leu Pro Val Phe Pro Cys Leu Lys Asp Asp Glu Asp Gln Lys Leu  
 145 150 155 160

Leu Ser Arg Leu Arg Asn Ala Asn Asn Val Thr Thr Arg Asn Asp Pro  
 165 170 175

Asp Gly Arg Ser Arg Leu Asn Val Asn Val Phe Thr Gly Asn Val Ile  
 180 185 190

Val Thr Asp Phe Gly Asp Glu Thr Gly Thr Ile Ser Asn Ile Gln Lys  
 195 200 205

Asp Lys Leu Thr Asp Val Phe Asp Lys Trp Leu Ser Ser Asp Leu Ala  
 210 215 220

Lys Ser Leu Asn Cys His Cys Ser Glu Phe Ser Cys Leu Gly Pro Asn  
 225 230 235 240

Val Leu Val Lys Asn Met Tyr Tyr Pro Asn Met Asp Phe Lys Asp Asn  
245 250 255

Glu Arg His Met His Lys Gln Pro Gln Ile Ile Gln Phe  
260 265

<210> 565

<211> 1047

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1024)

<223> RXA02323

<400> 565

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aaagtcaagt tttttgacct tcgcttttta ggagcacccc atg tca tct cat gat 115  
Met Ser Ser His Asp  
1 5

ctc gtt gac gta gtt gtc gtc ggc gcc ggc gct gca ggt ctc gcc gcc 163  
Leu Val Asp Val Val Val Val Gly Ala Gly Ala Gly Leu Ala Ala  
10 15 20

gct gtc gcg ctc ggc cgc tca ctg cgc agt gtc atc gtc atc gac gct 211  
Ala Val Ala Leu Gly Arg Ser Leu Arg Ser Val Ile Val Ile Asp Ala  
25 30 35

ggt caa ccc cgt aac agc tat gcg cac gct gct cac aat gtc ctc ggc 259  
Gly Gln Pro Arg Asn Ser Tyr Ala His Ala Ala His Asn Val Leu Gly  
40 45 50

cag gaa ggc att gcg ccc gcc gag ctg ctg gaa aaa ggc cgc gcc gaa 307  
Gln Glu Gly Ile Ala Pro Ala Glu Leu Leu Glu Lys Gly Arg Ala Glu  
55 60 65

gcg cgt tcc tat ggc gtc acc att gcg ccc ggg cgc gta gca aaa gtt 355  
Ala Arg Ser Tyr Gly Val Thr Ile Ala Pro Gly Arg Val Ala Lys Val  
70 75 80 85

gag cgc acc ggt tcc acc ttc gcc ata acg ctt gac gac gcc tcc ctc 403  
Glu Arg Thr Gly Ser Thr Phe Ala Ile Thr Leu Asp Asp Ala Ser Leu  
90 95 100

ctt cac tct cgg cgc atc att ttg gcc cac ggc gcc gtt gac gat ctg 451  
Leu His Ser Arg Arg Ile Ile Leu Ala His Gly Ala Val Asp Asp Leu  
105 110 115

cca gag gta gaa gga ctg tca gat ttt tgg gga acc aaa gtg ttg cac 499  
Pro Glu Val Glu Gly Leu Ser Asp Phe Trp Gly Thr Lys Val Leu His  
120 125 130

tgc gct tac tgc cac ggc ttt gag gcc cgc gat tct gaa atc gtc gtg 547  
Cys Ala Tyr Cys His Gly Phe Glu Ala Arg Asp Ser Glu Ile Val Val  
135 140 145

gtg ggt acc tcg ccc atg gct gcg cac caa gcg ttg atg ttc tcg cag 595

Val Gly Thr Ser Pro Met Ala Ala His Gln Ala Leu Met Phe Ser Gln  
 150 155 160 165  
 ttg tcc aaa act gtc agc ttg gtg ggc acg atc gac att gat gaa caa 643  
 Leu Ser Lys Thr Val Ser Leu Val Gly Thr Ile Asp Ile Asp Glu Gln  
 170 175 180  
 acc agc gag agc cta gat agt gct gga gta aaa gtg ttg ggc acc aat 691  
 Thr Ser Glu Ser Leu Asp Ser Ala Gly Val Lys Val Leu Gly Thr Asn  
 185 190 195  
 gcg gtg cgc gta tcc gcc gaa ggt gat ggc ctg tct gtg gaa ctg tcc 739  
 Ala Val Arg Val Ser Ala Glu Gly Asp Gly Leu Ser Val Glu Leu Ser  
 200 205 210  
 gaa ggc gat cat tta agc tgc gac aac atc gtg gtg gca tct cgt cca 787  
 Glu Gly Asp His Leu Ser Cys Asp Asn Ile Val Val Ala Ser Arg Pro  
 215 220 225  
 ctg gtg gat ggc acg ctg tac acc caa ctt ggt ggt cag atg gaa gaa 835  
 Leu Val Asp Gly Thr Leu Tyr Thr Gln Leu Gly Gly Gln Met Glu Glu  
 230 235 240 245  
 aac ccg atg ggc agg ttc att cca ggt acc caa acc ggg cgc act cct 883  
 Asn Pro Met Gly Arg Phe Ile Pro Gly Thr Gln Thr Gly Arg Thr Pro  
 250 255 260  
 att gaa ggt gtg tgg gct gcc gga aac gcg caa gct ccc atg gcg atg 931  
 Ile Glu Gly Val Trp Ala Ala Gly Asn Ala Gln Ala Pro Met Ala Met  
 265 270 275  
 gtc tat ggt tcc gct gct caa ggc gtg atg gct gga gca gag atc aac 979  
 Val Tyr Gly Ser Ala Ala Gln Gly Val Met Ala Gly Ala Glu Ile Asn  
 280 285 290  
 ttt gat ctg atc ctg gaa gat att tcc gtg gca agc gcg cag agc 1024  
 Phe Asp Leu Ile Leu Glu Asp Ile Ser Val Ala Ser Ala Gln Ser  
 295 300 305  
 taaactgcgt gaggttggtg cct 1047

&lt;210&gt; 566

&lt;211&gt; 308

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 566

Met Ser Ser His Asp Leu Val Asp Val Val Val Val Gly Ala Gly Ala  
 1 5 10 15  
 Ala Gly Leu Ala Ala Ala Val Ala Leu Gly Arg Ser Leu Arg Ser Val  
 20 25 30  
 Ile Val Ile Asp Ala Gly Gln Pro Arg Asn Ser Tyr Ala His Ala Ala  
 35 40 45  
 His Asn Val Leu Gly Gln Glu Gly Ile Ala Pro Ala Glu Leu Leu Glu  
 50 55 60  
 Lys Gly Arg Ala Glu Ala Arg Ser Tyr Gly Val Thr Ile Ala Pro Gly

65	70					75					80				
Arg Val Ala Lys Val Glu Arg Thr Gly Ser Thr Phe Ala Ile Thr Leu	85					90					95				
Asp Asp Ala Ser Leu Leu His Ser Arg Arg Ile Ile Leu Ala His Gly	100					105					110				
Ala Val Asp Asp Leu Pro Glu Val Glu Gly Leu Ser Asp Phe Trp Gly	115					120					125				
Thr Lys Val Leu His Cys Ala Tyr Cys His Gly Phe Glu Ala Arg Asp	130					135					140				
Ser Glu Ile Val Val Val Gly Thr Ser Pro Met Ala Ala His Gln Ala	145					150					155				
Leu Met Phe Ser Gln Leu Ser Lys Thr Val Ser Leu Val Gly Thr Ile	165					170					175				
Asp Ile Asp Glu Gln Thr Ser Glu Ser Leu Asp Ser Ala Gly Val Lys	180					185					190				
Val Leu Gly Thr Asn Ala Val Arg Val Ser Ala Glu Gly Asp Gly Leu	195					200					205				
Ser Val Glu Leu Ser Glu Gly Asp His Leu Ser Cys Asp Asn Ile Val	210					215					220				
Val Ala Ser Arg Pro Leu Val Asp Gly Thr Leu Tyr Thr Gln Leu Gly	225					230					235				
Gly Gln Met Glu Glu Asn Pro Met Gly Arg Phe Ile Pro Gly Thr Gln	245					250					255				
Thr Gly Arg Thr Pro Ile Glu Gly Val Trp Ala Ala Gly Asn Ala Gln	260					265					270				
Ala Pro Met Ala Met Val Tyr Gly Ser Ala Ala Gln Gly Val Met Ala	275					280					285				
Gly Ala Glu Ile Asn Phe Asp Leu Ile Leu Glu Asp Ile Ser Val Ala	290					295					300				
Ser Ala Gln Ser	305														

&lt;210&gt; 567

&lt;211&gt; 354

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(331)

&lt;223&gt; RXA01072

&lt;400&gt; 567

gtgtcgcctt gagcgatgca aagacttttaa aaacagatct aaaaaagtaa gatgaggcat 60

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tagcgtcaac cgctaaagcc gataagggaa ggtccaaaaa atg gca atc acc gtt 115
                                   Met Ala Ile Thr Val
                                   1      5

tac acc aag cca gct tgc gtc cag tgc aat gcc acc aag aag gcc ctc 163
Tyr Thr Lys Pro Ala Cys Val Gln Cys Asn Ala Thr Lys Lys Ala Leu
              10              15              20

gac cgc gct ggt ctt gag tat gac ctc gtt gat atc agc ctt gat gaa 211
Asp Arg Ala Gly Leu Glu Tyr Asp Leu Val Asp Ile Ser Leu Asp Glu
              25              30              35

gag gca cgt gag tac gtc ctc gca ctt ggc tac ctg cag gca cca gtt 259
Glu Ala Arg Glu Tyr Val Leu Ala Leu Gly Tyr Leu Gln Ala Pro Val
              40              45              50

gtc gtt gca gat ggc tcc cac tgg tcc ggt ttc cgc cca gag cgc atc 307
Val Val Ala Asp Gly Ser His Trp Ser Gly Phe Arg Pro Glu Arg Ile
              55              60              65

cgt gaa atg gca acc gca gct gcc taaactgcac ttcgtggcac gac 354
Arg Glu Met Ala Thr Ala Ala Ala
              70              75

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<210> 568  
 <211> 77  
 <212> PRT  
 <213> Corynebacterium glutamicum

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<400> 568
Met Ala Ile Thr Val Tyr Thr Lys Pro Ala Cys Val Gln Cys Asn Ala
 1              5              10              15

Thr Lys Lys Ala Leu Asp Arg Ala Gly Leu Glu Tyr Asp Leu Val Asp
              20              25              30

Ile Ser Leu Asp Glu Glu Ala Arg Glu Tyr Val Leu Ala Leu Gly Tyr
              35              40              45

Leu Gln Ala Pro Val Val Val Ala Asp Gly Ser His Trp Ser Gly Phe
              50              55              60

Arg Pro Glu Arg Ile Arg Glu Met Ala Thr Ala Ala Ala
 65              70              75

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<210> 569  
 <211> 684  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(661)  
 <223> RXA02436

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<400> 569
atccactact aacttgaggt tgccaatcgt gtcctatattc aactctcctt aaattgggtcg 60

cgttctttcta agaccccaca ttagtaaaaag catggggacat gtg gtt ggc att tcg 115

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<210> 570
<211> 187
<212> PRT
<213> Corynebacterium glutamicum
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<400> 570  
Val Val Gly Ile Ser Leu Asp Val Val Met Met Gly Val Met Thr Ser  
1 5 10 15

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<210> 571
<211> 900
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(877)
<223> RXN01837
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<400> 571
cccccatcat tccctcaagg tgtgaagata cggtaggat agaaaagaat ttttttgacg 60

ttggacattc tcaaaatcaa gtagcaaggg atcaaactct  gtg agt act aat aag 115
                                         Val Ser Thr Asn Lys
                                         1                               5

gaa cga cgc caa cag gcg ctt tcc cag ctg gag aaa gaa atc aaa agc 163
Glu Arg Arg Gln Gln Ala Leu Ser Gln Leu Glu Lys Glu Ile Lys Ser
                        10                        15                        20

cgg gac cgc aaa gaa aag acc aag cca cta acc gtg gtc ttt gct tcc 211
Arg Asp Arg Lys Glu Lys Thr Lys Pro Leu Thr Val Val Phe Ala Ser
                        25                        30                        35

ctg gct gtc atc ctg gtt gtc gtt ggc ggt atc tgg tac gca gct acc 259
Leu Ala Val Ile Leu Val Val Val Gly Gly Ile Trp Tyr Ala Ala Thr

```

40	45	50	
cgc agc acc gaa gac gaa gtc atc acc gct gat gaa aca tcc acc acc			307
Arg Ser Thr Glu Asp Glu Val Ile Thr Ala Asp Glu Thr Ser Thr Thr			
55	60	65	
gca gag acc cct gac tac cag cca ctg gcg ctg acc cgc acc acc gcg			355
Ala Glu Thr Pro Asp Tyr Gln Pro Leu Ala Leu Thr Arg Thr Thr Ala			
70	75	80	85
ctc ggc gac tcc gtg acc tgt gag tac cca gat gct ggc gag gct tcc			403
Leu Gly Asp Ser Val Thr Cys Glu Tyr Pro Asp Ala Gly Glu Ala Ser			
90	95		100
aag gat gtc tcc aag cct gct act gaa aac gtg cca gca acc ggc acc			451
Lys Asp Val Ser Lys Pro Ala Thr Glu Asn Val Pro Ala Thr Gly Thr			
105	110		115
gtg acc gtc aac ctg acc acc gcc cag ggc aac atc ggc atg gaa ctt			499
Val Thr Val Asn Leu Thr Thr Ala Gln Gly Asn Ile Gly Met Glu Leu			
120	125		130
gat cgc tcc gta tcc cct tgt acc gtc aac gct gtt gag cac atg gct			547
Asp Arg Ser Val Ser Pro Cys Thr Val Asn Ala Val Glu His Met Ala			
135	140		145
tcc gag ggc tac tac aac gat act gtc tgc cac cgc atc acc acc tct			595
Ser Glu Gly Tyr Tyr Asn Asp Thr Val Cys His Arg Ile Thr Thr Ser			
150	155		160
ggc att tac gtt ctc cag tgc ggc gat cca agc agc acc ggc gca ggc			643
Gly Ile Tyr Val Leu Gln Cys Gly Asp Pro Ser Ser Thr Gly Ala Gly			
170	175		180
ggc cca ggg ttc agc ttc gcc aac gaa tac cca acc gac gaa gca act			691
Gly Pro Gly Phe Ser Phe Ala Asn Glu Tyr Pro Thr Asp Glu Ala Thr			
185	190		195
gac cta acc acc cca gtc atc tac gag cgc ggc acc atc gcc atg gcc			739
Asp Leu Thr Thr Pro Val Ile Tyr Glu Arg Gly Thr Ile Ala Met Ala			
200	205		210
aac gct ggc gct gac acc aac ggg ctc cca gtt ctt cct caa cta cga			787
Asn Ala Gly Ala Asp Thr Asn Gly Leu Pro Val Leu Pro Gln Leu Arg			
215	220		225
gga ttc ccc act ggc acc gaa cta cac cta ctt cgg cca gat cac cga			835
Gly Phe Pro Thr Gly Thr Glu Leu His Leu Leu Arg Pro Asp His Arg			
230	235		240
aga agg cct tgc aac cct cga cgc cat cgc aga agt tgg cac			877
Arg Arg Pro Cys Asn Pro Arg Arg His Arg Arg Ser Trp His			
250	255		
tgaaggtgga accggcgacg gag			900

&lt;210&gt; 572

&lt;211&gt; 259

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 572

Val Ser Thr Asn Lys Glu Arg Arg Gln Gln Ala Leu Ser Gln Leu Glu  
 1 5 10 15

Lys Glu Ile Lys Ser Arg Asp Arg Lys Glu Lys Thr Lys Pro Leu Thr  
 20 25 30

Val Val Phe Ala Ser Leu Ala Val Ile Leu Val Val Val Gly Gly Ile  
 35 40 45

Trp Tyr Ala Ala Thr Arg Ser Thr Glu Asp Glu Val Ile Thr Ala Asp  
 50 55 60

Glu Thr Ser Thr Thr Ala Glu Thr Pro Asp Tyr Gln Pro Leu Ala Leu  
 65 70 75 80

Thr Arg Thr Thr Ala Leu Gly Asp Ser Val Thr Cys Glu Tyr Pro Asp  
 85 90 95

Ala Gly Glu Ala Ser Lys Asp Val Ser Lys Pro Ala Thr Glu Asn Val  
 100 105 110

Pro Ala Thr Gly Thr Val Thr Val Asn Leu Thr Thr Ala Gln Gly Asn  
 115 120 125

Ile Gly Met Glu Leu Asp Arg Ser Val Ser Pro Cys Thr Val Asn Ala  
 130 135 140

Val Glu His Met Ala Ser Glu Gly Tyr Tyr Asn Asp Thr Val Cys His  
 145 150 155 160

Arg Ile Thr Thr Ser Gly Ile Tyr Val Leu Gln Cys Gly Asp Pro Ser  
 165 170 175

Ser Thr Gly Ala Gly Gly Pro Gly Phe Ser Phe Ala Asn Glu Tyr Pro  
 180 185 190

Thr Asp Glu Ala Thr Asp Leu Thr Thr Pro Val Ile Tyr Glu Arg Gly  
 195 200 205

Thr Ile Ala Met Ala Asn Ala Gly Ala Asp Thr Asn Gly Leu Pro Val  
 210 215 220

Leu Pro Gln Leu Arg Gly Phe Pro Thr Gly Thr Glu Leu His Leu Leu  
 225 230 235 240

Arg Pro Asp His Arg Arg Arg Pro Cys Asn Pro Arg Arg His Arg Arg  
 245 250 255

Ser Trp His

&lt;210&gt; 573

&lt;211&gt; 416

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(393)

&lt;223&gt; FRXA01837

&lt;400&gt; 573

tcg gag ggc tac tac aac gat act gtc tgc cac cgc atc acc acc tct	48
Ser Glu Gly Tyr Tyr Asn Asp Thr Val Cys His Arg Ile Thr Thr Ser	
1 5 10 15	
ggc att tac gtt ctc cag tgc ggc gat cca agc agc acc ggc gca ggc	96
Gly Ile Tyr Val Leu Gln Cys Gly Asp Pro Ser Ser Thr Gly Ala Gly	
20 25 30	
ggc cca ggg ttc agc ttc gcc aac gaa tac cca acc gac gaa gca act	144
Gly Pro Gly Phe Ser Phe Ala Asn Glu Tyr Pro Thr Asp Glu Ala Thr	
35 40 45	
gac cta acc acc cca gtc atc tac gag cgc ggc acc atc gcc atg gcc	192
Asp Leu Thr Thr Pro Val Ile Tyr Glu Arg Gly Thr Ile Ala Met Ala	
50 55 60	
aac gct ggc gct gac acc aac ggc tcc cag ttc ttc ctc aac tac gag	240
Asn Ala Gly Ala Asp Thr Asn Gly Ser Gln Phe Phe Leu Asn Tyr Glu	
65 70 75 80	
gat tcc cca ctg gca ccg aac tac acc tac ttc ggc cag atc acc gaa	288
Asp Ser Pro Leu Ala Pro Asn Tyr Thr Tyr Phe Gly Gln Ile Thr Glu	
85 90 95	
gaa ggc ctt gca acc ctc gac gcc atc gca gaa gtt ggc act gaa ggt	336
Glu Gly Leu Ala Thr Leu Asp Ala Ile Ala Glu Val Gly Thr Glu Gly	
100 105 110	
gga acc ggc gac gga gca cca gcg caa gag gtt cgc att gaa tcc gca	384
Gly Thr Gly Asp Gly Ala Pro Ala Gln Glu Val Arg Ile Glu Ser Ala	
115 120 125	
gct gtt gcg taagttctaa gccctcttc ttt	416
Ala Val Ala	
130	

&lt;210&gt; 574

&lt;211&gt; 131

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 574

Ser Glu Gly Tyr Tyr Asn Asp Thr Val Cys His Arg Ile Thr Thr Ser	
1 5 10 15	
Gly Ile Tyr Val Leu Gln Cys Gly Asp Pro Ser Ser Thr Gly Ala Gly	
20 25 30	
Gly Pro Gly Phe Ser Phe Ala Asn Glu Tyr Pro Thr Asp Glu Ala Thr	
35 40 45	
Asp Leu Thr Thr Pro Val Ile Tyr Glu Arg Gly Thr Ile Ala Met Ala	
50 55 60	
Asn Ala Gly Ala Asp Thr Asn Gly Ser Gln Phe Phe Leu Asn Tyr Glu	
65 70 75 80	

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<210> 575
<211> 2127
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(2104)
<223> RXS01277
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<400> 575																										
tactactcgg	ttcacgttta	cgtcggctga	tccaattgga	ggcgcacctcg	gaagccgcct											60										
taaaaaaacct gccgggtcaaa agatcactaa cctgaacttc																atg	act	gat	tac	acg						115
																Met	Thr	Asp	Tyr	Thr						
																1				5						
ttc	ctc	gaa	gac	att	gac	acc	ccg	gaa	gcg	ctc	gcg	tgg	gcg	gaa	aaa	163										
Phe	Leu	Glu	Asp	Ile	Asp	Thr	Pro	Glu	Ala	Leu	Ala	Trp	Ala	Glu	Lys											
																10				15		20				
tgg	tcg	ggg	gaa	agc	gtc	gaa	aag	cta	aaa	agc	cca	gcc	aag	gac	gcc	211										
Trp	Ser	Gly	Glu	Ser	Val	Glu	Lys	Leu	Lys	Ser	Pro	Ala	Lys	Asp	Ala											
																25				30		35				
ctg	gaa	gcc	agg	ctg	ctg	gct	gcg	ttg	gac	acc	gat	gat	cgc	att	gcc	259										
Leu	Glu	Ala	Arg	Leu	Leu	Ala	Ala	Leu	Asp	Thr	Asp	Asp	Arg	Ile	Ala											
																40				45		50				
tac	gtg	agc	cgg	cgc	ggg	gag	aag	ctg	tac	aac	ttt	tgg	cgg	gac	gcg	307										
Tyr	Val	Ser	Arg	Arg	Gly	Glu	Lys	Leu	Tyr	Asn	Phe	Trp	Arg	Asp	Ala											
																55				60		65				
cag	cat	ccg	cgt	gga	gtg	tgg	cgc	acg	acc	acg	ttg	gag	tcg	tat	gaa	355										
Gln	His	Pro	Arg	Gly	Val	Trp	Arg	Thr	Thr	Thr	Leu	Glu	Ser	Tyr	Glu											
																70				75		80		85		
agt	gac	cag	ccg	gag	tgg	gac	gtg	ctc	att	gat	gtg	gat	gcg	ttg	gcg	403										
Ser	Asp	Gln	Pro	Glu	Trp	Asp	Val	Leu	Ile	Asp	Val	Asp	Ala	Leu	Ala											
																90				95		100				
gag	gat	gag	ggc	gaa	aac	tgg	gta	tgg	aag	ggc	gcg	gtt	gtg	cgc	tcg	451										
Glu	Asp	Glu	Gly	Glu	Asn	Trp	Val	Trp	Lys	Gly	Ala	Val	Val	Arg	Ser											
																105				110		115				
ccg	gag	ttt	gat	cgg	gcg	ttg	gtg	aag	ttc	tcg	cgg	ggc	ggg	gct	gat	499										
Pro	Glu	Phe	Asp	Arg	Ala	Leu	Val	Lys	Phe	Ser	Arg	Gly	Gly	Ala	Asp											

120					125					130						
gcg	acg	gtg	att	agg	gag	ttt	gat	ctg	gcc	acg	gct	gct	ttc	gtg	gat	547
Ala	Thr	Val	Ile	Arg	Glu	Phe	Asp	Leu	Ala	Thr	Ala	Ala	Phe	Val	Asp	
135					140					145						
gat	tcg	ccg	ttt	gaa	ttg	aag	gag	gcg	aag	tcc	gat	gtc	acg	tgg	gtt	595
Asp	Ser	Pro	Phe	Glu	Leu	Lys	Glu	Ala	Lys	Ser	Asp	Val	Thr	Trp	Val	
150					155					160					165	
gat	ctg	gat	acg	ttg	ctg	gtg	ggc	acg	gat	acc	ggc	gag	ggg	tca	ctg	643
Asp	Leu	Asp	Thr	Leu	Leu	Val	Gly	Thr	Asp	Thr	Gly	Glu	Gly	Ser	Leu	
170					175					180						
acg	gat	tct	ggg	tac	ccg	gcg	cgg	gtg	ctc	acg	tgg	aag	cgt	ggg	act	691
Thr	Asp	Ser	Gly	Tyr	Pro	Ala	Arg	Val	Leu	Thr	Trp	Lys	Arg	Gly	Thr	
185					190					195						
ccg	ctt	gag	cag	gcg	gag	ttg	ttc	ttt	gag	ggg	tcg	cgt	cag	gat	gtg	739
Pro	Leu	Glu	Gln	Ala	Glu	Leu	Phe	Phe	Glu	Gly	Ser	Arg	Gln	Asp	Val	
200					205					210						
gcg	act	cat	gcg	tgg	cgg	gat	tca	aca	cct	ggt	ttt	gag	cgg	acg	ttt	787
Ala	Thr	His	Ala	Trp	Arg	Asp	Ser	Thr	Pro	Gly	Phe	Glu	Arg	Thr	Phe	
215					220					225						
gtg	tca	agg	tcg	ttg	gat	ttc	tat	aat	tcg	gag	acg	tcg	ctg	gaa	acc	835
Val	Ser	Arg	Ser	Leu	Asp	Phe	Tyr	Asn	Ser	Glu	Thr	Ser	Leu	Glu	Thr	
230					235					240					245	
gag	ggt	ggc	ctg	gtc	aag	ctt	gat	gtg	ccg	acc	gat	tgc	gat	gtc	att	883
Glu	Gly	Gly	Leu	Val	Lys	Leu	Asp	Val	Pro	Thr	Asp	Cys	Asp	Val	Ile	
250					255					260						
gtg	aag	aag	cag	tgg	att	ttt	gtg	agt	cct	cgg	acg	gat	ttc	gct	ggg	931
Val	Lys	Lys	Gln	Trp	Ile	Phe	Val	Ser	Pro	Arg	Thr	Asp	Phe	Ala	Gly	
265					270					275						
att	cca	gca	ggt	ggc	ttg	gga	gtg	ctg	ctg	tta	aag	gag	ttc	ctt	gag	979
Ile	Pro	Ala	Gly	Gly	Leu	Gly	Val	Leu	Leu	Leu	Lys	Glu	Phe	Leu	Glu	
280					285					290						
ggc	ggg	cgc	gat	ttt	cag	cct	gtg	ttt	acg	cct	act	gag	tcg	acg	tcg	1027
Gly	Gly	Arg	Asp	Phe	Gln	Pro	Val	Phe	Thr	Pro	Thr	Glu	Ser	Thr	Ser	
295					300					305						
ctg	cag	gga	ttg	gcc	acg	aca	aag	aat	ttc	ctg	gtt	tta	acg	ctc	ctt	1075
Leu	Gln	Gly	Leu	Ala	Thr	Thr	Lys	Asn	Phe	Leu	Val	Leu	Thr	Leu	Leu	
310					315					320					325	
aat	aat	gtc	tcc	aca	gaa	atc	gtc	aca	gtg	ccg	ctc	aat	gat	ccg	aca	1123
Asn	Asn	Val	Ser	Thr	Glu	Ile	Val	Thr	Val	Pro	Leu	Asn	Asp	Pro	Thr	
330					335					340						
acg	gag	cat	gaa	cac	att	gac	ctc	cca	gag	cat	gtc	acc	gcg	cat	gtg	1171
Thr	Glu	His	Glu	His	Ile	Asp	Leu	Pro	Glu	His	Val	Thr	Ala	His	Val	
345					350					355						
gtt	gct	acc	tcc	ccg	ttg	gat	ggc	gat	gaa	att	tgg	gtg	cag	gca	gcg	1219
Val	Ala	Thr	Ser	Pro	Leu	Asp	Gly	Asp	Glu	Ile	Trp	Val	Gln	Ala	Ala	
360					365					370						

agt ttc acc gaa gcg cca acg ttg ctg cgt gcg gag ctg cct ggt gcg	1267
Ser Phe Thr Glu Ala Pro Thr Leu Leu Arg Ala Glu Leu Pro Gly Ala	
375 380 385	
ctt gag gct gtg aag aag gcg ccg ttg cag ttt gaa aat gct ggt cag	1315
Leu Glu Ala Val Lys Lys Ala Pro Leu Gln Phe Glu Asn Ala Gly Gln	
390 395 400 405	
gag act cgt cag cat tgg gca acc tcg gcg gat gga acg aag att ccg	1363
Glu Thr Arg Gln His Trp Ala Thr Ser Ala Asp Gly Thr Lys Ile Pro	
410 415 420	
tac ttt att aca gga gcc ttc gag gag gaa cca caa aac acc ctg gtc	1411
Tyr Phe Ile Thr Gly Ala Phe Glu Glu Glu Pro Gln Asn Thr Leu Val	
425 430 435	
cac gcc tac ggc ggc ttc gag gtt tcc ctt acc cca agc cac tcc ccg	1459
His Ala Tyr Gly Gly Phe Glu Val Ser Leu Thr Pro Ser His Ser Pro	
440 445 450	
acc cgc ggc atc gca tgg ttg gaa aag ggc tac tac ttt gtg gaa gcc	1507
Thr Arg Gly Ile Ala Trp Leu Glu Lys Gly Tyr Tyr Phe Val Glu Ala	
455 460 465	
aac ctg cgt ggt ggc ggt gaa ttc ggt ccg gaa tgg cat tcg cag gca	1555
Asn Leu Arg Gly Gly Gly Glu Phe Gly Pro Glu Trp His Ser Gln Ala	
470 475 480 485	
acc aag ctg aac cgc atg aag gtg tgg gag gat cac cgc gcg gtg ctc	1603
Thr Lys Leu Asn Arg Met Lys Val Trp Glu Asp His Arg Ala Val Leu	
490 495 500	
gcc gac ctt gtg gag cgc ggc tac gca acg ccg gag cag att gcg att	1651
Ala Asp Leu Val Glu Arg Gly Tyr Ala Thr Pro Glu Gln Ile Ala Ile	
505 510 515	
cgt ggc gga tcc aac ggt ggt ttg ctg aca agt ggc gcg tta act cag	1699
Arg Gly Gly Ser Asn Gly Gly Leu Leu Thr Ser Gly Ala Leu Thr Gln	
520 525 530	
tac cca gaa gca ttc ggt gcg gca gtt gtg cag gtg ccg ttg gct gat	1747
Tyr Pro Glu Ala Phe Gly Ala Ala Val Val Gln Val Pro Leu Ala Asp	
535 540 545	
atg ttg cgc tat cac acc tgg tca gcg ggt gct tcg tgg atg gcg gag	1795
Met Leu Arg Tyr His Thr Trp Ser Ala Gly Ala Ser Trp Met Ala Glu	
550 555 560 565	
tac ggc aac cct gac gat ccg gag gaa cgg gcg gtg att gag cag tac	1843
Tyr Gly Asn Pro Asp Asp Pro Glu Glu Arg Ala Val Ile Glu Gln Tyr	
570 575 580	
tcg ccg gtg cag gcg gtg gtg ggc gtc gag aag cga att tat cca ccc	1891
Ser Pro Val Gln Ala Val Val Gly Val Glu Lys Arg Ile Tyr Pro Pro	
585 590 595	
gca ttg gtg acg acc tca acc cgg gac gac cgc gtc cac ccc gcg cac	1939
Ala Leu Val Thr Thr Ser Thr Arg Asp Asp Arg Val His Pro Ala His	
600 605 610	

gcg cgc ctt ttt gct caa gct ttg ctt gat gcg ggc cag gcc gtg gat 1987  
 Ala Arg Leu Phe Ala Gln Ala Leu Leu Asp Ala Gly Gln Ala Val Asp  
 615 620 625

tac tac gaa aac acc gag ggc ggc cat gcc ggc gcg gcg gat aac aag 2035  
 Tyr Tyr Glu Asn Thr Glu Gly Gly His Ala Gly Ala Ala Asp Asn Lys  
 630 635 640 645

cag acc gcg ttt gtg gaa tcg ctg atc tac acc tgg atc gag aag act 2083  
 Gln Thr Ala Phe Val Glu Ser Leu Ile Tyr Thr Trp Ile Glu Lys Thr  
 650 655 660

ttg gat cag cag ggt agc att taatacctat gattatgcga agg 2127  
 Leu Asp Gln Gln Gly Ser Ile  
 665

<210> 576

<211> 668

<212> PRT

<213> Corynebacterium glutamicum

<400> 576

Met Thr Asp Tyr Thr Phe Leu Glu Asp Ile Asp Thr Pro Glu Ala Leu  
 1 5 10 15

Ala Trp Ala Glu Lys Trp Ser Gly Glu Ser Val Glu Lys Leu Lys Ser  
 20 25 30

Pro Ala Lys Asp Ala Leu Glu Ala Arg Leu Leu Ala Ala Leu Asp Thr  
 35 40 45

Asp Asp Arg Ile Ala Tyr Val Ser Arg Arg Gly Glu Lys Leu Tyr Asn  
 50 55 60

Phe Trp Arg Asp Ala Gln His Pro Arg Gly Val Trp Arg Thr Thr Thr  
 65 70 75 80

Leu Glu Ser Tyr Glu Ser Asp Gln Pro Glu Trp Asp Val Leu Ile Asp  
 85 90 95

Val Asp Ala Leu Ala Glu Asp Glu Gly Glu Asn Trp Val Trp Lys Gly  
 100 105 110

Ala Val Val Arg Ser Pro Glu Phe Asp Arg Ala Leu Val Lys Phe Ser  
 115 120 125

Arg Gly Gly Ala Asp Ala Thr Val Ile Arg Glu Phe Asp Leu Ala Thr  
 130 135 140

Ala Ala Phe Val Asp Asp Ser Pro Phe Glu Leu Lys Glu Ala Lys Ser  
 145 150 155 160

Asp Val Thr Trp Val Asp Leu Asp Thr Leu Leu Val Gly Thr Asp Thr  
 165 170 175

Gly Glu Gly Ser Leu Thr Asp Ser Gly Tyr Pro Ala Arg Val Leu Thr  
 180 185 190

Trp Lys Arg Gly Thr Pro Leu Glu Gln Ala Glu Leu Phe Phe Glu Gly  
 195 200 205

Ser Arg Gln Asp Val Ala Thr His Ala Trp Arg Asp Ser Thr Pro Gly  
 210 215 220  
 Phe Glu Arg Thr Phe Val Ser Arg Ser Leu Asp Phe Tyr Asn Ser Glu  
 225 230 235 240  
 Thr Ser Leu Glu Thr Glu Gly Gly Leu Val Lys Leu Asp Val Pro Thr  
 245 250 255  
 Asp Cys Asp Val Ile Val Lys Lys Gln Trp Ile Phe Val Ser Pro Arg  
 260 265 270  
 Thr Asp Phe Ala Gly Ile Pro Ala Gly Gly Leu Gly Val Leu Leu Leu  
 275 280 285  
 Lys Glu Phe Leu Glu Gly Gly Arg Asp Phe Gln Pro Val Phe Thr Pro  
 290 295 300  
 Thr Glu Ser Thr Ser Leu Gln Gly Leu Ala Thr Thr Lys Asn Phe Leu  
 305 310 315 320  
 Val Leu Thr Leu Leu Asn Asn Val Ser Thr Glu Ile Val Thr Val Pro  
 325 330 335  
 Leu Asn Asp Pro Thr Thr Glu His Glu His Ile Asp Leu Pro Glu His  
 340 345 350  
 Val Thr Ala His Val Val Ala Thr Ser Pro Leu Asp Gly Asp Glu Ile  
 355 360 365  
 Trp Val Gln Ala Ala Ser Phe Thr Glu Ala Pro Thr Leu Leu Arg Ala  
 370 375 380  
 Glu Leu Pro Gly Ala Leu Glu Ala Val Lys Lys Ala Pro Leu Gln Phe  
 385 390 395 400  
 Glu Asn Ala Gly Gln Glu Thr Arg Gln His Trp Ala Thr Ser Ala Asp  
 405 410 415  
 Gly Thr Lys Ile Pro Tyr Phe Ile Thr Gly Ala Phe Glu Glu Glu Pro  
 420 425 430  
 Gln Asn Thr Leu Val His Ala Tyr Gly Gly Phe Glu Val Ser Leu Thr  
 435 440 445  
 Pro Ser His Ser Pro Thr Arg Gly Ile Ala Trp Leu Glu Lys Gly Tyr  
 450 455 460  
 Tyr Phe Val Glu Ala Asn Leu Arg Gly Gly Gly Glu Phe Gly Pro Glu  
 465 470 475 480  
 Trp His Ser Gln Ala Thr Lys Leu Asn Arg Met Lys Val Trp Glu Asp  
 485 490 495  
 His Arg Ala Val Leu Ala Asp Leu Val Glu Arg Gly Tyr Ala Thr Pro  
 500 505 510  
 Glu Gln Ile Ala Ile Arg Gly Gly Ser Asn Gly Gly Leu Leu Thr Ser  
 515 520 525

Gly Ala Leu Thr Gln Tyr Pro Glu Ala Phe Gly Ala Ala Val Val Gln  
 530 535 540  
 Val Pro Leu Ala Asp Met Leu Arg Tyr His Thr Trp Ser Ala Gly Ala  
 545 550 555 560  
 Ser Trp Met Ala Glu Tyr Gly Asn Pro Asp Asp Pro Glu Glu Arg Ala  
 565 570 575  
 Val Ile Glu Gln Tyr Ser Pro Val Gln Ala Val Val Gly Val Glu Lys  
 580 585 590  
 Arg Ile Tyr Pro Pro Ala Leu Val Thr Thr Ser Thr Arg Asp Asp Arg  
 595 600 605  
 Val His Pro Ala His Ala Arg Leu Phe Ala Gln Ala Leu Leu Asp Ala  
 610 615 620  
 Gly Gln Ala Val Asp Tyr Tyr Glu Asn Thr Glu Gly Gly His Ala Gly  
 625 630 635 640  
 Ala Ala Asp Asn Lys Gln Thr Ala Phe Val Glu Ser Leu Ile Tyr Thr  
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 Trp Ile Glu Lys Thr Leu Asp Gln Gln Gly Ser Ile  
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<210> 577  
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 <213> Corynebacterium glutamicum

<220>  
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 <222> (1)..(192)  
 <223> FRXA02047

<400> 577  
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 1 5 10 15  
 ttg ctt gat gcg ggc cag gcc gtg gat tac tac gaa aac acc gag ggc 96  
 Leu Leu Asp Ala Gly Gln Ala Val Asp Tyr Tyr Glu Asn Thr Glu Gly  
 20 25 30  
 ggc cat gcc gcc gcg gcg gat aac aag cag acc gcg ttt gtg gaa tcg 144  
 Gly His Ala Gly Ala Ala Asp Asn Lys Gln Thr Ala Phe Val Glu Ser  
 35 40 45  
 ctg atc tac acc tgg atc gaa aag act ttg gat cag cag ggt agc att 192  
 Leu Ile Tyr Thr Trp Ile Glu Lys Thr Leu Asp Gln Gln Gly Ser Ile  
 50 55 60  
 taatacctat gattatgcga agg 215

<210> 578  
 <211> 64  
 <212> PRT

<213> Corynebacterium glutamicum

<400> 578

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Leu Leu Asp Ala Gly Gln Ala Val Asp Tyr Tyr Glu Asn Thr Glu Gly
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Gly His Ala Gly Ala Ala Asp Asn Lys Gln Thr Ala Phe Val Glu Ser
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<210> 579

<211> 477

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(454)

<223> RXA02174

<400> 579

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gaaacccaaa aatacgattt tcaaggagca tgtacagcac atg gaa aag cca cag 115
                                         Met Glu Lys Pro Gln
                                         1           5

att gag cta ccg gtc ggt cca gca ccg gaa gat ctc gta atc tct gac 163
Ile Glu Leu Pro Val Gly Pro Ala Pro Glu Asp Leu Val Ile Ser Asp
          10           15           20

atc atc gtt ggc gaa gga gca gaa gcc cgc cca ggt gga gaa gtt gag 211
Ile Ile Val Gly Glu Gly Ala Glu Ala Arg Pro Gly Gly Glu Val Glu
          25           30           35

gtc cac tat gtg ggc gtt gac ttt gaa acc ggc gag gag ttt gac tct 259
Val His Tyr Val Gly Val Asp Phe Glu Thr Gly Glu Glu Phe Asp Ser
          40           45           50

tcc tgg gat cgt gga cag acc agc cag ttc cca ctc aac ggc ctc att 307
Ser Trp Asp Arg Gly Gln Thr Ser Gln Phe Pro Leu Asn Gly Leu Ile
          55           60           65

gca ggt tgg caa gag gga att cca ggc atg aag gtc ggc gga cgt cgt 355
Ala Gly Trp Gln Glu Gly Ile Pro Gly Met Lys Val Gly Gly Arg Arg
          70           75           80           85

cag ctg acc att ccg cca gag gct gct tac ggc cct gag ggt tcc ggc 403
Gln Leu Thr Ile Pro Pro Glu Ala Ala Tyr Gly Pro Glu Gly Ser Gly
          90           95           100

cac cca ctg tct ggc cgt acc ctg gtg ttc atc atc gat ttg atc agc 451
His Pro Leu Ser Gly Arg Thr Leu Val Phe Ile Ile Asp Leu Ile Ser
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gca taattttctt tactgcgcta aac  
Ala

477

<210> 580  
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<212> PRT  
<213> Corynebacterium glutamicum

<400> 580  
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Leu Val Ile Ser Asp Ile Ile Val Gly Glu Gly Ala Glu Ala Arg Pro  
20 25 30  
Gly Gly Glu Val Glu Val His Tyr Val Gly Val Asp Phe Glu Thr Gly  
35 40 45  
Glu Glu Phe Asp Ser Ser Trp Asp Arg Gly Gln Thr Ser Gln Phe Pro  
50 55 60  
Leu Asn Gly Leu Ile Ala Gly Trp Gln Glu Gly Ile Pro Gly Met Lys  
65 70 75 80  
Val Gly Gly Arg Arg Gln Leu Thr Ile Pro Pro Glu Ala Ala Tyr Gly  
85 90 95  
Pro Glu Gly Ser Gly His Pro Leu Ser Gly Arg Thr Leu Val Phe Ile  
100 105 110  
Ile Asp Leu Ile Ser Ala  
115

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<212> DNA  
<213> Corynebacterium glutamicum

<220>  
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<222> (101)..(1447)  
<223> RXA00568

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Val Lys Ser Ser Val  
1 5  
gag aag ctg agc gac acc cgt tca aag atc acc gtt gag gtt cca ttt 163  
Glu Lys Leu Ser Asp Thr Arg Ser Lys Ile Thr Val Glu Val Pro Phe  
10 15 20  
tct gaa ctg aag cca gag atc gac cag gca tac gcc gct cta gcg cag 211  
Ser Glu Leu Lys Pro Glu Ile Asp Gln Ala Tyr Ala Ala Leu Ala Gln  
25 30 35

caa gtc cag atc cct ggt ttc cgt aag ggc aag gca ccg cgt cag ctt	259
Gln Val Gln Ile Pro Gly Phe Arg Lys Gly Lys Ala Pro Arg Gln Leu	
40 45 50	
atc gac gca cgc ttc ggc cgt ggt gcg gtt ctg gag cag gtt gtc aac	307
Ile Asp Ala Arg Phe Gly Arg Gly Ala Val Leu Glu Gln Val Val Asn	
55 60 65	
gac atg ctt cct aac cgc tac gca cag gca atc gaa gct gag ggc atc	355
Asp Met Leu Pro Asn Arg Tyr Ala Gln Ala Ile Glu Ala Glu Gly Ile	
70 75 80 85	
aag gca atc ggc cag cct aac gta gag gtc acc aag atc gaa gac aac	403
Lys Ala Ile Gly Gln Pro Asn Val Glu Val Thr Lys Ile Glu Asp Asn	
90 95 100	
gag ctc gtt gag ttc gtc gct gag gtt gac gtt cgc cca gag ttc gag	451
Glu Leu Val Glu Phe Val Ala Glu Val Asp Val Arg Pro Glu Phe Glu	
105 110 115	
ctt cct aag ttc gag gac atc act gtt gag gtc cca gct atc aag gct	499
Leu Pro Lys Phe Glu Asp Ile Thr Val Glu Val Pro Ala Ile Lys Ala	
120 125 130	
gac gaa gag gca atc gaa gca gag ctc gag acc ctg cgt gca cgt ttc	547
Asp Glu Glu Ala Ile Glu Ala Glu Leu Glu Thr Leu Arg Ala Arg Phe	
135 140 145	
tcc acc ttg aag gat cac aac cac aag ctg aag aag ggt gag ttc gtc	595
Ser Thr Leu Lys Asp His Asn His Lys Leu Lys Lys Gly Glu Phe Val	
150 155 160 165	
acc atc aac atc acc gca agc att gac ggt gag aag att gaa gag gca	643
Thr Ile Asn Ile Thr Ala Ser Ile Asp Gly Glu Lys Ile Glu Glu Ala	
170 175 180	
acc act gag ggt ctg tcc tac gaa atc gga tct gac gat ctg att gac	691
Thr Thr Glu Gly Leu Ser Tyr Glu Ile Gly Ser Asp Asp Leu Ile Asp	
185 190 195	
ggc ctg gac aag gct ctg atc ggc gct aag aag gat gaa acc gta gag	739
Gly Leu Asp Lys Ala Leu Ile Gly Ala Lys Lys Asp Glu Thr Val Glu	
200 205 210	
ttc acc tct gag ctg gca aac ggc gag cac aag ggc aag gaa gct caa	787
Phe Thr Ser Glu Leu Ala Asn Gly Glu His Lys Gly Lys Glu Ala Gln	
215 220 225	
atc agc gtt gag atc acc gca acc aag cag cgc gag ctg cct gag ctg	835
Ile Ser Val Glu Ile Thr Ala Thr Lys Gln Arg Glu Leu Pro Glu Leu	
230 235 240 245	
gat gat gag ttc gca cag ctg gct tct gag ttc gac acc atc gaa gag	883
Asp Asp Glu Phe Ala Gln Leu Ala Ser Glu Phe Asp Thr Ile Glu Glu	
250 255 260	
ctt cgt gag tcc acc gtg tct gac gtt gag gct aag cag aag aac gag	931
Leu Arg Glu Ser Thr Val Ser Asp Val Glu Ala Lys Gln Lys Asn Glu	
265 270 275	
cag gct gct gca atc cgc gac gaa gtt ctc gct gcg gct ctt ggc gag	979

Gln Ala Ala Ala Ile Arg Asp Glu Val Leu Ala Ala Ala Leu Gly Glu  
 280 285 290

gct gac ttc gct ctg cca cag tcc atc gtt gac gag cag gca cac tcc 1027  
 Ala Asp Phe Ala Leu Pro Gln Ser Ile Val Asp Glu Gln Ala His Ser  
 295 300 305

cag ctg cac cag ctc ctc ggc gag ctt gca cac gac gat gct gca ctg 1075  
 Gln Leu His Gln Leu Leu Gly Glu Leu Ala His Asp Asp Ala Ala Leu  
 310 315 320 325

aac tcc ctc ctt gag gct cag ggc acc act cgt gaa gag ttc gac aag 1123  
 Asn Ser Leu Leu Glu Ala Gln Gly Thr Thr Arg Glu Glu Phe Asp Lys  
 330 335 340

aag aac gtc gaa gat gct gag aag gct gtt cgc acc cag ctg ttc ctg 1171  
 Lys Asn Val Glu Asp Ala Glu Lys Ala Val Arg Thr Gln Leu Phe Leu  
 345 350 355

gac acc ctc tct gag gtt gag gag cct gag gtt tcc cag cag gag ctc 1219  
 Asp Thr Leu Ser Glu Val Glu Glu Pro Glu Val Ser Gln Gln Glu Leu  
 360 365 370

acc gac cac atc ctg ttc acc gca cag tct tac ggc atg gac cca aac 1267  
 Thr Asp His Ile Leu Phe Thr Ala Gln Ser Tyr Gly Met Asp Pro Asn  
 375 380 385

cag ttc atc ggt cag ctg cag cag tcc ggc cag atc gcg aac ctc ttc 1315  
 Gln Phe Ile Gly Gln Leu Gln Gln Ser Gly Gln Ile Ala Asn Leu Phe  
 390 395 400 405

tcc gac gtt cgc cgt ggc aag gct ctt gca cag gct atc tgc cgc gta 1363  
 Ser Asp Val Arg Arg Gly Lys Ala Leu Ala Gln Ala Ile Cys Arg Val  
 410 415 420

aac gtg aag gac tcc gag ggt aac gag atc gac cct aag gaa tac ttc 1411  
 Asn Val Lys Asp Ser Glu Gly Asn Glu Ile Asp Pro Lys Glu Tyr Phe  
 425 430 435

ggt gaa gaa gaa gta gct gag act gag tct gaa gct taaaaacttt 1457  
 Gly Glu Glu Glu Val Ala Glu Thr Glu Ser Glu Ala  
 440 445

aaagaaataa cgc 1470

&lt;210&gt; 582

&lt;211&gt; 449

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 582

Val Lys Ser Ser Val Glu Lys Leu Ser Asp Thr Arg Ser Lys Ile Thr  
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Val Glu Val Pro Phe Ser Glu Leu Lys Pro Glu Ile Asp Gln Ala Tyr  
 20 25 30

Ala Ala Leu Ala Gln Gln Val Gln Ile Pro Gly Phe Arg Lys Gly Lys  
 35 40 45

Ala Pro Arg Gln Leu Ile Asp Ala Arg Phe Gly Arg Gly Ala Val Leu  
 50 55 60  
 Glu Gln Val Val Asn Asp Met Leu Pro Asn Arg Tyr Ala Gln Ala Ile  
 65 70 75 80  
 Glu Ala Glu Gly Ile Lys Ala Ile Gly Gln Pro Asn Val Glu Val Thr  
 85 90 95  
 Lys Ile Glu Asp Asn Glu Leu Val Glu Phe Val Ala Glu Val Asp Val  
 100 105 110  
 Arg Pro Glu Phe Glu Leu Pro Lys Phe Glu Asp Ile Thr Val Glu Val  
 115 120 125  
 Pro Ala Ile Lys Ala Asp Glu Glu Ala Ile Glu Ala Glu Leu Glu Thr  
 130 135 140  
 Leu Arg Ala Arg Phe Ser Thr Leu Lys Asp His Asn His Lys Leu Lys  
 145 150 155 160  
 Lys Gly Glu Phe Val Thr Ile Asn Ile Thr Ala Ser Ile Asp Gly Glu  
 165 170 175  
 Lys Ile Glu Glu Ala Thr Thr Glu Gly Leu Ser Tyr Glu Ile Gly Ser  
 180 185 190  
 Asp Asp Leu Ile Asp Gly Leu Asp Lys Ala Leu Ile Gly Ala Lys Lys  
 195 200 205  
 Asp Glu Thr Val Glu Phe Thr Ser Glu Leu Ala Asn Gly Glu His Lys  
 210 215 220  
 Gly Lys Glu Ala Gln Ile Ser Val Glu Ile Thr Ala Thr Lys Gln Arg  
 225 230 235 240  
 Glu Leu Pro Glu Leu Asp Asp Glu Phe Ala Gln Leu Ala Ser Glu Phe  
 245 250 255  
 Asp Thr Ile Glu Glu Leu Arg Glu Ser Thr Val Ser Asp Val Glu Ala  
 260 265 270  
 Lys Gln Lys Asn Glu Gln Ala Ala Ala Ile Arg Asp Glu Val Leu Ala  
 275 280 285  
 Ala Ala Leu Gly Glu Ala Asp Phe Ala Leu Pro Gln Ser Ile Val Asp  
 290 295 300  
 Glu Gln Ala His Ser Gln Leu His Gln Leu Leu Gly Glu Leu Ala His  
 305 310 315 320  
 Asp Asp Ala Ala Leu Asn Ser Leu Leu Glu Ala Gln Gly Thr Thr Arg  
 325 330 335  
 Glu Glu Phe Asp Lys Lys Asn Val Glu Asp Ala Glu Lys Ala Val Arg  
 340 345 350  
 Thr Gln Leu Phe Leu Asp Thr Leu Ser Glu Val Glu Glu Pro Glu Val  
 355 360 365  
 Ser Gln Gln Glu Leu Thr Asp His Ile Leu Phe Thr Ala Gln Ser Tyr

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<211> 432
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(409)
<223> RXN03040
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<223> All occurrences of n = any nucleotide

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<223> All occurrences of Xaa = any amino acid
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ctctacatct tcgccgggttc cgggtgtgttc tctgaactag																		115
												Met	tca	tnc	ggt	gac		
												1				5		
aac gca ccg att gat gag gat gcg ttc aaa aac cgc gtc ttg gtt ggg																		163
Asn Ala Pro Ile Asp Glu Asp Ala Phe Lys Asn Arg Val Leu Val Gly																		
										10				15		20		
ttt gaa atc gaa gct atg tcc aac acc tgc acc cat aac ctc aag gct																		211
Phe Glu Ile Glu Ala Met Ser Asn Thr Cys Thr His Asn Leu Lys Ala																		
										25			30		35			
gcg acc gat caa atg ggc atc gac aac atc aac tac gat ttc cga cca																		259
Ala Thr Asp Gln Met Gly Ile Asp Asn Ile Asn Tyr Asp Phe Arg Pro																		
										40			45		50			
acc gga acc cac gcc tgg gat tac tgg aac gaa gcg ctc cac cgc ttc																		307
Thr Gly Thr His Ala Trp Asp Tyr Trp Asn Glu Ala Leu His Arg Phe																		
										55			60		65			
ttc ccg ttg atg atg cag ggc ttc ggc ctc gac ggt ggt ccc atc ccg																		355
Phe Pro Leu Met Met Gln Gly Phe Gly Leu Asp Gly Gly Pro Ile Pro																		
										70			75		80	85		

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<400> 585
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ggaactcccg ctgcctaagc gggacatagt tgcaggggac atg cgt tca gat gtt 115
                                         Met Arg Ser Asp Val
                                         1                               5

atc gag tta ccg gag ggg gta agc aag gag aaa gct gac cag cta gaa 163
Ile Glu Leu Pro Glu Gly Val Ser Lys Glu Lys Ala Asp Gln Leu Glu
                        10                        15                        20

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gtt gcg gaa gcg cga ctt aac gag ggt gca cga ctg atg gca acc acc	211
Val Ala Glu Ala Arg Leu Asn Glu Gly Ala Arg Leu Met Ala Thr Thr	
25 30 35	
ggg tgt gag gtt atg tgg cca acg ggc ttc tca gtt tgt ggc cga att	259
Gly Cys Glu Val Met Trp Pro Thr Gly Phe Ser Val Cys Gly Arg Ile	
40 45 50	
ctt gac acc tat cgc cag gtt gga ggt cag ttg tca tgg ctt ggg cca	307
Leu Asp Thr Tyr Arg Gln Val Gly Gly Gln Leu Ser Trp Leu Gly Pro	
55 60 65	
ccg aag tca aac gag ttg acc aat ccc gac ggt gtt ggc aaa aga agt	355
Pro Lys Ser Asn Glu Leu Thr Asn Pro Asp Gly Val Gly Lys Arg Ser	
70 75 80 85	
gaa ttt ttt ggt gga gcc atc tat tgg cac cca gac aca ggc gct tat	403
Glu Phe Phe Gly Gly Ala Ile Tyr Trp His Pro Asp Thr Gly Ala Tyr	
90 95 100	
gca gtg acc ttg gac ggt ttg cga cag tgg ggg acc ttg aac tgg gaa	451
Ala Val Thr Leu Asp Gly Leu Arg Gln Trp Gly Thr Leu Asn Trp Glu	
105 110 115	
tca ggg cca ttg ggg tac cca acc tct ggt ccg atg gat aca aac tat	499
Ser Gly Pro Leu Gly Tyr Pro Thr Ser Gly Pro Met Asp Thr Asn Tyr	
120 125 130	
ccc ctt act cag cga cag act ttt caa ggt ggt gac aac tac tac aac	547
Pro Leu Thr Gln Arg Gln Thr Phe Gln Gly Gly Asp Asn Tyr Tyr Asn	
135 140 145	
cca ttg act ggc ggt gct gtg tgg ggc gat att aaa cag cgc tac gaa	595
Pro Leu Thr Gly Gly Ala Val Trp Gly Asp Ile Lys Gln Arg Tyr Glu	
150 155 160 165	
gaa ctt ggc ggc tcg aat cat gcc att ggc atc ccg atc act aat gag	643
Glu Leu Gly Gly Ser Asn His Ala Ile Gly Ile Pro Ile Thr Asn Glu	
170 175 180	
cta cct agc ggt act gag tat ttt tac aat aat ttc tcc aat gga aca	691
Leu Pro Ser Gly Thr Glu Tyr Phe Tyr Asn Asn Phe Ser Asn Gly Thr	
185 190 195	
att tcg tgg cga aat gat cgt cag aca cgg ttt atg tat ttg gct acg	739
Ile Ser Trp Arg Asn Asp Arg Gln Thr Arg Phe Met Tyr Leu Ala Thr	
200 205 210	
cag cgg gtg tgg gat gcg ttg ggt cgg gag acg ggt cgt tta ggt ttt	787
Gln Arg Val Trp Asp Ala Leu Gly Arg Glu Thr Gly Arg Leu Gly Phe	
215 220 225	
cct gaa gca gat gaa aca cct gag gtt tct ggt cta ttc cat gtg gcg	835
Pro Glu Ala Asp Glu Thr Pro Glu Val Ser Gly Leu Phe His Val Ala	
230 235 240 245	

&lt;210&gt; 586

&lt;211&gt; 245

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 586

Met Arg Ser Asp Val Ile Glu Leu Pro Glu Gly Val Ser Lys Glu Lys  
 1 5 10 15  
 Ala Asp Gln Leu Glu Val Ala Glu Ala Arg Leu Asn Glu Gly Ala Arg  
 20 25 30  
 Leu Met Ala Thr Thr Gly Cys Glu Val Met Trp Pro Thr Gly Phe Ser  
 35 40 45  
 Val Cys Gly Arg Ile Leu Asp Thr Tyr Arg Gln Val Gly Gly Gln Leu  
 50 55 60  
 Ser Trp Leu Gly Pro Pro Lys Ser Asn Glu Leu Thr Asn Pro Asp Gly  
 65 70 75 80  
 Val Gly Lys Arg Ser Glu Phe Phe Gly Gly Ala Ile Tyr Trp His Pro  
 85 90 95  
 Asp Thr Gly Ala Tyr Ala Val Thr Leu Asp Gly Leu Arg Gln Trp Gly  
 100 105 110  
 Thr Leu Asn Trp Glu Ser Gly Pro Leu Gly Tyr Pro Thr Ser Gly Pro  
 115 120 125  
 Met Asp Thr Asn Tyr Pro Leu Thr Gln Arg Gln Thr Phe Gln Gly Gly  
 130 135 140  
 Asp Asn Tyr Tyr Asn Pro Leu Thr Gly Gly Ala Val Trp Gly Asp Ile  
 145 150 155 160  
 Lys Gln Arg Tyr Glu Glu Leu Gly Gly Ser Asn His Ala Ile Gly Ile  
 165 170 175  
 Pro Ile Thr Asn Glu Leu Pro Ser Gly Thr Glu Tyr Phe Tyr Asn Asn  
 180 185 190  
 Phe Ser Asn Gly Thr Ile Ser Trp Arg Asn Asp Arg Gln Thr Arg Phe  
 195 200 205  
 Met Tyr Leu Ala Thr Gln Arg Val Trp Asp Ala Leu Gly Arg Glu Thr  
 210 215 220  
 Gly Arg Leu Gly Phe Pro Glu Ala Asp Glu Thr Pro Glu Val Ser Gly  
 225 230 235 240  
 Leu Phe His Val Ala  
 245

&lt;210&gt; 587

&lt;211&gt; 456

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(433)

&lt;223&gt; RXN02949

&lt;400&gt; 587

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tgttatcgcc cctggatgag tagtgattta gaggagtgcgt gtg agc gac gag cag 115  
Val Ser Asp Glu Gln  
1 5

aat tct ggc gta ggc gga acg tct cgc cca acg ggt aaa cgc cag ctg 163  
Asn Ser Gly Val Gly Gly Thr Ser Arg Pro Thr Gly Lys Arg Gln Leu  
10 15 20

tcg ggt gct tcc act acc tct acc tct tct tat gag gct aag cag gta 211  
Ser Gly Ala Ser Thr Thr Ser Thr Ser Ser Tyr Glu Ala Lys Gln Val  
25 30 35

tct aca cag aag aag tca tcc ggt tcg gat tct aag cct ggc ggc ggt 259  
Ser Thr Gln Lys Lys Ser Ser Gly Ser Asp Ser Lys Pro Gly Gly Gly  
40 45 50

gtt att tct ttt ctg cct gag gtt gtg gga gaa gtc cgt aag gtt att 307  
Val Ile Ser Phe Leu Pro Glu Val Val Gly Glu Val Arg Lys Val Ile  
55 60 65

tgg cct act gcg cgc cag atg gtc acg tac acc ctt gtc gtt ttg gga 355  
Trp Pro Thr Ala Arg Gln Met Val Thr Tyr Thr Leu Val Val Leu Gly  
70 75 80 85

ttc ttg att gtt ttg acc gct ttg gtg tct ggt gtg gat ttc cta gct 403  
Phe Leu Ile Val Leu Thr Ala Leu Val Ser Gly Val Asp Phe Leu Ala  
90 95 100

ggt ctt gga gtt gag aag att ctg act ccg taggtaggat gtgtaacatc ttt 456  
Gly Leu Gly Val Glu Lys Ile Leu Thr Pro  
105 110

&lt;210&gt; 588

&lt;211&gt; 111

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 588

Val Ser Asp Glu Gln Asn Ser Gly Val Gly Gly Thr Ser Arg Pro Thr  
1 5 10 15

Gly Lys Arg Gln Leu Ser Gly Ala Ser Thr Thr Ser Thr Ser Ser Tyr  
20 25 30

Glu Ala Lys Gln Val Ser Thr Gln Lys Lys Ser Ser Gly Ser Asp Ser  
35 40 45

Lys Pro Gly Gly Gly Val Ile Ser Phe Leu Pro Glu Val Val Gly Glu  
50 55 60

Val Arg Lys Val Ile Trp Pro Thr Ala Arg Gln Met Val Thr Tyr Thr  
65 70 75 80

Leu Val Val Leu Gly Phe Leu Ile Val Leu Thr Ala Leu Val Ser Gly  
85 90 95

Val Asp Phe Leu Ala Gly Leu Gly Val Glu Lys Ile Leu Thr Pro

100

105

110

&lt;210&gt; 589

&lt;211&gt; 618

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(595)

&lt;223&gt; RXN00833

&lt;400&gt; 589

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tttctagcac caaaacaaaa ctctccctag tatgggggtcc atg gct aaa aca cat 115  
 Met Ala Lys Thr His  
 1 5

ttt caa ggc aac gaa act gct acc tcc ggc gaa ctg cca cag gtc ggc 163  
 Phe Gln Gly Asn Glu Thr Ala Thr Ser Gly Glu Leu Pro Gln Val Gly  
 10 15 20

gac aac ctc gca gag ttc aac ctc gtc aac acc gaa ctg ggc gag gtc 211  
 Asp Asn Leu Ala Glu Phe Asn Leu Val Asn Thr Glu Leu Gly Glu Val  
 25 30 35

tcc tca aag gac ttc cag ggc cgc aag ctt gtc ctg aac atc ttc cca 259  
 Ser Ser Lys Asp Phe Gln Gly Arg Lys Leu Val Leu Asn Ile Phe Pro  
 40 45 50

tcc gtt gac acc ggc gtt tgt gca aca tca gtc cgc aag ttc aac gag 307  
 Ser Val Asp Thr Gly Val Cys Ala Thr Ser Val Arg Lys Phe Asn Glu  
 55 60 65

gca gca gca agc ctg gaa aac acc acc gtg ctg tgc atc tcc aag gat 355  
 Ala Ala Ala Ser Leu Glu Asn Thr Thr Val Leu Cys Ile Ser Lys Asp  
 70 75 80 85

ctt cca ttc gca ctg ggc cgt ttc tgc tcc gca gaa ggc atc gag aac 403  
 Leu Pro Phe Ala Leu Gly Arg Phe Cys Ser Ala Glu Gly Ile Glu Asn  
 90 95 100

gtc acc cca gta tcc gca ttc cgt tcc acc ttc ggt gaa gac aac ggc 451  
 Val Thr Pro Val Ser Ala Phe Arg Ser Thr Phe Gly Glu Asp Asn Gly  
 105 110 115

atc gtg ctc gaa ggc tca cca ctt aag ggt ctt ctt gca cgc agc gtc 499  
 Ile Val Leu Glu Gly Ser Pro Leu Lys Gly Leu Leu Ala Arg Ser Val  
 120 125 130

atc gtc gtc gat gaa aac ggc aag gtt gct tac acc cag ttg gtt gat 547  
 Ile Val Val Asp Glu Asn Gly Lys Val Ala Tyr Thr Gln Leu Val Asp  
 135 140 145

gag atc ttc act gaa cct gat tac gac gct gca ctt gct ggg ctg aac 595  
 Glu Ile Phe Thr Glu Pro Asp Tyr Asp Ala Leu Ala Gly Leu Asn  
 150 155 160 165

taattttactt cgctcagggg aat 618

<210> 590  
 <211> 165  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 590  
 Met Ala Lys Thr His Phe Gln Gly Asn Glu Thr Ala Thr Ser Gly Glu  
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 Leu Pro Gln Val Gly Asp Asn Leu Ala Glu Phe Asn Leu Val Asn Thr  
                     20                    25                    30  
 Glu Leu Gly Glu Val Ser Ser Lys Asp Phe Gln Gly Arg Lys Leu Val  
             35                    40                    45  
 Leu Asn Ile Phe Pro Ser Val Asp Thr Gly Val Cys Ala Thr Ser Val  
     50                    55                    60  
 Arg Lys Phe Asn Glu Ala Ala Ala Ser Leu Glu Asn Thr Thr Val Leu  
     65                    70                    75                    80  
 Cys Ile Ser Lys Asp Leu Pro Phe Ala Leu Gly Arg Phe Cys Ser Ala  
                     85                    90                    95  
 Glu Gly Ile Glu Asn Val Thr Pro Val Ser Ala Phe Arg Ser Thr Phe  
             100                    105                    110  
 Gly Glu Asp Asn Gly Ile Val Leu Glu Gly Ser Pro Leu Lys Gly Leu  
             115                    120                    125  
 Leu Ala Arg Ser Val Ile Val Val Asp Glu Asn Gly Lys Val Ala Tyr  
     130                    135                    140  
 Thr Gln Leu Val Asp Glu Ile Phe Thr Glu Pro Asp Tyr Asp Ala Ala  
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 <213> Corynebacterium glutamicum

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 <223> RXN01676

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   Met Ile Leu His Gly  
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 Val Val Phe Tyr Ala Gly Leu Leu Val Leu Leu Val Pro Leu Gly Leu

10					15					20					
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Gly Ala Gly Ile Leu Gly Glu Leu Phe Ile Thr Gln Arg Gln Thr Ile															
25 30 35															
atc gtg gtt tca tgc atc gtg ctg att atc cta ggt ttt gtc cag atc	259														
Ile Val Val Ser Ser Ile Val Leu Ile Ile Leu Gly Phe Val Gln Ile															
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Phe Gly Gly Gly Phe Asp Phe Gly Lys Ala Leu Pro Gly Leu Asp Arg															
55 60 65															
ctg caa tct aag gcc act gtg acc tca ggt cta gga aag agc ttt tta	355														
Leu Gln Ser Lys Ala Thr Val Thr Ser Gly Leu Gly Lys Ser Phe Leu															
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cta gga atg acc agt agt att gcc ggt ttt tgt tcc gga cca atc ctc	403														
Leu Gly Met Thr Ser Ser Ile Ala Gly Phe Cys Ser Gly Pro Ile Leu															
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Gly Ala Val Leu Thr Leu Ala Ala Thr Ser Gly Asn Ser Ile Thr Ser															
105 110 115															
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Ala Leu Ile Leu Ser Ala Tyr Gly Ala Gly Met Val Leu Pro Leu Met															
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Ala Ile Ala Ala Leu Trp Ala Lys Leu Gly Gln Arg Gly Gln Gln Met															
135 140 145															
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Leu Arg Gly Arg Glu Phe Thr Phe Leu Gly Arg Gln Trp His Ile Val															
150 155 160 165															
tct gtc att agc ggt gcc ctg atc atc gct gtc gga atc ctc ttt tgg	643														
Ser Val Ile Ser Gly Ala Leu Ile Ile Ala Val Gly Ile Leu Phe Trp															
170 175 180															
tcc acg aac ggc ctt gtc agc atg ccg gag ctc gtt cca atg gac acc	691														
Ser Thr Asn Gly Leu Val Ser Met Pro Glu Leu Val Pro Met Asp Thr															
185 190 195															
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Gln Ile Trp Leu Gln Glu Ala Thr Phe Ser Leu Gly Ser Pro Leu Phe															
200 205 210															
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Asp Ile Ala Leu Ile Ile Val Ala Ala Gly Leu Phe Leu Tyr Phe Trp															
215 220 225															
aac aaa cga caa aag cga aaa gaa gaa gct cag cga ccc aaa gaa agt	835														
Asn Lys Arg Gln Lys Arg Lys Glu Glu Ala Gln Arg Pro Lys Glu Ser															
230 235 240 245															
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Gly Trp Val Ile Asn Pro Arg															
250															

&lt;210&gt; 592

&lt;211&gt; 252

&lt;212&gt; PRT

<213> *Corynebacterium glutamicum*

&lt;400&gt; 592

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          20           25           30

Gln Arg Gln Thr Ile Ile Val Val Ser Ser Ile Val Leu Ile Ile Leu
          35           40           45

Gly Phe Val Gln Ile Phe Gly Gly Gly Phe Asp Phe Gly Lys Ala Leu
 50           55           60

Pro Gly Leu Asp Arg Leu Gln Ser Lys Ala Thr Val Thr Ser Gly Leu
 65           70           75           80

Gly Lys Ser Phe Leu Leu Gly Met Thr Ser Ser Ile Ala Gly Phe Cys
          85           90           95

Ser Gly Pro Ile Leu Gly Ala Val Leu Thr Leu Ala Ala Thr Ser Gly
          100          105          110

Asn Ser Ile Thr Ser Ala Leu Ile Leu Ser Ala Tyr Gly Ala Gly Met
          115          120          125

Val Leu Pro Leu Met Ala Ile Ala Ala Leu Trp Ala Lys Leu Gly Gln
          130          135          140

Arg Gly Gln Gln Met Leu Arg Gly Arg Glu Phe Thr Phe Leu Gly Arg
          145          150          155          160

Gln Trp His Ile Val Ser Val Ile Ser Gly Ala Leu Ile Ile Ala Val
          165          170          175

Gly Ile Leu Phe Trp Ser Thr Asn Gly Leu Val Ser Met Pro Glu Leu
          180          185          190

Val Pro Met Asp Thr Gln Ile Trp Leu Gln Glu Ala Thr Phe Ser Leu
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Gly Ser Pro Leu Phe Asp Ile Ala Leu Ile Ile Val Ala Ala Gly Leu
          210          215          220

Phe Leu Tyr Phe Trp Asn Lys Arg Gln Lys Arg Lys Glu Glu Ala Gln
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Arg Pro Lys Glu Ser Gly Trp Val Ile Asn Pro Arg
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&lt;210&gt; 593

&lt;211&gt; 744

&lt;212&gt; DNA

<213> *Corynebacterium glutamicum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(721)

&lt;223&gt; RXN00380

&lt;400&gt; 593

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Val Arg Leu Thr Lys
1 5

cta gca gca aca atc ggc tgc gtg aca ctc agc gga ctt gcg cta gta 163
Leu Ala Ala Thr Ile Gly Cys Val Thr Leu Ser Gly Leu Ala Leu Val
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gcc tgc agc agt gac agt acc gct ggt act gac gct gtt gct gtc ggc 211
Ala Cys Ser Ser Asp Ser Thr Ala Gly Thr Asp Ala Val Ala Val Gly
25 30 35

gga acc ttc caa ttc cac tcc ccg gat gga aag atg gaa att ttc tac 259
Gly Thr Phe Gln Phe His Ser Pro Asp Gly Lys Met Glu Ile Phe Tyr
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gac gag gct gac cgt caa caa ctc ccc gac att ggt gga gat tcc ctc 307
Asp Glu Ala Asp Arg Gln Gln Leu Pro Asp Ile Gly Gly Asp Ser Leu
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Met Glu Glu Gly Thr Gln Ile Asn Leu Ser Asp Phe Glu Asn Gln Val
70 75 80 85

gtc atc ctc aat gcg tgg ggg cag tgg tgt gca ccg tgc cgc tcc gaa 403
Val Ile Leu Asn Ala Trp Gly Gln Trp Cys Ala Pro Cys Arg Ser Glu
90 95 100

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Ser Asp Asp Leu Gln Ile Ile His Glu Glu Leu Gln Ala Ala Gly Asn
105 110 115

ggc gac acc cct ggt ggc acc gtg ttg ggt atc aat gtg cgt gat tac 499
Gly Asp Thr Pro Gly Gly Thr Val Leu Gly Ile Asn Val Arg Asp Tyr
120 125 130

tcc cgc gac atc gcc caa gac ttt gtc acc gac aac ggc ctt gat tac 547
Ser Arg Asp Ile Ala Gln Asp Phe Val Thr Asp Asn Gly Leu Asp Tyr
135 140 145

cca agc att tac gat cca cca ttt atg aca gca gca tcc ctc ggt ggt 595
Pro Ser Ile Tyr Asp Pro Pro Phe Met Thr Ala Ala Ser Leu Gly Gly
150 155 160 165

gtt ccc gca tcg gtg atc cca acc acc atc gtg ctg gat aaa cag cac 643
Val Pro Ala Ser Val Ile Pro Thr Thr Ile Val Leu Asp Lys Gln His
170 175 180

cgc ccc gca gca gtg ttc ttg cgc gaa gtc acc tcc aaa gat gtg ttg 691
Arg Pro Ala Ala Val Phe Leu Arg Glu Val Thr Ser Lys Asp Val Leu
185 190 195

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 Gly Gly Asp Ser Leu Met Glu Glu Gly Thr Gln Ile Asn Leu Ser Asp  
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                           85                          90                          95  
 Pro Cys Arg Ser Glu Ser Asp Asp Leu Gln Ile Ile His Glu Glu Leu  
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 Gln Ala Ala Gly Asn Gly Asp Thr Pro Gly Gly Thr Val Leu Gly Ile  
                           115                          120                          125  
 Asn Val Arg Asp Tyr Ser Arg Asp Ile Ala Gln Asp Phe Val Thr Asp  
   130                          135                          140  
 Asn Gly Leu Asp Tyr Pro Ser Ile Tyr Asp Pro Pro Phe Met Thr Ala  
   145                          150                          155                          160  
 Ala Ser Leu Gly Gly Val Pro Ala Ser Val Ile Pro Thr Thr Ile Val  
                           165                          170                          175  
 Leu Asp Lys Gln His Arg Pro Ala Ala Val Phe Leu Arg Glu Val Thr  
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 <223> RXN02325

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Glu Asp Pro Ile Glu Lys Ser Arg Arg Asp Pro Asp Asp Val Asn Lys

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Ala Leu Ala Ala Ala Asp Met Tyr Val Leu Met Asn Gln Pro Asp Thr			
230	235	240	245
gcg ctc gcg cac ctt gca gca cta ttg cca aaa ccg gag gct gcc cgg			883
Ala Leu Ala His Leu Ala Ala Leu Leu Pro Lys Pro Glu Ala Ala Arg			
	250	255	260
cgg atc gtg gag ttg ctg aac ttg ttt gat ccg ctg gac ctg gtc gca			931
Arg Ile Val Glu Leu Leu Asn Leu Phe Asp Pro Leu Asp Leu Val Ala			
	265	270	275
ttg gaa atc agg gcg cag gtg ggg aat gca atg agc taagaaaaca			977
Leu Glu Ile Arg Ala Gln Val Gly Asn Ala Met Ser			
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ctttaaatat tct			990

&lt;210&gt; 596

&lt;211&gt; 289

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 596

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20 25 30

Pro His Glu Gly Lys Val Ala Asn Ile Thr Lys Val Thr Ser Ser Asn
35 40 45

Met Glu His Thr Ile Thr Gln Ala Ser Lys Ala Lys Glu Val Val Val
50 55 60

Leu Ile Gly His Ser Leu Leu Pro Thr Phe Gln Asp Leu Glu Lys Asp
65 70 75 80

Ile Leu His Phe Gln Ala Gly Asn Lys Gly Arg Phe Ser Val Ala Ile
85 90 95

Val Asp Pro Asp Arg Ser Ala Asp Val Val Ala Arg Phe Arg Pro Lys
100 105 110

Gln Ile Pro Val Ala Tyr Val Val Lys Asp Gly Ala Ser Ile Ala Glu
115 120 125

Phe Asn Ser Leu Asn Lys Glu Pro Val Ala Gln Trp Leu Asp His Phe
130 135 140

Val Ser Arg Glu Thr Ile Pro Asn Glu Lys Glu Gly Asp Val Asp Lys
145 150 155 160

Gln Ile Asp Pro Arg Leu Trp Arg Ala Ala Glu Leu Val Asn Ala Gly
165 170 175

Asp Phe Arg Ala Ala Leu Ala Leu Tyr Glu Gln Leu Pro Gln Asp Ala
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180					185					190						
Thr	Val	Lys	Arg	Ala	His	Ala	Ala	Val	Ser	Val	Leu	Ala	Arg	Met	Ser	
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210					215					220						
Asp	Asp	Val	Asn	Lys	Ala	Leu	Ala	Ala	Ala	Asp	Met	Tyr	Val	Leu	Met	
225					230					235					240	
Asn	Gln	Pro	Asp	Thr	Ala	Leu	Ala	His	Leu	Ala	Ala	Leu	Leu	Pro	Lys	
245					250					255						
Pro	Glu	Ala	Ala	Arg	Arg	Ile	Val	Glu	Leu	Leu	Asn	Leu	Phe	Asp	Pro	
260					265					270						
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Ser																

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 <223> RXN00493

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 Met Ala Lys Leu Ile 5  
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 Ala Phe Asp Gln Asp Ala Arg Glu Gly Ile Leu Arg Gly Val Asp Ala 20  
 10 15  
 ctg gca aac gct gtc aag gta acc ctc ggc cca cgc ggc cgt aac gtg 211  
 Leu Ala Asn Ala Val Lys Val Thr Leu Gly Pro Arg Gly Arg Asn Val 35  
 25 30  
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 Val Leu Asp Lys Ala Phe Gly Gly Pro Leu Val Thr Asn Asp Gly Val 50  
 40 45  
 acc att gcc cgc gac atc gac ctt gag gat cct ttt gag aac ctc ggt 307  
 Thr Ile Ala Arg Asp Ile Asp Leu Glu Asp Pro Phe Glu Asn Leu Gly 65  
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 Ala Gln Leu Val Lys Ser Val Ala Val Lys Thr Asn Asp Ile Ala Gly 85  
 70 75 80

gac ggc acc acg act gca act ctg ctt gct cag gca ctc att gct gaa	403
Asp Gly Thr Thr Thr Ala Thr Leu Leu Ala Gln Ala Leu Ile Ala Glu	
90 95 100	
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Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro Met Glu Leu Asn Lys	
105 110 115	
ggt att tct gca gct gca gaa aag acc ttg gaa gag ttg aag gca cgc	499
Gly Ile Ser Ala Ala Ala Glu Lys Thr Leu Glu Glu Leu Lys Ala Arg	
120 125 130	
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Ala Thr Glu Val Ser Asp Thr Lys Glu Ile Ala Asn Val Ala Thr Val	
135 140 145	
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Ser Ser Arg Asp Glu Val Val Gly Glu Ile Val Ala Ala Ala Met Glu	
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Lys Val Gly Lys Asp Gly Val Val Thr Val Glu Glu Ser Gln Ser Ile	
170 175 180	
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Glu Thr Ala Leu Glu Val Thr Glu Gly Ile Ser Phe Asp Lys Gly Tyr	
185 190 195	
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Leu Ser Pro Tyr Phe Ile Asn Asp Asn Asp Thr Gln Gln Ala Val Leu	
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Asp Asn Pro Ala Val Leu Leu Val Arg Asn Lys Ile Ser Ser Leu Pro	
215 220 225	
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Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Pro Leu Gln Thr Leu Val	
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Val Asn Ser Ile Arg Lys Thr Ile Lys Val Val Ala Val Lys Ser Pro	
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Tyr Phe Gly Asp Arg Arg Lys Ala Phe Met Asp Asp Leu Ala Ile Val	
280 285 290	
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Thr Lys Ala Thr Val Val Asp Pro Glu Val Gly Ile Asn Leu Asn Glu	
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Ala Gly Glu Glu Val Phe Gly Thr Ala Arg Arg Ile Thr Val Ser Lys	
310 315 320 325	
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Trp	Asp	Arg	Glu	Lys	Ala	Glu	Glu	Arg	Leu	Ala	Lys	Leu	Ser	Gly	Gly		
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Ile	Ala	Val	Ile	Arg	Val	Gly	Ala	Ala	Thr	Glu	Thr	Glu	Val	Asn	Asp		
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Arg	Lys	Leu	Arg	Val	Glu	Asp	Ala	Ile	Asn	Ala	Ala	Arg	Ala	Ala	Ala		
390					395				400						405		
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Gln	Glu	Gly	Val	Ile	Ala	Gly	Gly	Gly	Ser	Ala	Leu	Val	Gln	Ile	Ala		
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gct	ctg	cca	aac	ggc	gag	ggc	ttc	aac	gct	gca	act	ttg	gaa	tac	gga	1555	
Ala	Leu	Pro	Asn	Gly	Glu	Gly	Phe	Asn	Ala	Ala	Thr	Leu	Glu	Tyr	Gly		
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Asn	Leu	Ile	Asn	Asp	Gly	Val	Ile	Asp	Pro	Val	Lys	Val	Thr	His	Ser		
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Gly	His	His	His	His													
					535												

&lt;210&gt; 598

&lt;211&gt; 538

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 598

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 35 40 45  
 Thr Asn Asp Gly Val Thr Ile Ala Arg Asp Ile Asp Leu Glu Asp Pro  
 50 55 60  
 Phe Glu Asn Leu Gly Ala Gln Leu Val Lys Ser Val Ala Val Lys Thr  
 65 70 75 80  
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 85 90 95  
 Ala Leu Ile Ala Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro  
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 Met Glu Leu Asn Lys Gly Ile Ser Ala Ala Ala Glu Lys Thr Leu Glu  
 115 120 125  
 Glu Leu Lys Ala Arg Ala Thr Glu Val Ser Asp Thr Lys Glu Ile Ala  
 130 135 140  
 Asn Val Ala Thr Val Ser Ser Arg Asp Glu Val Val Gly Glu Ile Val  
 145 150 155 160  
 Ala Ala Ala Met Glu Lys Val Gly Lys Asp Gly Val Val Thr Val Glu  
 165 170 175  
 Glu Ser Gln Ser Ile Glu Thr Ala Leu Glu Val Thr Glu Gly Ile Ser  
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 Gln Gln Ala Val Leu Asp Asn Pro Ala Val Leu Leu Val Arg Asn Lys  
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 Ile Ser Ser Leu Pro Asp Phe Leu Pro Leu Leu Glu Lys Val Val Glu  
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 Ser Asn Arg Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Pro  
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 Leu Gln Thr Leu Val Val Asn Ser Ile Arg Lys Thr Ile Lys Val Val  
 260 265 270  
 Ala Val Lys Ser Pro Tyr Phe Gly Asp Arg Arg Lys Ala Phe Met Asp  
 275 280 285  
 Asp Leu Ala Ile Val Thr Lys Ala Thr Val Val Asp Pro Glu Val Gly  
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 Ile Asn Leu Asn Glu Ala Gly Glu Glu Val Phe Gly Thr Ala Arg Arg  
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Ile Thr Val Ser Lys Asp Glu Thr Ile Ile Val Asp Gly Ala Gly Ser  
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 Asn Thr Asp Ser Thr Trp Asp Arg Glu Lys Ala Glu Glu Arg Leu Ala  
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 Lys Leu Ser Gly Gly Ile Ala Val Ile Arg Val Gly Ala Ala Thr Glu  
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 Thr Glu Val Asn Asp Arg Lys Leu Arg Val Glu Asp Ala Ile Asn Ala  
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 Ala Arg Ala Ala Ala Gln Glu Gly Val Ile Ala Gly Gly Gly Ser Ala  
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 Leu Val Gln Ile Ala Glu Thr Leu Lys Ala Tyr Ala Glu Glu Phe Glu  
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 Pro Ala Tyr Trp Ile Ala Ser Asn Ala Gly Leu Asp Gly Ser Val Val  
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 <223> RXN02543

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 Met Gly Arg Ala Val  
 1 5  
  
 gga att gac ctt gga acc acc aac tct gtg gtt tcc gta ctt gaa ggc 163

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Gly	Glu	Pro	Val	Val	Ile	Ala	Asn	Ala	Glu	Gly	Ser	Arg	Thr	Thr	Pro	
			25					30					35			
tcc	gtc	gtt	gca	ttc	gca	aag	aac	ggg	gaa	gtt	cta	gtc	ggc	cag	tcc	259
Ser	Val	Val	Ala	Phe	Ala	Lys	Asn	Gly	Glu	Val	Leu	Val	Gly	Gln	Ser	
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gct	aag	aac	cag	gcg	gtc	acc	aac	gtt	gac	cgc	acc	att	cgc	tcc	gtc	307
Ala	Lys	Asn	Gln	Ala	Val	Thr	Asn	Val	Asp	Arg	Thr	Ile	Arg	Ser	Val	
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aag	cgc	cac	atc	ggc	acc	gac	tgg	tcc	gtt	gct	atc	gat	gac	aag	aac	355
Lys	Arg	His	Ile	Gly	Thr	Asp	Trp	Ser	Val	Ala	Ile	Asp	Asp	Lys	Asn	
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Tyr	Thr	Ser	Gln	Glu	Ile	Ser	Ala	Arg	Thr	Leu	Met	Lys	Leu	Lys	Arg	
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Asp	Ala	Glu	Ala	Tyr	Leu	Gly	Glu	Asp	Val	Thr	Asp	Ala	Val	Ile	Thr	
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gtt	cct	gca	tac	ttc	gag	gac	tca	cag	cgc	cag	gca	acc	aag	gaa	gct	499
Val	Pro	Ala	Tyr	Phe	Glu	Asp	Ser	Gln	Arg	Gln	Ala	Thr	Lys	Glu	Ala	
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Gly	Gln	Ile	Ala	Gly	Leu	Asn	Val	Leu	Arg	Ile	Val	Asn	Glu	Pro	Thr	
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gcg	gct	gca	ctt	gca	tac	ggc	ctt	gag	aag	ggc	gag	cag	gag	cag	acc	595
Ala	Ala	Ala	Leu	Ala	Tyr	Gly	Leu	Glu	Lys	Gly	Glu	Gln	Glu	Gln	Thr	
	150				155					160					165	
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Ile	Leu	Val	Phe	Asp	Leu	Gly	Gly	Gly	Thr	Phe	Asp	Val	Ser	Leu	Leu	
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Glu	Ile	Gly	Asp	Gly	Val	Val	Glu	Val	Arg	Ala	Thr	Ser	Gly	Asp	Asn	
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gag	ctc	ggg	ggc	gac	gac	tgg	gat	cag	cgt	atc	gtt	gac	tgg	ctg	gta	739
Glu	Leu	Gly	Gly	Asp	Asp	Trp	Asp	Gln	Arg	Ile	Val	Asp	Trp	Leu	Val	
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Glu	Lys	Phe	Gln	Ser	Ser	Asn	Gly	Ile	Asp	Leu	Thr	Lys	Asp	Lys	Met	
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Ala	Leu	Gln	Arg	Leu	Arg	Glu	Ala	Ala	Glu	Lys	Ala	Lys	Ile	Glu	Leu	
	230				235					240					245	
tcc	tct	tcc	cag	agt	gca	aac	atc	aac	ctt	cct	tac	atc	acc	gtt	gat	883
Ser	Ser	Ser	Gln	Ser	Ala	Asn	Ile	Asn	Leu	Pro	Tyr	Ile	Thr	Val	Asp	

250										255					260					
gca	gac	aag	aac	cca	ctg	ttc	ttg	gat	gag	acc	ctt	tcc	cgt	gcc	gag	931				
Ala	Asp	Lys	Asn	Pro	Leu	Phe	Leu	Asp	Glu	Thr	Leu	Ser	Arg	Ala	Glu					
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ttc	cag	cgc	atc	acc	cag	gac	ctc	ctg	gcc	cgc	acc	aag	act	cct	ttc	979				
Phe	Gln	Arg	Ile	Thr	Gln	Asp	Leu	Leu	Ala	Arg	Thr	Lys	Thr	Pro	Phe					
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aac	cag	gtt	gtt	aag	gac	gct	ggc	gtg	tcc	gtc	tcg	gag	atc	gac	cac	1027				
Asn	Gln	Val	Val	Lys	Asp	Ala	Gly	Val	Ser	Val	Ser	Glu	Ile	Asp	His					
		295				300					305									
gtt	gtt	ctc	gtc	ggc	ggc	tcc	acc	cgt	atg	cct	gct	gtt	acc	gaa	ctg	1075				
Val	Val	Leu	Val	Gly	Gly	Ser	Thr	Arg	Met	Pro	Ala	Val	Thr	Glu	Leu					
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Gly	Glu	Val	Lys	Asp	Val	Leu	Leu	Leu	Asp	Val	Thr	Pro	Leu	Ser	Leu					
		360				365						370								
ggc	att	gag	acc	aag	ggc	gtg	atg	acc	aag	ctc	atc	gag	cgc	aac		1267				
Gly	Ile	Glu	Thr	Lys	Gly	Gly	Val	Met	Thr	Lys	Leu	Ile	Glu	Arg	Asn					
	375					380					385									
acc	acc	atc	cct	acc	aag	cgt	tcc	gag	acc	ttc	acc	acc	gca	gag	gac	1315				
Thr	Thr	Ile	Pro	Thr	Lys	Arg	Ser	Glu	Thr	Phe	Thr	Thr	Ala	Glu	Asp					
390					395					400					405					
aac	cag	cct	tct	gtt	cag	atc	cag	gtc	ttc	cag	ggc	gag	cgt	gaa	atc	1363				
Asn	Gln	Pro	Ser	Val	Gln	Ile	Gln	Val	Phe	Gln	Gly	Glu	Arg	Glu	Ile					
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gca	acc	gcc	aac	aag	ctg	ctc	gga	tcc	ttc	gag	ctc	ggc	ggc	atc	gca	1411				
Ala	Thr	Ala	Asn	Lys	Leu	Leu	Gly	Ser	Phe	Glu	Leu	Gly	Gly	Ile	Ala					
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Pro	Ala	Pro	Arg	Gly	Val	Pro	Gln	Ile	Glu	Val	Thr	Phe	Asp	Ile	Asp					
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gcc	aac	ggc	atc	gtc	cac	gtc	acc	gca	aag	gac	aag	ggc	act	ggc	aag	1507				
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	455					460					465									
gaa	aac	acc	atc	acc	att	cag	gac	ggc	tcc	ggc	ctc	tcc	cag	gat	gaa	1555				
Glu	Asn	Thr	Ile	Thr	Ile	Gln	Asp	Gly	Ser	Gly	Leu	Ser	Gln	Asp	Glu					
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Ile	Asp	Arg	Met	Ile	Lys	Asp	Ala	Glu	Ala	His	Ala	Asp	Glu	Asp	Lys					
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Lys Arg Arg Glu Glu Gln Glu Val Arg Asn Asn Ala Glu Ser Leu Val  
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520 525 530  
  
gac ctc aag gca aag gtc gaa gag gca gcc aag ggc gtt gaa gaa gca 1747  
Asp Leu Lys Ala Lys Val Glu Glu Ala Ala Lys Gly Val Glu Glu Ala  
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ctc aag ggc gag gac ctc gag gca atc aag gct gca gtt gag aag ctg 1795  
Leu Lys Gly Glu Asp Leu Glu Ala Ile Lys Ala Ala Val Glu Lys Leu  
550 555 560 565  
  
aac acc gag tcc cag gaa atg ggt aag gct atc tac gag gct gac gct 1843  
Asn Thr Glu Ser Gln Glu Met Gly Lys Ala Ile Tyr Glu Ala Asp Ala  
570 575 580  
  
gct gct ggt gca acc cag gct gac gca ggt gca gaa ggc gct gca gat 1891  
Ala Ala Gly Ala Thr Gln Ala Asp Ala Gly Ala Glu Gly Ala Ala Asp  
585 590 595  
  
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&lt;210&gt; 600

&lt;211&gt; 618

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 600

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Ser Val Leu Glu Gly Gly Glu Pro Val Val Ile Ala Asn Ala Glu Gly  
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Ser Arg Thr Thr Pro Ser Val Val Ala Phe Ala Lys Asn Gly Glu Val  
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Leu Val Gly Gln Ser Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg  
50 55 60  
  
Thr Ile Arg Ser Val Lys Arg His Ile Gly Thr Asp Trp Ser Val Ala  
65 70 75 80  
  
Ile Asp Asp Lys Asn Tyr Thr Ser Gln Glu Ile Ser Ala Arg Thr Leu  
85 90 95  
  
Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu Asp Val Thr  
100 105 110

Asp Ala Val Ile Thr Val Pro Ala Tyr Phe Glu Asp Ser Gln Arg Gln  
 115 120 125  
 Ala Thr Lys Glu Ala Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile  
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 Val Asn Glu Pro Thr Ala Ala Ala Leu Ala Tyr Gly Leu Glu Lys Gly  
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 Glu Gln Glu Gln Thr Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe  
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 Thr Ser Gly Asp Asn Glu Leu Gly Gly Asp Asp Trp Asp Gln Arg Ile  
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 Val Asp Trp Leu Val Glu Lys Phe Gln Ser Ser Asn Gly Ile Asp Leu  
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 Thr Lys Asp Lys Met Ala Leu Gln Arg Leu Arg Glu Ala Ala Glu Lys  
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 Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Ala Asn Ile Asn Leu Pro  
 245 250 255  
 Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Thr  
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 Thr Lys Thr Pro Phe Asn Gln Val Val Lys Asp Ala Gly Val Ser Val  
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 Ser Glu Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro  
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 Ala Gly Val Leu Arg Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val  
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 Thr Pro Leu Ser Leu Gly Ile Glu Thr Lys Gly Gly Val Met Thr Lys  
 370 375 380  
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 405 410 415  
 Gly Glu Arg Glu Ile Ala Thr Ala Asn Lys Leu Leu Gly Ser Phe Glu  
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 Leu Gly Gly Ile Ala Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val

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Lys	Gly	Thr	Gly	Lys	Glu	Asn	Thr	Ile	Thr	Ile	Gln	Asp	Gly	Ser	Gly
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Leu	Ser	Gln	Asp	Glu	Ile	Asp	Arg	Met	Ile	Lys	Asp	Ala	Glu	Ala	His
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Ala	Asp	Glu	Asp	Lys	Lys	Arg	Arg	Glu	Glu	Gln	Glu	Val	Arg	Asn	Asn
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Ala	Glu	Ser	Leu	Val	Tyr	Gln	Thr	Arg	Lys	Phe	Val	Glu	Glu	Asn	Ser
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Ala	Val	Glu	Lys	Leu	Asn	Thr	Glu	Ser	Gln	Glu	Met	Gly	Lys	Ala	Ile
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Tyr	Glu	Ala	Asp	Ala	Ala	Ala	Gly	Ala	Thr	Gln	Ala	Asp	Ala	Gly	Ala
			580					585					590		
Glu	Gly	Ala	Ala	Asp	Asp	Asn	Val	Val	Asp	Ala	Glu	Val	Val	Glu	Asp
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&lt;210&gt; 601

&lt;211&gt; 1575

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1552)

&lt;223&gt; RXN01345

&lt;400&gt; 601

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gac	ttg	gga	act	acc	cgc	aca	atc	gcg	gcc	gcc	gtg	gac	cgc	gga	aac	163
Asp	Leu	Gly	Thr	Thr	Arg	Thr	Ile	Ala	Ala	Ala	Val	Asp	Arg	Gly	Asn	
			10					15						20		

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Tyr	Pro	Ile	Val	Thr	Val	Glu	Asp	Ser	Leu	Gly	Asp	Thr	His	Asp	Phe	
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Ile Pro Ser Val Val Ala Leu Lys Ala Asp Arg Ile Val Ala Gly Trp	
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Asp Ala Ile Glu Val Gly Gln Asp His Pro Ser Phe Val Arg Ser Phe	
55 60 65	
aaa cgc cta ctc tct gaa ccc aat gtc acg gaa gcc acc ccg gtc tac	355
Lys Arg Leu Leu Ser Glu Pro Asn Val Thr Glu Ala Thr Pro Val Tyr	
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Leu Gly Asp His Val His Pro Leu Gly Ala Val Leu Glu Ala Phe Ala	
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Glu Asn Val Val Thr Ala Leu Arg Ala Phe Gln Thr Gln Leu Gly Asp	
105 110 115	
acc tcc ccg atc gaa gta gtc att ggt gtg ccc gcc aac tcc cac agc	499
Thr Ser Pro Ile Glu Val Val Ile Gly Val Pro Ala Asn Ser His Ser	
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Ala Gln Arg Leu Leu Thr Met Ser Ala Phe Ser Ala Thr Gly Ile Thr	
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Val Val Gly Leu Val Asn Glu Pro Ser Ala Ala Ala Phe Glu Tyr Thr	
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His Arg His Ala Arg Thr Leu Asn Ser Lys Arg Gln Ala Ile Val Val	
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Tyr Asp Leu Gly Gly Gly Thr Phe Asp Ser Ser Leu Ile Arg Ile Asp	
185 190 195	
ggc acc cac cac gag gtt gtg tcc tcc att ggc att tca cgc ctt ggt	739
Gly Thr His His Glu Val Val Ser Ser Ile Gly Ile Ser Arg Leu Gly	
200 205 210	
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Gly Asp Asp Phe Asp Glu Ile Leu Leu Gln Cys Ala Leu Lys Ala Ala	
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Gly Arg Gln His Asp Ala Phe Gly Lys Arg Ala Lys Asn Thr Leu Leu	
230 235 240 245	
gac gaa tcc cgc aac gcg aag gaa gct ctt gtt ccg caa tcc cgt cgc	883
Asp Glu Ser Arg Asn Ala Lys Glu Ala Leu Val Pro Gln Ser Arg Arg	
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Leu Val Leu Glu Ile Gly Asp Asp Asp Ile Thr Val Pro Val Asn Lys	
265 270 275	
ttc tac gag gct gcc act ccc ctg gtg gaa aaa tcc ttg tcc atc atg	979

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Ile	Tyr	Leu	Val	Gly	Gly	Gly	Ser	Ser	Leu	Pro	Leu	Val	Ser	Arg	Leu	
310				315					320					325		
ctc	cgc	gag	cgt	ttc	ggc	cgc	cgt	gtc	cac	cgc	tcc	cca	ttc	ccc	tca	1123
Leu	Arg	Glu	Arg	Phe	Gly	Arg	Arg	Val	His	Arg	Ser	Pro	Phe	Pro	Ser	
				330					335					340		
ggg	tcc	act	gcg	gtg	ggg	ctg	gcc	atc	gcg	gct	gac	cct	tcc	tct	ggg	1171
Gly	Ser	Thr	Ala	Val	Gly	Leu	Ala	Ile	Ala	Ala	Asp	Pro	Ser	Ser	Gly	
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ttc	cac	cta	agg	gac	cgc	gtt	gcg	cga	ggc	atc	ggg	gtg	ttc	cgt	gag	1219
Phe	His	Leu	Arg	Asp	Arg	Val	Ala	Arg	Gly	Ile	Gly	Val	Phe	Arg	Glu	
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cac	gat	tct	ggg	cgt	gcc	gtg	agc	ttt	gac	ccg	ctg	atc	gcc	ccg	gac	1267
His	Asp	Ser	Gly	Arg	Ala	Val	Ser	Phe	Asp	Pro	Leu	Ile	Ala	Pro	Asp	
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Thr	Asp	Ser	Ala	Thr	Val	Ala	Lys	Arg	Cys	Tyr	Lys	Ala	Val	His	Asn	
390					395				400					405		
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Ile	Gly	Trp	Phe	Arg	Phe	Val	Glu	Tyr	Ser	Thr	Val	Ser	Glu	Asp	Gly	
			410					415					420			
agc	ccc	gga	gat	att	tcc	ctg	ctc	agt	gaa	atc	aag	att	cct	ttt	gat	1411
Ser	Pro	Gly	Asp	Ile	Ser	Leu	Leu	Ser	Glu	Ile	Lys	Ile	Pro	Phe	Asp	
			425					430					435			
agc	tcc	atc	acc	gat	gtg	gat	gct	acc	gag	att	tca	cgt	ttc	gat	ggc	1459
Ser	Ser	Ile	Thr	Asp	Val	Asp	Ala	Thr	Glu	Ile	Ser	Arg	Phe	Asp	Gly	
		440				445						450				
cca	gaa	gta	gaa	gaa	acc	atc	aca	gtc	aat	gac	aac	ggc	gtg	gct	tcc	1507
Pro	Glu	Val	Glu	Glu	Thr	Ile	Thr	Val	Asn	Asp	Asn	Gly	Val	Ala	Ser	
	455					460					465					
att	tcc	atc	aag	ata	ctc	ggc	ggc	gtt	acc	gtc	gag	cac	aca	att		1552
Ile	Ser	Ile	Lys	Ile	Leu	Gly	Gly	Val	Thr	Val	Glu	His	Thr	Ile		
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&lt;210&gt; 602

&lt;211&gt; 484

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 602

Met Arg Phe Gly Leu Asp Leu Gly Thr Thr Arg Thr Ile Ala Ala Ala

1	5	10	15
Val Asp Arg Gly Asn Tyr Pro Ile Val Thr Val Glu Asp Ser Leu Gly	20	25	30
Asp Thr His Asp Phe Ile Pro Ser Val Val Ala Leu Lys Ala Asp Arg	35	40	45
Ile Val Ala Gly Trp Asp Ala Ile Glu Val Gly Gln Asp His Pro Ser	50	55	60
Phe Val Arg Ser Phe Lys Arg Leu Leu Ser Glu Pro Asn Val Thr Glu	65	70	75
Ala Thr Pro Val Tyr Leu Gly Asp His Val His Pro Leu Gly Ala Val	85	90	95
Leu Glu Ala Phe Ala Glu Asn Val Val Thr Ala Leu Arg Ala Phe Gln	100	105	110
Thr Gln Leu Gly Asp Thr Ser Pro Ile Glu Val Val Ile Gly Val Pro	115	120	125
Ala Asn Ser His Ser Ala Gln Arg Leu Leu Thr Met Ser Ala Phe Ser	130	135	140
Ala Thr Gly Ile Thr Val Val Gly Leu Val Asn Glu Pro Ser Ala Ala	145	150	155
Ala Phe Glu Tyr Thr His Arg His Ala Arg Thr Leu Asn Ser Lys Arg	165	170	175
Gln Ala Ile Val Val Tyr Asp Leu Gly Gly Gly Thr Phe Asp Ser Ser	180	185	190
Leu Ile Arg Ile Asp Gly Thr His His Glu Val Val Ser Ser Ile Gly	195	200	205
Ile Ser Arg Leu Gly Gly Asp Asp Phe Asp Glu Ile Leu Leu Gln Cys	210	215	220
Ala Leu Lys Ala Ala Gly Arg Gln His Asp Ala Phe Gly Lys Arg Ala	225	230	235
Lys Asn Thr Leu Leu Asp Glu Ser Arg Asn Ala Lys Glu Ala Leu Val	245	250	255
Pro Gln Ser Arg Arg Leu Val Leu Glu Ile Gly Asp Asp Asp Ile Thr	260	265	270
Val Pro Val Asn Lys Phe Tyr Glu Ala Ala Thr Pro Leu Val Glu Lys	275	280	285
Ser Leu Ser Ile Met Glu Pro Leu Ile Gly Val Asp Asp Leu Lys Asp	290	295	300
Ser Asp Ile Ala Gly Ile Tyr Leu Val Gly Gly Gly Ser Ser Leu Pro	305	310	315
Leu Val Ser Arg Leu Leu Arg Glu Arg Phe Gly Arg Arg Val His Arg	325	330	335

Ser Pro Phe Pro Ser Gly Ser Thr Ala Val Gly Leu Ala Ile Ala Ala  
 340 345 350  
 Asp Pro Ser Ser Gly Phe His Leu Arg Asp Arg Val Ala Arg Gly Ile  
 355 360 365  
 Gly Val Phe Arg Glu His Asp Ser Gly Arg Ala Val Ser Phe Asp Pro  
 370 375 380  
 Leu Ile Ala Pro Asp Thr Asp Ser Ala Thr Val Ala Lys Arg Cys Tyr  
 385 390 395 400  
 Lys Ala Val His Asn Ile Gly Trp Phe Arg Phe Val Glu Tyr Ser Thr  
 405 410 415  
 Val Ser Glu Asp Gly Ser Pro Gly Asp Ile Ser Leu Leu Ser Glu Ile  
 420 425 430  
 Lys Ile Pro Phe Asp Ser Ser Ile Thr Asp Val Asp Ala Thr Glu Ile  
 435 440 445  
 Ser Arg Phe Asp Gly Pro Glu Val Glu Glu Thr Ile Thr Val Asn Asp  
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 Glu His Thr Ile

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 <212> DNA  
 <213> Corynebacterium glutamicum

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 <223> RXN02736

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 Met Ile Phe Glu Leu  
 1 5  
 ccg gat acc acc acc cag caa att tcc aag acc cta act cga ctg cgt 163  
 Pro Asp Thr Thr Thr Gln Gln Ile Ser Lys Thr Leu Thr Arg Leu Arg  
 10 15 20  
 gaa tcg ggc acc cag gtc acc acc ggc cga gtg ctc acc ctc atc gtg 211  
 Glu Ser Gly Thr Gln Val Thr Thr Gly Arg Val Leu Thr Leu Ile Val  
 25 30 35  
 gtc act gac tcc gaa agc gat gtc gct gca gtt acc gag tcc acc aat 259  
 Val Thr Asp Ser Glu Ser Asp Val Ala Ala Val Thr Glu Ser Thr Asn  
 40 45 50

gaa gcc tcg cgc gag cac cca tct cgc gtg atc att ttg gtg gtt ggc	307
Glu Ala Ser Arg Glu His Pro Ser Arg Val Ile Ile Leu Val Val Gly	
55 60 65	
gat aaa act gca gaa aac aaa gtt gac gca gaa gtc cgt atc ggt ggc	355
Asp Lys Thr Ala Glu Asn Lys Val Asp Ala Glu Val Arg Ile Gly Gly	
70 75 80 85	
gac gct ggt gct tcc gag atg atc atc atg cat ctc aac gga cct gtc	403
Asp Ala Gly Ala Ser Glu Met Ile Ile Met His Leu Asn Gly Pro Val	
90 95 100	
gct gac aag ctc cag tat gtc gtc aca cca ctg ttg ctt cct gac acc	451
Ala Asp Lys Leu Gln Tyr Val Val Thr Pro Leu Leu Leu Pro Asp Thr	
105 110 115	
ccc atc gtt gct tgg tgg cca ggt gaa tca cca aag aat cct tcc cag	499
Pro Ile Val Ala Trp Trp Pro Gly Glu Ser Pro Lys Asn Pro Ser Gln	
120 125 130	
gac cca att gga cgc atc gca caa cga cgc atc act gat gct ttg tac	547
Asp Pro Ile Gly Arg Ile Ala Gln Arg Arg Ile Thr Asp Ala Leu Tyr	
135 140 145	
gac cgt gat gac gca cta gaa gat cgt gtt gag aac tat cac cca ggt	595
Asp Arg Asp Asp Ala Leu Glu Asp Arg Val Glu Asn Tyr His Pro Gly	
150 155 160 165	
gat acc gac atg acg tgg gcg cgc ctt acc cag tgg cgg gga ctt gtt	643
Asp Thr Asp Met Thr Trp Ala Arg Leu Thr Gln Trp Arg Gly Leu Val	
170 175 180	
gcc tcc tca ttg gat cac cca cca cac agc gaa atc act tcc gtg agg	691
Ala Ser Ser Leu Asp His Pro Pro His Ser Glu Ile Thr Ser Val Arg	
185 190 195	
ctg acc ggt gca agc ggc agt acc tcg gtg gat ttg gct gca ggc tgg	739
Leu Thr Gly Ala Ser Gly Ser Thr Ser Val Asp Leu Ala Ala Gly Trp	
200 205 210	
ttg gcg cgg agg ctg aaa gtg cct gtg atc cgc gag gtg aca gat gct	787
Leu Ala Arg Arg Leu Lys Val Pro Val Ile Arg Glu Val Thr Asp Ala	
215 220 225	
ccc acc gtg cca acc gat gag ttt ggt act cca ctg ctg gct atc cag	835
Pro Thr Val Pro Thr Asp Glu Phe Gly Thr Pro Leu Leu Ala Ile Gln	
230 235 240 245	
cgc ctg gag atc gtt cgc acc acc ggc tcg atc atc atc acc atc tat	883
Arg Leu Glu Ile Val Arg Thr Thr Gly Ser Ile Ile Ile Thr Ile Tyr	
250 255 260	
gac gct cat acc ctt cag gta gag atg ccg gaa tcc ggc aat gcc cca	931
Asp Ala His Thr Leu Gln Val Glu Met Pro Glu Ser Gly Asn Ala Pro	
265 270 275	
tcg ctg gtg gct att ggt cgt cga agt gag tcc gac tgc ttg tct gag	979
Ser Leu Val Ala Ile Gly Arg Arg Ser Glu Ser Asp Cys Leu Ser Glu	
280 285 290	
gag ctt cgc cac atg gat cca gat ttg ggc tac cag cac gca cta tcc	1027

Glu Leu Arg His Met Asp Pro Asp Leu Gly Tyr Gln His Ala Leu Ser  
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 Gly Leu Ser Ser Val Lys Leu Glu Thr Val  
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<210> 604

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 604

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Leu Thr Leu Ile Val Val Thr Asp Ser Glu Ser Asp Val Ala Ala Val  
 35 40 45

Thr Glu Ser Thr Asn Glu Ala Ser Arg Glu His Pro Ser Arg Val Ile  
 50 55 60

Ile Leu Val Val Gly Asp Lys Thr Ala Glu Asn Lys Val Asp Ala Glu  
 65 70 75 80

Val Arg Ile Gly Gly Asp Ala Gly Ala Ser Glu Met Ile Ile Met His  
 85 90 95

Leu Asn Gly Pro Val Ala Asp Lys Leu Gln Tyr Val Val Thr Pro Leu  
 100 105 110

Leu Leu Pro Asp Thr Pro Ile Val Ala Trp Trp Pro Gly Glu Ser Pro  
 115 120 125

Lys Asn Pro Ser Gln Asp Pro Ile Gly Arg Ile Ala Gln Arg Arg Ile  
 130 135 140

Thr Asp Ala Leu Tyr Asp Arg Asp Asp Ala Leu Glu Asp Arg Val Glu  
 145 150 155 160

Asn Tyr His Pro Gly Asp Thr Asp Met Thr Trp Ala Arg Leu Thr Gln  
 165 170 175

Trp Arg Gly Leu Val Ala Ser Ser Leu Asp His Pro Pro His Ser Glu  
 180 185 190

Ile Thr Ser Val Arg Leu Thr Gly Ala Ser Gly Ser Thr Ser Val Asp  
 195 200 205

Leu Ala Ala Gly Trp Leu Ala Arg Arg Leu Lys Val Pro Val Ile Arg  
 210 215 220

Glu Val Thr Asp Ala Pro Thr Val Pro Thr Asp Glu Phe Gly Thr Pro  
 225 230 235 240

Leu Leu Ala Ile Gln Arg Leu Glu Ile Val Arg Thr Thr Gly Ser Ile  
 245 250 255

Ile Ile Thr Ile Tyr Asp Ala His Thr Leu Gln Val Glu Met Pro Glu  
 260 265 270  
 Ser Gly Asn Ala Pro Ser Leu Val Ala Ile Gly Arg Arg Ser Glu Ser  
 275 280 285  
 Asp Cys Leu Ser Glu Glu Leu Arg His Met Asp Pro Asp Leu Gly Tyr  
 290 295 300  
 Gln His Ala Leu Ser Gly Leu Ser Ser Val Lys Leu Glu Thr Val  
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 <213> Corynebacterium glutamicum

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 <223> RXN02280

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 Met Gln Glu Ser Ser  
 1 5  
 cgt gat aat ttc caa gtt gac ctc ggc ggc gtt gtt gat ctt ttg agt 163  
 Arg Asp Asn Phe Gln Val Asp Leu Gly Gly Val Val Asp Leu Leu Ser  
 10 15 20  
 cgc cac att tat tcc ggt ccg agg gtg tat gtg cgt gag ttg ctg cag 211  
 Arg His Ile Tyr Ser Gly Pro Arg Val Tyr Val Arg Glu Leu Leu Gln  
 25 30 35  
 aat gcg gtt gat gct tgt act gca cgt tct gaa cag ggt gag gag ggc 259  
 Asn Ala Val Asp Ala Cys Thr Ala Arg Ser Glu Gln Gly Glu Glu Gly  
 40 45 50  
 tac gag ccg agt att cgt att ccg ccg gtg acc aag gat cgt gcc acg 307  
 Tyr Glu Pro Ser Ile Arg Ile Arg Pro Val Thr Lys Asp Arg Ala Thr  
 55 60 65  
 ttt tca ctg gtt gat aat ggt acg ggc ctg acc gcg cag gag gcg cgg 355  
 Phe Ser Leu Val Asp Asn Gly Thr Gly Leu Thr Ala Gln Glu Ala Arg  
 70 75 80 85  
 gaa ttg ctg gcg acg gtg ggg ccg acg tcg aaa cgc gat gaa ttc ggt 403  
 Glu Leu Leu Ala Thr Val Gly Arg Thr Ser Lys Arg Asp Glu Phe Gly  
 90 95 100  
 ctg cag ccg gaa ggt cgc ctg ggg caa ttt ggc atc ggg ctg ctt agt 451  
 Leu Gln Arg Glu Gly Arg Leu Gly Gln Phe Gly Ile Gly Leu Leu Ser  
 105 110 115  
 tgt ttc atg gtg gcg gat gag atc acc atg gtg tcg cat gcg gag ggt 499  
 Cys Phe Met Val Ala Asp Glu Ile Thr Met Val Ser His Ala Glu Gly

120	125	130	
gcg tcg gcg att cgg tgg act ggt cat gcg gat ggc acc ttt aac ctg Ala Ser Ala Ile Arg Trp Thr Gly His Ala Asp Gly Thr Phe Asn Leu 135 140 145			547
gag att ctt ggg gat gac gca acg gat gtc att ccg gtg ggc acg act Glu Ile Leu Gly Asp Asp Ala Thr Asp Val Ile Pro Val Gly Thr Thr 150 155 160 165			595
gtg cac ctg act ccg cgc cct gat gag cgc acg ttg ctg acg gaa aat Val His Leu Thr Pro Arg Pro Asp Glu Arg Thr Leu Leu Thr Glu Asn 170 175 180			643
tcc gtg gtc acc att gct agt aat tat ggc cgc tac ctg ccg att cct Ser Val Val Thr Ile Ala Ser Asn Tyr Gly Arg Tyr Leu Pro Ile Pro 185 190 195			691
att gtg gtg cag ggt gag aaa aac acc acc atc act aca tcg ccg gtg Ile Val Val Gln Gly Glu Lys Asn Thr Thr Ile Thr Thr Ser Pro Val 200 205 210			739
ttt gca aag gat act gat cag cag cac agg ctg tat gcc ggc cgg gag Phe Ala Lys Asp Thr Asp Gln Gln His Arg Leu Tyr Ala Gly Arg Glu 215 220 225			787
cgc ctt ggt aaa act cct ttt gat gtc atc gat ctc acc ggt cct ggc Arg Leu Gly Lys Thr Pro Phe Asp Val Ile Asp Leu Thr Gly Pro Gly 230 235 240 245			835
atc gag ggt gtg gct tat gta ttg ccg gag gcc cag gct ccg cat atg Ile Glu Gly Val Ala Tyr Val Leu Pro Glu Ala Gln Ala Pro His Met 250 255 260			883
tcc agg cgt cac agt att tat gtc aac cgc atg ttg gtc tct gat ggg Ser Arg Arg His Ser Ile Tyr Val Asn Arg Met Leu Val Ser Asp Gly 265 270 275			931
cct tcc acg gtg ctg ccc aac tgg gcg ttc ttt gtg gaa tgt gaa atc Pro Ser Thr Val Leu Pro Asn Trp Ala Phe Phe Val Glu Cys Glu Ile 280 285 290			979
aat tca acc gat ttg gaa ccc acc gca tcg cgt gaa gcg ctc atg gat Asn Ser Thr Asp Leu Glu Pro Thr Ala Ser Arg Glu Ala Leu Met Asp 295 300 305			1027
gac acc gcg ttc gcg gca acc agg gaa cat atc ggt gag tgc att aaa Asp Thr Ala Phe Ala Ala Thr Arg Glu His Ile Gly Glu Cys Ile Lys 310 315 320 325			1075
tcg tgg ctg att aat ctc gcc atg acc aag cct cac cgc gtg cgg gaa Ser Trp Leu Ile Asn Leu Ala Met Thr Lys Pro His Arg Val Arg Glu 330 335 340			1123
ttt act gcg att cat gat ctt gcc ctg cgc gag ctg tgc caa tcg gac Phe Thr Ala Ile His Asp Leu Ala Leu Arg Glu Leu Cys Gln Ser Asp 345 350 355			1171
gcg gac ctg gct gaa acc atg ttg ggt ctt ctc acc ttg gag acc tcc Ala Asp Leu Ala Glu Thr Met Leu Gly Leu Leu Thr Leu Glu Thr Ser 360 365 370			1219

cgt ggt cgc atc tcg atc ggt gag atc acc acg ttg tcc atc acc gag	1267
Arg Gly Arg Ile Ser Ile Gly Glu Ile Thr Thr Leu Ser Ile Thr Glu	
375 380 385	
gat gtg tcg ctg cag ctg gct acc acg ttg gat gat ttc agg cag ctc	1315
Asp Val Ser Leu Gln Leu Ala Thr Thr Leu Asp Asp Phe Arg Gln Leu	
390 395 400 405	
aac acc att gcg cgc ccg gac acc ttg att att aat ggc ggc tac att	1363
Asn Thr Ile Ala Arg Pro Asp Thr Leu Ile Ile Asn Gly Gly Tyr Ile	
410 415 420	
cac gac agc gat ctg gct cgg ctc att ccc gtt cac tac cca ccg ctt	1411
His Asp Ser Asp Leu Ala Arg Leu Ile Pro Val His Tyr Pro Pro Leu	
425 430 435	
acg gta tct act gct gac ctg cgc gaa tcc atg gat ctg atg gag ctt	1459
Thr Val Ser Thr Ala Asp Leu Arg Glu Ser Met Asp Leu Met Glu Leu	
440 445 450	
ccg ccg ctg cag gac att gag aaa gcc aag gca ctg gat gcg cag gtc	1507
Pro Pro Leu Gln Asp Ile Glu Lys Ala Lys Ala Leu Asp Ala Gln Val	
455 460 465	
acg gaa tca ttg aag gat ttt cag atc aag ggc gca acg agg gtt ttt	1555
Thr Glu Ser Leu Lys Asp Phe Gln Ile Lys Gly Ala Thr Arg Val Phe	
470 475 480 485	
gaa ccc gca gat gtt cct gcc gtg gtg atc att gat tcc aag gcg cag	1603
Glu Pro Ala Asp Val Pro Ala Val Val Ile Ile Asp Ser Lys Ala Gln	
490 495 500	
gcc tca ccg gat cgc aat gaa aca caa agc gca acc act gat cgt tgg	1651
Ala Ser Arg Asp Arg Asn Glu Thr Gln Ser Ala Thr Thr Asp Arg Trp	
505 510 515	
gct gac att ttg gca acg gtg gat aac acg ttg agc cgt caa aca gcc	1699
Ala Asp Ile Leu Ala Thr Val Asp Asn Thr Leu Ser Arg Gln Thr Ala	
520 525 530	
aac att cca cag gat cag gga ctg tcg gcg ttg tgc ttg aat tgg aac	1747
Asn Ile Pro Gln Asp Gln Gly Leu Ser Ala Leu Cys Leu Asn Trp Asn	
535 540 545	
aat tcg ctg gtc agg aaa ttg gcg tcc act gat gac acc gcc gtg gtg	1795
Asn Ser Leu Val Arg Lys Leu Ala Ser Thr Asp Asp Thr Ala Val Val	
550 555 560 565	
tcg cgc acg gtg cgt ttg ctc tac gtt cag gca ttg ttg tcc agc aag	1843
Ser Arg Thr Val Arg Leu Leu Tyr Val Gln Ala Leu Leu Ser Ser Lys	
570 575 580	
agg cca ctg ccg gtg aag gaa cgc gcg ctg ctt aat gat tcg ctg gca	1891
Arg Pro Leu Arg Val Lys Glu Arg Ala Leu Leu Asn Asp Ser Leu Ala	
585 590 595	
gat ctg gtt tct ttg tct ttg tca tcc gat atc taagacaatc ctccgcta	1944
Asp Leu Val Ser Leu Ser Leu Ser Ser Asp Ile	
600 605	

ctt

1947

&lt;210&gt; 606

&lt;211&gt; 608

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 606

Met Gln Glu Ser Ser Arg Asp Asn Phe Gln Val Asp Leu Gly Gly Val  
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Val Asp Leu Leu Ser Arg His Ile Tyr Ser Gly Pro Arg Val Tyr Val  
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Arg Glu Leu Leu Gln Asn Ala Val Asp Ala Cys Thr Ala Arg Ser Glu  
 35 40 45

Gln Gly Glu Glu Gly Tyr Glu Pro Ser Ile Arg Ile Arg Pro Val Thr  
 50 55 60

Lys Asp Arg Ala Thr Phe Ser Leu Val Asp Asn Gly Thr Gly Leu Thr  
 65 70 75 80

Ala Gln Glu Ala Arg Glu Leu Leu Ala Thr Val Gly Arg Thr Ser Lys  
 85 90 95

Arg Asp Glu Phe Gly Leu Gln Arg Glu Gly Arg Leu Gly Gln Phe Gly  
 100 105 110

Ile Gly Leu Leu Ser Cys Phe Met Val Ala Asp Glu Ile Thr Met Val  
 115 120 125

Ser His Ala Glu Gly Ala Ser Ala Ile Arg Trp Thr Gly His Ala Asp  
 130 135 140

Gly Thr Phe Asn Leu Glu Ile Leu Gly Asp Asp Ala Thr Asp Val Ile  
 145 150 155 160

Pro Val Gly Thr Thr Val His Leu Thr Pro Arg Pro Asp Glu Arg Thr  
 165 170 175

Leu Leu Thr Glu Asn Ser Val Val Thr Ile Ala Ser Asn Tyr Gly Arg  
 180 185 190

Tyr Leu Pro Ile Pro Ile Val Val Gln Gly Glu Lys Asn Thr Thr Ile  
 195 200 205

Thr Thr Ser Pro Val Phe Ala Lys Asp Thr Asp Gln Gln His Arg Leu  
 210 215 220

Tyr Ala Gly Arg Glu Arg Leu Gly Lys Thr Pro Phe Asp Val Ile Asp  
 225 230 235 240

Leu Thr Gly Pro Gly Ile Glu Gly Val Ala Tyr Val Leu Pro Glu Ala  
 245 250 255

Gln Ala Pro His Met Ser Arg Arg His Ser Ile Tyr Val Asn Arg Met  
 260 265 270

Leu Val Ser Asp Gly Pro Ser Thr Val Leu Pro Asn Trp Ala Phe Phe

275					280					285					
Val	Glu	Cys	Glu	Ile	Asn	Ser	Thr	Asp	Leu	Glu	Pro	Thr	Ala	Ser	Arg
290						295					300				
Glu	Ala	Leu	Met	Asp	Asp	Thr	Ala	Phe	Ala	Ala	Thr	Arg	Glu	His	Ile
305					310					315					320
Gly	Glu	Cys	Ile	Lys	Ser	Trp	Leu	Ile	Asn	Leu	Ala	Met	Thr	Lys	Pro
				325					330					335	
His	Arg	Val	Arg	Glu	Phe	Thr	Ala	Ile	His	Asp	Leu	Ala	Leu	Arg	Glu
			340					345					350		
Leu	Cys	Gln	Ser	Asp	Ala	Asp	Leu	Ala	Glu	Thr	Met	Leu	Gly	Leu	Leu
		355					360					365			
Thr	Leu	Glu	Thr	Ser	Arg	Gly	Arg	Ile	Ser	Ile	Gly	Glu	Ile	Thr	Thr
		370				375					380				
Leu	Ser	Ile	Thr	Glu	Asp	Val	Ser	Leu	Gln	Leu	Ala	Thr	Thr	Leu	Asp
385					390					395					400
Asp	Phe	Arg	Gln	Leu	Asn	Thr	Ile	Ala	Arg	Pro	Asp	Thr	Leu	Ile	Ile
				405					410					415	
Asn	Gly	Gly	Tyr	Ile	His	Asp	Ser	Asp	Leu	Ala	Arg	Leu	Ile	Pro	Val
			420					425					430		
His	Tyr	Pro	Pro	Leu	Thr	Val	Ser	Thr	Ala	Asp	Leu	Arg	Glu	Ser	Met
		435					440					445			
Asp	Leu	Met	Glu	Leu	Pro	Pro	Leu	Gln	Asp	Ile	Glu	Lys	Ala	Lys	Ala
		450				455					460				
Leu	Asp	Ala	Gln	Val	Thr	Glu	Ser	Leu	Lys	Asp	Phe	Gln	Ile	Lys	Gly
465					470					475					480
Ala	Thr	Arg	Val	Phe	Glu	Pro	Ala	Asp	Val	Pro	Ala	Val	Val	Ile	Ile
				485					490					495	
Asp	Ser	Lys	Ala	Gln	Ala	Ser	Arg	Asp	Arg	Asn	Glu	Thr	Gln	Ser	Ala
			500					505					510		
Thr	Thr	Asp	Arg	Trp	Ala	Asp	Ile	Leu	Ala	Thr	Val	Asp	Asn	Thr	Leu
		515					520					525			
Ser	Arg	Gln	Thr	Ala	Asn	Ile	Pro	Gln	Asp	Gln	Gly	Leu	Ser	Ala	Leu
		530				535					540				
Cys	Leu	Asn	Trp	Asn	Asn	Ser	Leu	Val	Arg	Lys	Leu	Ala	Ser	Thr	Asp
545					550					555					560
Asp	Thr	Ala	Val	Val	Ser	Arg	Thr	Val	Arg	Leu	Leu	Tyr	Val	Gln	Ala
				565					570					575	
Leu	Leu	Ser	Ser	Lys	Arg	Pro	Leu	Arg	Val	Lys	Glu	Arg	Ala	Leu	Leu
			580					585					590		
Asn	Asp	Ser	Leu	Ala	Asp	Leu	Val	Ser	Leu	Ser	Leu	Ser	Ser	Asp	Ile
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<223> RXS00170
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Met Leu Leu Ala Ile 5															
ggg gtt gca tct ccg gta gct caa gca caa gtg gaa gat caa ttt gag 163															
Gly Val Ala Ser Pro Val Ala Gln Ala Gln Val Glu Asp Gln Phe Glu 20															
ctt gta aaa gaa atc agt gat gag cag ttt gct gat gat ggt gtt gac 211															
Leu Val Lys Glu Ile Ser Asp Glu Gln Phe Ala Asp Asp Gly Val Asp 35															
tat gtt ccc aat agg aat gct ccg act gtt aag gaa caa ctt gag gat 259															
Tyr Val Pro Asn Arg Asn Ala Pro Thr Val Lys Glu Gln Leu Glu Asp 50															
ttc gaa tca gca cat cca gaa gta gtc att gag tat cac gag cac gtc 307															
Phe Glu Ser Ala His Pro Glu Val Val Ile Glu Tyr His Glu His Val 65															
aac gat agt aaa gac aat gtt gag gaa ctt ccg cta cct aag cgg gac 355															
Asn Asp Ser Lys Asp Asn Val Glu Glu Leu Pro Leu Pro Lys Arg Asp 85															
atc gtt gca ggg gaa atg cgc tca gat gtc atc gag tta ccg gag ggg 403															
Ile Val Ala Gly Glu Met Arg Ser Asp Val Ile Glu Leu Pro Glu Gly 100															
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Val Ser Lys Asp Glu Ala Asp Gln Val Glu Val Ala Glu Ala Arg Leu 115															
aat gag ggc gca cga ttg atg gct gca act ggg tgt gag gct atg tgg 499															
Asn Glu Gly Ala Arg Leu Met Ala Ala Thr Gly Cys Glu Ala Met Trp 130															
cca aca ggt ttc tca gtt tgt ggc cgg att ctt gac gct tat cgg cag 547															
Pro Thr Gly Phe Ser Val Cys Gly Arg Ile Leu Asp Ala Tyr Arg Gln 145															
gtt gga ggt cag ttg tca tgg ctt ggg cca cca aag tca aac gag ttg 595															
Val Gly Gly Gln Leu Ser Trp Leu Gly Pro Pro Lys Ser Asn Glu Leu 165															
acc aat ccc gac ggt gtt ggc aaa aga agt gaa ttt gtt ggg ggt gcc 643															
Thr Asn Pro Asp Gly Val Gly Lys Arg Ser Glu Phe Val Gly Gly Ala															

170										175					180					
atc	tat	tgg	cat	cca	gac	aca	ggc	gct	tat	gca	gtg	acc	ctg	gac	ggc	691				
Ile	Tyr	Trp	His	Pro	Asp	Thr	Gly	Ala	Tyr	Ala	Val	Thr	Leu	Asp	Gly					
			185					190					195							
ttg	agg	cag	tgg	ggg	acc	ttg	aac	tgg	gaa	tca	ggg	cca	ttg	ggg	tac	739				
Leu	Arg	Gln	Trp	Gly	Thr	Leu	Asn	Trp	Glu	Ser	Gly	Pro	Leu	Gly	Tyr					
		200					205					210								
cca	acc	tct	ggc	ccg	atg	gat	aca	aac	tat	ccc	ctt	act	cag	cga	cag	787				
Pro	Thr	Ser	Gly	Pro	Met	Asp	Thr	Asn	Tyr	Pro	Leu	Thr	Gln	Arg	Gln					
		215				220					225									
act	ttt	caa	ggc	ggc	gac	aac	tat	tac	aac	cca	ttg	act	ggc	ggc	gct	835				
Thr	Phe	Gln	Gly	Gly	Asp	Asn	Tyr	Tyr	Asn	Pro	Leu	Thr	Gly	Gly	Ala					
230					235					240					245					
gtg	tgg	ggc	gat	att	aaa	cag	cgc	tac	gaa	gaa	ctt	ggc	ggc	tcg	aat	883				
Val	Trp	Gly	Asp	Ile	Lys	Gln	Arg	Tyr	Glu	Glu	Leu	Gly	Gly	Ser	Asn					
				250					255					260						
cat	gcc	att	ggc	atc	ccg	atc	act	aat	gag	cta	cct	agc	ggc	act	gag	931				
His	Ala	Ile	Gly	Ile	Pro	Ile	Thr	Asn	Glu	Leu	Pro	Ser	Gly	Thr	Glu					
			265					270					275							
tat	ttt	tac	aat	aat	ttc	ttc	aat	gga	aca	att	tcg	tgg	cga	aat	gat	979				
Tyr	Phe	Tyr	Asn	Asn	Phe	Phe	Asn	Gly	Thr	Ile	Ser	Trp	Arg	Asn	Asp					
		280					285					290								
cgt	cag	aca	cgg	ttt	atg	tat	ttg	gct	acg	cag	cgg	gtg	tgg	gat	gcg	1027				
Arg	Gln	Thr	Arg	Phe	Met	Tyr	Leu	Ala	Thr	Gln	Arg	Val	Trp	Asp	Ala					
	295					300					305									
ttg	ggc	cgg	gag	acg	ggc	cgt	tta	ggc	ttt	cct	gaa	gca	gat	gaa	aca	1075				
Leu	Gly	Arg	Glu	Thr	Gly	Arg	Leu	Gly	Phe	Pro	Glu	Ala	Asp	Glu	Thr					
310					315					320					325					
cct	gag	gtt	tct	ggc	cta	ttc	cat	gtg	gtg	aat	ttt	gcg	gag	cgc	ggc	1123				
Pro	Glu	Val	Ser	Gly	Leu	Phe	His	Val	Val	Asn	Phe	Ala	Glu	Arg	Gly					
				330					335					340						
gtg	att	gcg	tgg	aat	gga	atc	cta	ggc	gcc	aga	gag	ctg	tat	ggc	gat	1171				
Val	Ile	Ala	Trp	Asn	Gly	Ile	Leu	Gly	Ala	Arg	Glu	Leu	Tyr	Gly	Asp					
			345					350					355							
gtt	tac	tcc	ctg	tgg	ctg	caa	tac	caa	aat	acc	gat	act	cct	tta	ggc	1219				
Val	Tyr	Ser	Leu	Trp	Leu	Gln	Tyr	Gln	Asn	Thr	Asp	Thr	Pro	Leu	Gly					
		360					365					370								
tgg	ccg	ata	cca	tca	ttg	aca	tca	tta	aat	gag	tca	ctc	gaa	caa	gaa	1267				
Trp	Pro	Ile	Pro	Ser	Leu	Thr	Ser	Leu	Asn	Glu	Ser	Leu	Glu	Gln	Glu					
	375					380					385									
ttc	acc	aga	ggc	gtt	gtt	tta	ggc	tca	ggc	gat	gca	ctg	aca	tgg	att	1315				
Phe	Thr	Arg	Gly	Val	Val	Leu	Gly	Ser	Gly	Asp	Ala	Leu	Thr	Trp	Ile					
390					395					400					405					
cct	gac	gat	gaa	gaa	aga	agt	ttg	gag	gat	ttc	ctc	cca	att	gga	agt	1363				
Pro	Asp	Asp	Glu	Glu	Arg	Ser	Leu	Glu	Asp	Phe	Leu	Pro	Ile	Gly	Ser					
				410					415					420						

agc ggc tca tcc tca tcg agc caa gag atg acc ctg ttt tcc cag cgt 1411  
 Ser Gly Ser Ser Ser Ser Ser Ser Gln Glu Met Thr Leu Phe Ser Gln Arg  
 425 430 435

gca caa tac gtg gat tgc aag aat ctt ccc gat tta gat gag cag aga 1459  
 Ala Gln Tyr Val Asp Cys Lys Asn Leu Pro Asp Leu Asp Glu Gln Arg  
 440 445 450

aaa act gaa aac aac att gaa aag aat ggt ggc ccg atc aaa aaa gag 1507  
 Lys Thr Glu Asn Asn Ile Glu Lys Asn Gly Gly Pro Ile Lys Lys Glu  
 455 460 465

tat agt tcg cga ggt ttc ccc acc gag ttc aga ttt gtc gtg aga aaa 1555  
 Tyr Ser Ser Arg Gly Phe Pro Thr Glu Phe Arg Phe Val Val Arg Lys  
 470 475 480 485

ggg cat tat gac cgt tac agg aat gaa ggc tgg gga tat tta aaa aac 1603  
 Gly His Tyr Asp Arg Tyr Arg Asn Glu Gly Trp Gly Tyr Leu Lys Asn  
 490 495 500

tat tgc aaa cac aac ttc gcc aac cac gct atg gct gag gcc gta gta 1651  
 Tyr Cys Lys His Asn Phe Ala Asn His Ala Met Ala Glu Ala Val Val  
 505 510 515

gat aaa gcg gtg att gat tat ggc tca tcg cca gga acc agc tat tac 1699  
 Asp Lys Ala Val Ile Asp Tyr Gly Ser Ser Pro Gly Thr Ser Tyr Tyr  
 520 525 530

aag ttc gag aaa acg gtg tac ttt cta gat tgc aga act tat aca ttc 1747  
 Lys Phe Glu Lys Thr Val Tyr Phe Leu Asp Cys Arg Thr Tyr Thr Phe  
 535 540 545

aat aag aac tca gga tgt aaa gaa atg cac gct ccg caa tgg gtg act 1795  
 Asn Lys Asn Ser Gly Cys Lys Glu Met His Ala Pro Gln Trp Val Thr  
 550 555 560 565

att att tac aat cct cat act ttc act gga gca aat tcg aac aga ccc 1843  
 Ile Ile Tyr Asn Pro His Thr Phe Thr Gly Ala Asn Ser Asn Arg Pro  
 570 575 580

aag ggg gta att tca gca tgg tgt aat tca acc cca cct ggt gga atc 1891  
 Lys Gly Val Ile Ser Ala Trp Cys Asn Ser Thr Pro Pro Gly Gly Ile  
 585 590 595

gaa cac gag ccg gaa att tcc caa tgt cct gat cat gtg aat ctt tat 1939  
 Glu His Glu Pro Glu Ile Ser Gln Cys Pro Asp His Val Asn Leu Tyr  
 600 605 610

aat aag ctt cgc ata tgacagaacc ccatcaactg tgc 1977  
 Asn Lys Leu Arg Ile  
 615

&lt;210&gt; 608

&lt;211&gt; 618

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 608

Met Leu Leu Ala Ile Gly Val Ala Ser Pro Val Ala Gln Ala Gln Val

1	5	10	15
Glu Asp Gln Phe	Glu Leu Val Lys	Glu Ile Ser Asp	Glu Gln Phe Ala
20	25	30	
Asp Asp Gly Val	Asp Tyr Val Pro	Asn Arg Asn Ala	Pro Thr Val Lys
35	40	45	
Glu Gln Leu Glu	Asp Phe Glu Ser	Ala His Pro Glu	Val Val Ile Glu
50	55	60	
Tyr His Glu His	Val Asn Asp Ser	Lys Asp Asn Val	Glu Glu Leu Pro
65	70	75	80
Leu Pro Lys Arg	Asp Ile Val Ala	Gly Glu Met Arg	Ser Asp Val Ile
85	90	95	
Glu Leu Pro Glu	Gly Val Ser Lys	Asp Glu Ala Asp	Gln Val Glu Val
100	105	110	
Ala Glu Ala Arg	Leu Asn Glu Gly	Ala Arg Leu Met	Ala Ala Thr Gly
115	120	125	
Cys Glu Ala Met	Trp Pro Thr Gly	Phe Ser Val Cys	Gly Arg Ile Leu
130	135	140	
Asp Ala Tyr Arg	Gln Val Gly Gly	Gln Leu Ser Trp	Leu Gly Pro Pro
145	150	155	160
Lys Ser Asn Glu	Leu Thr Asn Pro	Asp Gly Val Gly	Lys Arg Ser Glu
165	170	175	
Phe Val Gly Gly	Ala Ile Tyr Trp	His Pro Asp Thr	Gly Ala Tyr Ala
180	185	190	
Val Thr Leu Asp	Gly Leu Arg Gln	Trp Gly Thr Leu	Asn Trp Glu Ser
195	200	205	
Gly Pro Leu Gly	Tyr Pro Thr Ser	Gly Pro Met Asp	Thr Asn Tyr Pro
210	215	220	
Leu Thr Gln Arg	Gln Thr Phe Gln	Gly Gly Asp Asn	Tyr Tyr Asn Pro
225	230	235	240
Leu Thr Gly Gly	Ala Val Trp Gly	Asp Ile Lys Gln	Arg Tyr Glu Glu
245	250	255	
Leu Gly Gly Ser	Asn His Ala Ile	Gly Ile Pro Ile	Thr Asn Glu Leu
260	265	270	
Pro Ser Gly Thr	Glu Tyr Phe Tyr	Asn Asn Phe Phe	Asn Gly Thr Ile
275	280	285	
Ser Trp Arg Asn	Asp Arg Gln Thr	Arg Phe Met Tyr	Leu Ala Thr Gln
290	295	300	
Arg Val Trp Asp	Ala Leu Gly Arg	Glu Thr Gly Arg	Leu Gly Phe Pro
305	310	315	320
Glu Ala Asp Glu	Thr Pro Glu Val	Ser Gly Leu Phe	His Val Val Asn
325	330	335	

Phe Ala Glu Arg Gly Val Ile Ala Trp Asn Gly Ile Leu Gly Ala Arg  
                   340                  345                  350  
 Glu Leu Tyr Gly Asp Val Tyr Ser Leu Trp Leu Gln Tyr Gln Asn Thr  
                   355                  360                  365  
 Asp Thr Pro Leu Gly Trp Pro Ile Pro Ser Leu Thr Ser Leu Asn Glu  
                   370                  375                  380  
 Ser Leu Glu Gln Glu Phe Thr Arg Gly Val Val Leu Gly Ser Gly Asp  
                   385                  390                  395                  400  
 Ala Leu Thr Trp Ile Pro Asp Asp Glu Glu Arg Ser Leu Glu Asp Phe  
                   405                  410                  415  
 Leu Pro Ile Gly Ser Ser Gly Ser Ser Ser Ser Ser Gln Glu Met Thr  
                   420                  425                  430  
 Leu Phe Ser Gln Arg Ala Gln Tyr Val Asp Cys Lys Asn Leu Pro Asp  
                   435                  440                  445  
 Leu Asp Glu Gln Arg Lys Thr Glu Asn Asn Ile Glu Lys Asn Gly Gly  
                   450                  455                  460  
 Pro Ile Lys Lys Glu Tyr Ser Ser Arg Gly Phe Pro Thr Glu Phe Arg  
                   465                  470                  475                  480  
 Phe Val Val Arg Lys Gly His Tyr Asp Arg Tyr Arg Asn Glu Gly Trp  
                   485                  490                  495  
 Gly Tyr Leu Lys Asn Tyr Cys Lys His Asn Phe Ala Asn His Ala Met  
                   500                  505                  510  
 Ala Glu Ala Val Val Asp Lys Ala Val Ile Asp Tyr Gly Ser Ser Pro  
                   515                  520                  525  
 Gly Thr Ser Tyr Tyr Lys Phe Glu Lys Thr Val Tyr Phe Leu Asp Cys  
                   530                  535                  540  
 Arg Thr Tyr Thr Phe Asn Lys Asn Ser Gly Cys Lys Glu Met His Ala  
                   545                  550                  555                  560  
 Pro Gln Trp Val Thr Ile Ile Tyr Asn Pro His Thr Phe Thr Gly Ala  
                   565                  570                  575  
 Asn Ser Asn Arg Pro Lys Gly Val Ile Ser Ala Trp Cys Asn Ser Thr  
                   580                  585                  590  
 Pro Pro Gly Gly Ile Glu His Glu Pro Glu Ile Ser Gln Cys Pro Asp  
                   595                  600                  605  
 His Val Asn Leu Tyr Asn Lys Leu Arg Ile  
                   610                  615

&lt;210&gt; 609

&lt;211&gt; 2199

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(2176)

&lt;223&gt; RXS02641

&lt;400&gt; 609

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aggcttctca gttgtttcat atagtctcag ccgcaccaat atcatcaggg agaacatcgt 60

gcagcaacga cgccgcatca gcgagactcg gaaaaaacccg atg ctc gct att att 115
                                   Met Leu Ala Ile Ile
                                   1 5

ttg acc gcc gta ttg ggc gca tct ggc ctt gca gcc gct ggc act cag 163
Leu Thr Ala Val Leu Gly Ala Ser Gly Leu Ala Ala Ala Gly Thr Gln
                                   10 15 20

tac ctc aat act cag ggc gaa ggc atc ggt ccg gtc gcc gtc caa aac 211
Tyr Leu Asn Thr Gln Gly Glu Gly Ile Gly Pro Val Ala Val Gln Asn
                                   25 30 35

gac agt gaa tcg ttt aat tcc ggc acc aac gtg gtt gtt gaa gac gca 259
Asp Ser Glu Ser Phe Asn Ser Gly Thr Asn Val Val Val Glu Asp Ala
                                   40 45 50

gca gtc acc gcc cag ggt gaa ggc gga ggc gct cgc acc gtc aag gaa 307
Ala Val Thr Ala Gln Gly Glu Gly Gly Gly Ala Arg Thr Val Lys Glu
                                   55 60 65

ttc cag cgt gac cag caa ttc tct agt ttt gct ctt acc tgg acc ggt 355
Phe Gln Arg Asp Gln Gln Phe Ser Ser Phe Ala Leu Thr Trp Thr Gly
                                   70 75 80 85

aaa aaa gac atc act gct ttt gtt cgc gca gaa cag gaa gac ggc acc 403
Lys Lys Asp Ile Thr Ala Phe Val Arg Ala Glu Gln Glu Asp Gly Thr
                                   90 95 100

tgg tca cag tgg tac gac ttg gag cca atg gtc aat gaa gat caa ggc 451
Trp Ser Gln Trp Tyr Asp Leu Glu Pro Met Val Asn Glu Asp Gln Gly
                                   105 110 115

acc aac gga act gag ctg atc tgg cac ggc cct acc aac aag atc cag 499
Thr Asn Gly Thr Glu Leu Ile Trp His Gly Pro Thr Asn Lys Ile Gln
                                   120 125 130

gtt tcc acc ctc aac gtg gat ctc ttt gga gca gat gct gca gcc gct 547
Val Ser Thr Leu Asn Val Asp Leu Phe Gly Ala Asp Ala Ala Ala Ala
                                   135 140 145

gat gaa aac ggt caa gac att cca gca gta gat gca gcc gag gca gcg 595
Asp Glu Asn Gly Gln Asp Ile Pro Ala Val Asp Ala Ala Glu Ala Ala
                                   150 155 160 165

cca gca gca gaa cct gca cca gct gaa gca cca gtc gag gaa gct cct 643
Pro Ala Ala Glu Pro Ala Pro Ala Glu Ala Pro Val Glu Glu Ala Pro
                                   170 175 180

gca cct gtc gca gaa cca gca cca gct gct gaa cct atc gct gag cca 691
Ala Pro Val Ala Glu Pro Ala Pro Ala Ala Glu Pro Ile Ala Glu Pro
                                   185 190 195

gtc gct gat tac tca gca aat gac ggc ctc gct ccc ctg cca tcc aac 739

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Val	Ala	Asp	Tyr	Ser	Ala	Asn	Asp	Gly	Leu	Ala	Pro	Leu	Pro	Ser	Asn		
		200					205					210					
tat	ggc	gac	atc	cag	cct	gtt	gcc	gat	gtt	gat	gac	ggc	cta	aac	gca	787	
Tyr	Gly	Asp	Ile	Gln	Pro	Val	Ala	Asp	Val	Asp	Asp	Gly	Leu	Asn	Ala		
	215					220				225							
gta	ttt	atc	gat	ggc	aac	gct	gat	gca	ggc	gtg	ggg	atc	gct	aac	gtt	835	
Val	Phe	Ile	Asp	Gly	Asn	Ala	Asp	Ala	Gly	Val	Gly	Ile	Ala	Asn	Val		
230					235					240					245		
gct	gac	acc	gat	ggc	atg	cca	aag	gtg	att	tct	cgt	gct	ggg	tgg	ggg	883	
Ala	Asp	Thr	Asp	Gly	Met	Pro	Lys	Val	Ile	Ser	Arg	Ala	Gly	Trp	Gly		
				250					255					260			
gcg	gac	gaa	agt	ctg	cgc	tgc	tca	aac	cca	act	att	gat	gat	ggc	gtt	931	
Ala	Asp	Glu	Ser	Leu	Arg	Cys	Ser	Asn	Pro	Thr	Ile	Asp	Asp	Gly	Val		
			265					270					275				
tct	gcg	atc	acc	att	cac	cac	act	gcg	ggg	tcc	aac	aac	tac	acc	gag	979	
Ser	Ala	Ile	Thr	Ile	His	His	Thr	Ala	Gly	Ser	Asn	Asn	Tyr	Thr	Glu		
		280					285					290					
gcg	cag	gct	gca	gcc	cag	gtt	cgt	agt	gct	tac	agc	tac	cac	gcc	aag	1027	
Ala	Gln	Ala	Ala	Ala	Gln	Val	Arg	Ser	Ala	Tyr	Ser	Tyr	His	Ala	Lys		
	295					300					305						
aac	ctc	ggc	tgg	tgc	gat	atc	gga	tac	cag	tca	ttg	gtt	gat	aag	tac	1075	
Asn	Leu	Gly	Trp	Cys	Asp	Ile	Gly	Tyr	Gln	Ser	Leu	Val	Asp	Lys	Tyr		
310					315				320						325		
ggc	aac	atc	tac	gaa	ggc	cgt	gcc	ggc	ggc	atg	acc	aat	gct	gtt	cag	1123	
Gly	Asn	Ile	Tyr	Glu	Gly	Arg	Ala	Gly	Gly	Met	Thr	Asn	Ala	Val	Gln		
				330					335					340			
ggg	gct	cac	gct	ggc	ggc	ttc	aac	cag	aat	act	tgg	gca	atc	tcc	atg	1171	
Gly	Ala	His	Ala	Gly	Gly	Phe	Asn	Gln	Asn	Thr	Trp	Ala	Ile	Ser	Met		
			345					350					355				
att	ggc	gac	tat	tcc	tac	aac	gct	ccc	cct	cag	gaa	acc	atc	aat	gct	1219	
Ile	Gly	Asp	Tyr	Ser	Tyr	Asn	Ala	Pro	Pro	Gln	Glu	Thr	Ile	Asn	Ala		
		360					365					370					
gtc	ggg	gag	ctt	gct	ggg	tgg	cgt	gca	aag	gtt	gcc	ggg	ttc	gac	cca	1267	
Val	Gly	Glu	Leu	Ala	Gly	Trp	Arg	Ala	Lys	Val	Ala	Gly	Phe	Asp	Pro		
	375					380					385						
act	ggg	act	gat	act	cac	tac	tcg	gag	ggg	act	tct	tac	gcg	aag	tac	1315	
Thr	Gly	Thr	Asp	Thr	His	Tyr	Ser	Glu	Gly	Thr	Ser	Tyr	Ala	Lys	Tyr		
390					395					400					405		
tcc	tat	ggc	acc	cga	gtg	tca	ctt	cct	aat	atc	ttg	gct	cac	cgc	aat	1363	
Ser	Tyr	Gly	Thr	Arg	Val	Ser	Leu	Pro	Asn	Ile	Leu	Ala	His	Arg	Asn		
				410					415					420			
gtc	ggc	ctg	acc	gca	tgt	cct	ggc	gat	gct	ggc	tat	gcg	caa	atg	gag	1411	
Val	Gly	Leu	Thr	Ala	Cys	Pro	Gly	Asp	Ala	Gly	Tyr	Ala	Gln	Met	Glu		
			425					430				435					
aat	atc	cgc	cag	atc	gtt	aag	gca	aag	tac	acc	agc	ttg	cag	aat	ggc	1459	
Asn	Ile	Arg	Gln	Ile	Val	Lys	Ala	Lys	Tyr	Thr	Ser	Leu	Gln	Asn	Gly		

440	445	450	
aac aca ggt ggc acg act acc acc ccg gcg aca acg ccg aag gag acg Asn Thr Gly Gly Thr Thr Thr Thr Pro Ala Thr Thr Pro Lys Glu Thr 455 460 465			1507
tcg aca agc aat gct cct tcg acg acc act gcc cag ctt gta act ccc Ser Thr Ser Asn Ala Pro Ser Thr Thr Thr Ala Gln Leu Val Thr Pro 470 475 480 485			1555
gct gaa cct cag cag tac agc gaa tcc gat gcc ctg gca gct ctg ctg Ala Glu Pro Gln Gln Tyr Ser Glu Ser Asp Ala Leu Ala Ala Leu Leu 490 495 500			1603
aca ggt ggc tct tcc ggc ggc acc gac ctg ctc aat ggc gca aac tct Thr Gly Gly Ser Ser Gly Gly Thr Asp Leu Leu Asn Gly Ala Asn Ser 505 510 515			1651
gag cag ctc ctg act ggc ctg ggt tcc att gcg gct gtg ctg att gct Glu Gln Leu Leu Thr Gly Leu Gly Ser Ile Ala Ala Val Leu Ile Ala 520 525 530			1699
gcg tct ttg gct gat ggt ggc ctg aat ggt ctg atc agc aat gtt ggt Ala Ser Leu Ala Asp Gly Gly Leu Asn Gly Leu Ile Ser Asn Val Gly 535 540 545			1747
agc aac aac ggc gtc cca gtg ctt ggc gat atc aag atc act gac gtc Ser Asn Asn Gly Val Pro Val Leu Gly Asp Ile Lys Ile Thr Asp Val 550 555 560 565			1795
atc cca atc gtt gat acc gcg atc aac cta acc gga gac aat aag tac Ile Pro Ile Val Asp Thr Ala Ile Asn Leu Thr Gly Asp Asn Lys Tyr 570 575 580			1843
tct cgc ggt tgg aac gac ctg aac aac acg ctt gga cca gtg ctt ggc Ser Arg Gly Trp Asn Asp Leu Asn Asn Thr Leu Gly Pro Val Leu Gly 585 590 595			1891
gct gcc act ggt ggc gaa acc acc gtg aag tac acc agc gac cag aac Ala Ala Thr Gly Gly Glu Thr Thr Val Lys Tyr Thr Ser Asp Gln Asn 600 605 610			1939
tct gag gtt act ttc gtg ccg ttt gaa aat ggc atc atg gtg tct tcc Ser Glu Val Thr Phe Val Pro Phe Glu Asn Gly Ile Met Val Ser Ser 615 620 625			1987
cct gag gct gga act cac ggc ctg tgg ggc gca atc ggt gac gcg tgg Pro Glu Ala Gly Thr His Gly Leu Trp Gly Ala Ile Gly Asp Ala Trp 630 635 640 645			2035
gct cag cag ggc gct gac ctt ggc cct ctg gga ctt cca acc agt aat Ala Gln Gln Gly Ala Asp Leu Gly Pro Leu Gly Leu Pro Thr Ser Asn 650 655 660			2083
gaa tac acc gtt ggc gaa cag ctt cgt gtt gat ttc cag aat ggt tac Glu Tyr Thr Val Gly Glu Gln Leu Arg Val Asp Phe Gln Asn Gly Tyr 665 670 675			2131
atc act tac gat tct gcg act ggc cag gca agc att cag ctg aac Ile Thr Tyr Asp Ser Ala Thr Gly Gln Ala Ser Ile Gln Leu Asn 680 685 690			2176

tagtctcaat tagagccgaa aac

2199

&lt;210&gt; 610

&lt;211&gt; 692

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 610

Met Leu Ala Ile Ile Leu Thr Ala Val Leu Gly Ala Ser Gly Leu Ala  
 1 5 10 15

Ala Ala Gly Thr Gln Tyr Leu Asn Thr Gln Gly Glu Gly Ile Gly Pro  
 20 25 30

Val Ala Val Gln Asn Asp Ser Glu Ser Phe Asn Ser Gly Thr Asn Val  
 35 40 45

Val Val Glu Asp Ala Ala Val Thr Ala Gln Gly Glu Gly Gly Gly Ala  
 50 55 60

Arg Thr Val Lys Glu Phe Gln Arg Asp Gln Gln Phe Ser Ser Phe Ala  
 65 70 75 80

Leu Thr Trp Thr Gly Lys Lys Asp Ile Thr Ala Phe Val Arg Ala Glu  
 85 90 95

Gln Glu Asp Gly Thr Trp Ser Gln Trp Tyr Asp Leu Glu Pro Met Val  
 100 105 110

Asn Glu Asp Gln Gly Thr Asn Gly Thr Glu Leu Ile Trp His Gly Pro  
 115 120 125

Thr Asn Lys Ile Gln Val Ser Thr Leu Asn Val Asp Leu Phe Gly Ala  
 130 135 140

Asp Ala Ala Ala Ala Asp Glu Asn Gly Gln Asp Ile Pro Ala Val Asp  
 145 150 155 160

Ala Ala Glu Ala Ala Pro Ala Ala Glu Pro Ala Pro Ala Glu Ala Pro  
 165 170 175

Val Glu Glu Ala Pro Ala Pro Val Ala Glu Pro Ala Pro Ala Ala Glu  
 180 185 190

Pro Ile Ala Glu Pro Val Ala Asp Tyr Ser Ala Asn Asp Gly Leu Ala  
 195 200 205

Pro Leu Pro Ser Asn Tyr Gly Asp Ile Gln Pro Val Ala Asp Val Asp  
 210 215 220

Asp Gly Leu Asn Ala Val Phe Ile Asp Gly Asn Ala Asp Ala Gly Val  
 225 230 235 240

Gly Ile Ala Asn Val Ala Asp Thr Asp Gly Met Pro Lys Val Ile Ser  
 245 250 255

Arg Ala Gly Trp Gly Ala Asp Glu Ser Leu Arg Cys Ser Asn Pro Thr  
 260 265 270

Ile Asp Asp Gly Val Ser Ala Ile Thr Ile His His Thr Ala Gly Ser  
 275 280 285  
 Asn Asn Tyr Thr Glu Ala Gln Ala Ala Ala Gln Val Arg Ser Ala Tyr  
 290 295 300  
 Ser Tyr His Ala Lys Asn Leu Gly Trp Cys Asp Ile Gly Tyr Gln Ser  
 305 310 315 320  
 Leu Val Asp Lys Tyr Gly Asn Ile Tyr Glu Gly Arg Ala Gly Gly Met  
 325 330 335  
 Thr Asn Ala Val Gln Gly Ala His Ala Gly Gly Phe Asn Gln Asn Thr  
 340 345 350  
 Trp Ala Ile Ser Met Ile Gly Asp Tyr Ser Tyr Asn Ala Pro Pro Gln  
 355 360 365  
 Glu Thr Ile Asn Ala Val Gly Glu Leu Ala Gly Trp Arg Ala Lys Val  
 370 375 380  
 Ala Gly Phe Asp Pro Thr Gly Thr Asp Thr His Tyr Ser Glu Gly Thr  
 385 390 395 400  
 Ser Tyr Ala Lys Tyr Ser Tyr Gly Thr Arg Val Ser Leu Pro Asn Ile  
 405 410 415  
 Leu Ala His Arg Asn Val Gly Leu Thr Ala Cys Pro Gly Asp Ala Gly  
 420 425 430  
 Tyr Ala Gln Met Glu Asn Ile Arg Gln Ile Val Lys Ala Lys Tyr Thr  
 435 440 445  
 Ser Leu Gln Asn Gly Asn Thr Gly Gly Thr Thr Thr Thr Pro Ala Thr  
 450 455 460  
 Thr Pro Lys Glu Thr Ser Thr Ser Asn Ala Pro Ser Thr Thr Thr Ala  
 465 470 475 480  
 Gln Leu Val Thr Pro Ala Glu Pro Gln Gln Tyr Ser Glu Ser Asp Ala  
 485 490 495  
 Leu Ala Ala Leu Leu Thr Gly Gly Ser Ser Gly Gly Thr Asp Leu Leu  
 500 505 510  
 Asn Gly Ala Asn Ser Glu Gln Leu Leu Thr Gly Leu Gly Ser Ile Ala  
 515 520 525  
 Ala Val Leu Ile Ala Ala Ser Leu Ala Asp Gly Gly Leu Asn Gly Leu  
 530 535 540  
 Ile Ser Asn Val Gly Ser Asn Asn Gly Val Pro Val Leu Gly Asp Ile  
 545 550 555 560  
 Lys Ile Thr Asp Val Ile Pro Ile Val Asp Thr Ala Ile Asn Leu Thr  
 565 570 575  
 Gly Asp Asn Lys Tyr Ser Arg Gly Trp Asn Asp Leu Asn Asn Thr Leu  
 580 585 590  
 Gly Pro Val Leu Gly Ala Ala Thr Gly Gly Glu Thr Thr Val Lys Tyr

595	600	605
Thr Ser Asp Gln Asn Ser Glu Val Thr Phe Val Pro Phe Glu Asn Gly		
610	615	620
Ile Met Val Ser Ser Pro Glu Ala Gly Thr His Gly Leu Trp Gly Ala		
625	630	635
Ile Gly Asp Ala Trp Ala Gln Gln Gly Ala Asp Leu Gly Pro Leu Gly		
	645	650
Leu Pro Thr Ser Asn Glu Tyr Thr Val Gly Glu Gln Leu Arg Val Asp		
	660	665
Phe Gln Asn Gly Tyr Ile Thr Tyr Asp Ser Ala Thr Gly Gln Ala Ser		
	675	680
Ile Gln Leu Asn		
690		

<210> 611  
 <211> 702  
 <212> DNA  
 <213> Corynebacterium glutamicum

<220>  
 <221> CDS  
 <222> (101)..(679)  
 <223> RXS02650

<400> 611  
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 attgagcctg ggtggaagtt tctaccgctc atggggaaaag atg gtc aac gtg acc 115  
 Met Val Asn Val Thr  
 1 5  
 tca aag gat gca ggg gca aac gtg acc ccc atg agt aag aaa gaa aag 163  
 Ser Lys Asp Ala Gly Ala Asn Val Thr Pro Met Ser Lys Lys Glu Lys  
 10 15 20  
 agg aca acc gtt aaa cag gtg gtt gcc ttg atg gcc gcc atc gtt gtg 211  
 Arg Thr Thr Val Lys Gln Val Val Ala Leu Met Ala Ala Ile Val Val  
 25 30 35  
 gtg att gcg tcc cta gac caa ata gtc aag cag att atg ctt agt tgg 259  
 Val Ile Ala Ser Leu Asp Gln Ile Val Lys Gln Ile Met Leu Ser Trp  
 40 45 50  
 ttg gaa cct ggc gtt ccc gtt ccc atc att ggg gat tgg ttc cgc ttc 307  
 Leu Glu Pro Gly Val Pro Val Pro Ile Ile Gly Asp Trp Phe Arg Phe  
 55 60 65  
 tac ctc ctg ttt aac ccc gga gcc gca ttt tcg atg ggt ggg gaa aac 355  
 Tyr Leu Leu Phe Asn Pro Gly Ala Ala Phe Ser Met Gly Gly Glu Asn  
 70 75 80 85  
 agc acc tgg atc ttt aca acc atc cag ttg agc ttc gtc atc ggt atc 403  
 Ser Thr Trp Ile Phe Thr Thr Ile Gln Leu Ser Phe Val Ile Gly Ile  
 90 95 100

gca att tat gcc cca cgc atc aaa cac aag tgg atc gcg gca gga ctt 451  
 Ala Ile Tyr Ala Pro Arg Ile Lys His Lys Trp Ile Ala Ala Gly Leu  
                   105                                  110                                  115

gcc ctt gtt gcc ggt gga gcc ttg gga aac gtg ttg gac cgg ttg ttc 499  
 Ala Leu Val Ala Gly Gly Ala Leu Gly Asn Val Leu Asp Arg Leu Phe  
                   120                                  125                                  130

aga gat cct tcc ttc ttc ttc gga cat gtt gtt gat tac atc tcc gta 547  
 Arg Asp Pro Ser Phe Phe Phe Gly His Val Val Asp Tyr Ile Ser Val  
                   135                                  140                                  145

gga aac ttt gca gta ttt aat atc gcc gat gcc tcg att tct tgc ggc 595  
 Gly Asn Phe Ala Val Phe Asn Ile Ala Asp Ala Ser Ile Ser Cys Gly  
                   150                                  155                                  160                                  165

gtc gtg gtg ttc ctg atc gga atg ttc ctt gag gac cgt gaa aac gcc 643  
 Val Val Val Phe Leu Ile Gly Met Phe Leu Glu Asp Arg Glu Asn Ala  
                                   170                                  175                                  180

cag cat gcc aaa gca act gac gag aag gat gag gcc tgatgaacaa 689  
 Gln His Ala Lys Ala Thr Asp Glu Lys Asp Glu Ala  
                                   185                                  190

ccgacaaagc aga 702

&lt;210&gt; 612

&lt;211&gt; 193

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 612

Met Val Asn Val Thr Ser Lys Asp Ala Gly Ala Asn Val Thr Pro Met  
   1                                  5                                  10                                  15

Ser Lys Lys Glu Lys Arg Thr Thr Val Lys Gln Val Val Ala Leu Met  
                   20                                  25                                  30

Ala Ala Ile Val Val Val Ile Ala Ser Leu Asp Gln Ile Val Lys Gln  
                   35                                  40                                  45

Ile Met Leu Ser Trp Leu Glu Pro Gly Val Pro Val Pro Ile Ile Gly  
                   50                                  55                                  60

Asp Trp Phe Arg Phe Tyr Leu Leu Phe Asn Pro Gly Ala Ala Phe Ser  
   65                                  70                                  75                                  80

Met Gly Gly Glu Asn Ser Thr Trp Ile Phe Thr Thr Ile Gln Leu Ser  
                   85                                  90                                  95

Phe Val Ile Gly Ile Ala Ile Tyr Ala Pro Arg Ile Lys His Lys Trp  
                   100                                  105                                  110

Ile Ala Ala Gly Leu Ala Leu Val Ala Gly Gly Ala Leu Gly Asn Val  
                   115                                  120                                  125

Leu Asp Arg Leu Phe Arg Asp Pro Ser Phe Phe Phe Gly His Val Val  
   130                                  135                                  140

Asp Tyr Ile Ser Val Gly Asn Phe Ala Val Phe Asn Ile Ala Asp Ala  
145 150 155 160

Ser Ile Ser Cys Gly Val Val Val Phe Leu Ile Gly Met Phe Leu Glu  
165 170 175

Asp Arg Glu Asn Ala Gln His Ala Lys Ala Thr Asp Glu Lys Asp Glu  
180 185 190

Ala

<210> 613

<211> 1494

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1471)

<223> RXS00076

<400> 613

tctaggagtg ttaaacagcc tggacttgaa acacctttaa ctacttgatt ttcacaccct 60

tggtttccata aaaggggtca cgaaaggcaa cttcaaacac atg aca act ccc ctg 115  
Met Thr Thr Pro Leu  
1 5

cgc gta gcc gtc atc gga gct ggc cct gct ggc att tac gca tcc gac 163  
Arg Val Ala Val Ile Gly Ala Gly Pro Ala Gly Ile Tyr Ala Ser Asp  
10 15 20

ctc ctc atc cgc aat gaa gag cgc gaa gtg ttc gtt gac ctt ttc gag 211  
Leu Leu Ile Arg Asn Glu Glu Arg Glu Val Phe Val Asp Leu Phe Glu  
25 30 35

caa atg cct gca ccg ttc gga ctc atc cgt tac ggc gtt gct cca gac 259  
Gln Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr Gly Val Ala Pro Asp  
40 45 50

cac cca cgc atc aag ggc atc gtt aag tcc ctg cac aac gtg ttg gac 307  
His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu His Asn Val Leu Asp  
55 60 65

aag cca cgc ctg cgc ctg ctc ggt aac att gaa atc ggc aaa gac atc 355  
Lys Pro Arg Leu Arg Leu Leu Gly Asn Ile Glu Ile Gly Lys Asp Ile  
70 75 80 85

acc gtc gaa gaa ctc cgc gac tac tac gat gca gtc gtg ttc tcc acc 403  
Thr Val Glu Glu Leu Arg Asp Tyr Tyr Asp Ala Val Val Phe Ser Thr  
90 95 100

ggc gca gtt gca gac cgc gac ctc aac atc ccc gga att gaa gca gaa 451  
Gly Ala Val Ala Asp Arg Asp Leu Asn Ile Pro Gly Ile Glu Ala Glu  
105 110 115

ggc tcc ttc ggt gcc ggc gag ttc gtt ggc ttc tac gac ggc aac cca 499  
Gly Ser Phe Gly Ala Gly Glu Phe Val Gly Phe Tyr Asp Gly Asn Pro  
120 125 130

cgc ttc gag cgc tcc tgg gat ctg tct gca cag tcc gtc gct gtt atc	547
Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln Ser Val Ala Val Ile	
135 140 145	
ggc gtt ggt aac gtc ggc ctc gac gta gcc cgc atc ctg gct aag aca	595
Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg Ile Leu Ala Lys Thr	
150 155 160 165	
ggc gac gag ctc aaa gtc acc gaa att tcc gac aac gtc tac gac tcc	643
Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp Asn Val Tyr Asp Ser	
170 175 180	
ctc aaa gaa aac aag gcc act gaa gtg cac gtt ttc gga cgt cgt ggc	691
Leu Lys Glu Asn Lys Ala Thr Glu Val His Val Phe Gly Arg Arg Gly	
185 190 195	
cca gca cag gtc aag ttc acc cca cag gaa ctc aaa gaa ctc gac cac	739
Pro Ala Gln Val Lys Phe Thr Pro Gln Glu Leu Lys Glu Leu Asp His	
200 205 210	
tcc ccc acc atc aac gtg gtt gtt gat cca gaa gac atc gac tac gac	787
Ser Pro Thr Ile Asn Val Val Val Asp Pro Glu Asp Ile Asp Tyr Asp	
215 220 225	
ggc gcc tct gaa gaa gcc cgc cgc gca tcc aag tcc cag gac ctg gtc	835
Gly Ala Ser Glu Glu Ala Arg Arg Ala Ser Lys Ser Gln Asp Leu Val	
230 235 240 245	
tgc cag atc ctg gaa cag tac gca atc cgc gag cca aag gac gct ccg	883
Cys Gln Ile Leu Glu Gln Tyr Ala Ile Arg Glu Pro Lys Asp Ala Pro	
250 255 260	
cac acc ctg cag atc cac ctc ttt gaa aac cca gtt gag gtt ctt caa	931
His Thr Leu Gln Ile His Leu Phe Glu Asn Pro Val Glu Val Leu Gln	
265 270 275	
aag gac ggc aag gtt gtt ggc ctg cgc acc gaa cgc acc tca ctt gat	979
Lys Asp Gly Lys Val Val Gly Leu Arg Thr Glu Arg Thr Ser Leu Asp	
280 285 290	
ggc aac ggc ggc gta aac gga acc ggc gaa ttc aag gac tgg cca gtc	1027
Gly Asn Gly Gly Val Asn Gly Thr Gly Glu Phe Lys Asp Trp Pro Val	
295 300 305	
cag gct gtc tac cgc gca gtc ggc tac aag tcc gac ccc atc gac ggc	1075
Gln Ala Val Tyr Arg Ala Val Gly Tyr Lys Ser Asp Pro Ile Asp Gly	
310 315 320 325	
gtc cca ttc gat gag aac aag cac gtc atc cct aat gac ggc gga cat	1123
Val Pro Phe Asp Glu Asn Lys His Val Ile Pro Asn Asp Gly Gly His	
330 335 340	
gtc ctc acc gct cca ggc gca gaa cca gta cca ggc ctc tat gca acc	1171
Val Leu Thr Ala Pro Gly Ala Glu Pro Val Pro Gly Leu Tyr Ala Thr	
345 350 355	
ggc tgg atc aag cgt gga cca atc ggt cta atc ggc aac acc aag tcc	1219
Gly Trp Ile Lys Arg Gly Pro Ile Gly Leu Ile Gly Asn Thr Lys Ser	
360 365 370	

gac gcc aag gaa acc acc gac atc ctc atc aag gat gcc gtc gcc ggt 1267  
 Asp Ala Lys Glu Thr Thr Asp Ile Leu Ile Lys Asp Ala Val Ala Gly  
 375 380 385  
  
 gta ctt gaa gct cca aag cac cag ggc gaa gaa gcc atc atc gag ctt 1315  
 Val Leu Glu Ala Pro Lys His Gln Gly Glu Glu Ala Ile Ile Glu Leu  
 390 395 400 405  
  
 ctc gat tcc cgc aac atc cca ttc acc acc tgg gaa ggc tgg tac aaa 1363  
 Leu Asp Ser Arg Asn Ile Pro Phe Thr Thr Trp Glu Gly Trp Tyr Lys  
 410 415 420  
  
 ctc gac gca gca gag cgc gca ctc ggt gaa gcc gaa ggc cgc gag cgc 1411  
 Leu Asp Ala Ala Glu Arg Ala Leu Gly Glu Ala Glu Gly Arg Glu Arg  
 425 430 435  
  
 aag aag att gtt gat tgg gaa gaa atg gtc cgc cag gcc cgc gaa gct 1459  
 Lys Lys Ile Val Asp Trp Glu Glu Met Val Arg Gln Ala Arg Glu Ala  
 440 445 450  
  
 cca gca att gtc taaattgttt taacgcgtga agc 1494  
 Pro Ala Ile Val  
 455

&lt;210&gt; 614

&lt;211&gt; 457

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium glutamicum

&lt;400&gt; 614

Met Thr Thr Pro Leu Arg Val Ala Val Ile Gly Ala Gly Pro Ala Gly  
 1 5 10 15  
  
 Ile Tyr Ala Ser Asp Leu Leu Ile Arg Asn Glu Glu Arg Glu Val Phe  
 20 25 30  
  
 Val Asp Leu Phe Glu Gln Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr  
 35 40 45  
  
 Gly Val Ala Pro Asp His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu  
 50 55 60  
  
 His Asn Val Leu Asp Lys Pro Arg Leu Arg Leu Leu Gly Asn Ile Glu  
 65 70 75 80  
  
 Ile Gly Lys Asp Ile Thr Val Glu Glu Leu Arg Asp Tyr Tyr Asp Ala  
 85 90 95  
  
 Val Val Phe Ser Thr Gly Ala Val Ala Asp Arg Asp Leu Asn Ile Pro  
 100 105 110  
  
 Gly Ile Glu Ala Glu Gly Ser Phe Gly Ala Gly Glu Phe Val Gly Phe  
 115 120 125  
  
 Tyr Asp Gly Asn Pro Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln  
 130 135 140  
  
 Ser Val Ala Val Ile Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg  
 145 150 155 160

Ile Leu Ala Lys Thr Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp  
 165 170 175  
 Asn Val Tyr Asp Ser Leu Lys Glu Asn Lys Ala Thr Glu Val His Val  
 180 185 190  
 Phe Gly Arg Arg Gly Pro Ala Gln Val Lys Phe Thr Pro Gln Glu Leu  
 195 200 205  
 Lys Glu Leu Asp His Ser Pro Thr Ile Asn Val Val Val Asp Pro Glu  
 210 215 220  
 Asp Ile Asp Tyr Asp Gly Ala Ser Glu Glu Ala Arg Arg Ala Ser Lys  
 225 230 235 240  
 Ser Gln Asp Leu Val Cys Gln Ile Leu Glu Gln Tyr Ala Ile Arg Glu  
 245 250 255  
 Pro Lys Asp Ala Pro His Thr Leu Gln Ile His Leu Phe Glu Asn Pro  
 260 265 270  
 Val Glu Val Leu Gln Lys Asp Gly Lys Val Val Gly Leu Arg Thr Glu  
 275 280 285  
 Arg Thr Ser Leu Asp Gly Asn Gly Gly Val Asn Gly Thr Gly Glu Phe  
 290 295 300  
 Lys Asp Trp Pro Val Gln Ala Val Tyr Arg Ala Val Gly Tyr Lys Ser  
 305 310 315 320  
 Asp Pro Ile Asp Gly Val Pro Phe Asp Glu Asn Lys His Val Ile Pro  
 325 330 335  
 Asn Asp Gly Gly His Val Leu Thr Ala Pro Gly Ala Glu Pro Val Pro  
 340 345 350  
 Gly Leu Tyr Ala Thr Gly Trp Ile Lys Arg Gly Pro Ile Gly Leu Ile  
 355 360 365  
 Gly Asn Thr Lys Ser Asp Ala Lys Glu Thr Thr Asp Ile Leu Ile Lys  
 370 375 380  
 Asp Ala Val Ala Gly Val Leu Glu Ala Pro Lys His Gln Gly Glu Glu  
 385 390 395 400  
 Ala Ile Ile Glu Leu Leu Asp Ser Arg Asn Ile Pro Phe Thr Thr Trp  
 405 410 415  
 Glu Gly Trp Tyr Lys Leu Asp Ala Ala Glu Arg Ala Leu Gly Glu Ala  
 420 425 430  
 Glu Gly Arg Glu Arg Lys Lys Ile Val Asp Trp Glu Glu Met Val Arg  
 435 440 445  
 Gln Ala Arg Glu Ala Pro Ala Ile Val  
 450 455

&lt;210&gt; 615

&lt;211&gt; 1488

&lt;212&gt; DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1465)

<223> RXS01438

<400> 615

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tccacatttt ttagaacccc ttttaaggaat cgaactttat atg tct cgc cct ttg 115
                                         Met Ser Arg Pro Leu
                                         1 5
cgt gtt gcc gtt gtc ggt gca ggt cca gca gga atc tac gcg tct gat 163
Arg Val Ala Val Val Gly Ala Gly Pro Ala Gly Ile Tyr Ala Ser Asp
                        10 15 20
ttg ttg atg aaa tcc gac acg gac gtg cag att gat ctt ttt gaa cgt 211
Leu Leu Met Lys Ser Asp Thr Asp Val Gln Ile Asp Leu Phe Glu Arg
                        25 30 35
atg cca gcg cct ttc ggt ttg atc cgt tat ggt gtt gcg cct gat cac 259
Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr Gly Val Ala Pro Asp His
                        40 45 50
cct cgc atc aag ggc atc gtg aag tcc ctg cac aat gtg atg gac aag 307
Pro Arg Ile Lys Gly Ile Val Lys Ser Leu His Asn Val Met Asp Lys
                        55 60 65
gag cag ctg cgt ttc ttg ggc aac att gag gtc ggc aag gac atc act 355
Glu Gln Leu Arg Phe Leu Gly Asn Ile Glu Val Gly Lys Asp Ile Thr
                        70 75 80 85
gtt gag gag ttg cgt gag ttt tat gac gcg atc gtg ttc tcc act ggc 403
Val Glu Glu Leu Arg Glu Phe Tyr Asp Ala Ile Val Phe Ser Thr Gly
                        90 95 100
gct act ggc gac cag gat ctt cgg gtt cca ggt tct gat ctg gaa ggt 451
Ala Thr Gly Asp Gln Asp Leu Arg Val Pro Gly Ser Asp Leu Glu Gly
                        105 110 115
tcg tgg ggc gct ggc gag ttc gtt ggt ttc tat gat ggc aac ccg aac 499
Ser Trp Gly Ala Gly Glu Phe Val Gly Phe Tyr Asp Gly Asn Pro Asn
                        120 125 130
ttt gaa cgc aac tgg gat ctt tct gct gag aag gta gcg gtt gtt ggt 547
Phe Glu Arg Asn Trp Asp Leu Ser Ala Glu Lys Val Ala Val Val Gly
                        135 140 145
gtc ggt aac gtg gcg ttg gac gtt gct cgt att ttg gcg aag act ggc 595
Val Gly Asn Val Ala Leu Asp Val Ala Arg Ile Leu Ala Lys Thr Gly
                        150 155 160 165
gat gag ctg cta gtt act gaa atc cct gac aat gtc tat gag agc ttg 643
Asp Glu Leu Leu Val Thr Glu Ile Pro Asp Asn Val Tyr Glu Ser Leu
                        170 175 180
gct aag aat cag gct aag gaa gtg cac gtt ttt ggt cgt cgt gga cct 691
Ala Lys Asn Gln Ala Lys Glu Val His Val Phe Gly Arg Arg Gly Pro
                        185 190 195
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gct cag gcg aag ttc act ccg ttg gag ctg aag gaa ctt gac cat tcc	739
Ala Gln Ala Lys Phe Thr Pro Leu Glu Leu Lys Glu Leu Asp His Ser	
200 205 210	
gac acc atc gag gtg atc gtg aac cct gag gac att gat tac gat gca	787
Asp Thr Ile Glu Val Ile Val Asn Pro Glu Asp Ile Asp Tyr Asp Ala	
215 220 225	
gct tcg gag cag gct cgt cgt gat tcc aag tct cag gac ctc gtg tgc	835
Ala Ser Glu Gln Ala Arg Arg Asp Ser Lys Ser Gln Asp Leu Val Cys	
230 235 240 245	
cag act ttg gaa agc tac gcg atg cgc gat cct aag ggc gct cct cac	883
Gln Thr Leu Glu Ser Tyr Ala Met Arg Asp Pro Lys Gly Ala Pro His	
250 255 260	
aag ctg ttc att cac ttc ttt gag tcc cca gtg gag atc ctc ggt gag	931
Lys Leu Phe Ile His Phe Phe Glu Ser Pro Val Glu Ile Leu Gly Glu	
265 270 275	
gac ggc aag gtt gtt ggc ctc aag act gag cgt act cag ctg gac ggc	979
Asp Gly Lys Val Val Gly Leu Lys Thr Glu Arg Thr Gln Leu Asp Gly	
280 285 290	
aac ggt ggc gtg act ggc acc ggc gag ttc aag acc tgg gat atg cag	1027
Asn Gly Gly Val Thr Gly Thr Gly Glu Phe Lys Thr Trp Asp Met Gln	
295 300 305	
tca gtt tac cgc gcg gta ggt tac cgt tct gat gcg atc gag ggt gtt	1075
Ser Val Tyr Arg Ala Val Gly Tyr Arg Ser Asp Ala Ile Glu Gly Val	
310 315 320 325	
cct ttt gac gat gag cgc gcg gtt gtc ccc aac gac ggc ggc cac atc	1123
Pro Phe Asp Asp Glu Arg Ala Val Val Pro Asn Asp Gly Gly His Ile	
330 335 340	
atc gat cct gag gtc ggc tcc ccc atc act ggc ctg tac gcc act ggc	1171
Ile Asp Pro Glu Val Gly Ser Pro Ile Thr Gly Leu Tyr Ala Thr Gly	
345 350 355	
tgg atc aag cgt ggc cca att gga ctg atc ggc aac acc aag tcc gac	1219
Trp Ile Lys Arg Gly Pro Ile Gly Leu Ile Gly Asn Thr Lys Ser Asp	
360 365 370	
gcc aag gaa acc act gag atg ctg ctt gct gat cac gct gct ggt tct	1267
Ala Lys Glu Thr Thr Glu Met Leu Leu Ala Asp His Ala Ala Gly Ser	
375 380 385	
ttg cct gcg cct gca aag cct gag ttg gag tcc atc att gag ttc ctc	1315
Leu Pro Ala Pro Ala Lys Pro Glu Leu Glu Ser Ile Ile Glu Phe Leu	
390 395 400 405	
gat gag cgc aag gtt gcg ttc acc aca tgg gat ggc tgg cac ctg ctg	1363
Asp Glu Arg Lys Val Ala Phe Thr Thr Trp Asp Gly Trp His Leu Leu	
410 415 420	
gat gct gcg gag cgc gcg ctg ggt gag cct gag ggc cgc gag cgc aag	1411
Asp Ala Ala Glu Arg Ala Leu Gly Glu Pro Glu Gly Arg Glu Arg Lys	
425 430 435	

aag atc gtt gag tgg aat gac atg gtg cgc cat gct cgt cca gaa tac 1459  
 Lys Ile Val Glu Trp Asn Asp Met Val Arg His Ala Arg Pro Glu Tyr  
           440                                  445                                  450

gac atc taaagtcgct taaagcctca aaa 1488  
 Asp Ile  
       455

<210> 616  
 <211> 455  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 616  
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Ile Tyr Ala Ser Asp Leu Leu Met Lys Ser Asp Thr Asp Val Gln Ile  
                                   20                                  25                                  30

Asp Leu Phe Glu Arg Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr Gly  
                                   35                                  40                                  45

Val Ala Pro Asp His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu His  
                                   50                                  55                                  60

Asn Val Met Asp Lys Glu Gln Leu Arg Phe Leu Gly Asn Ile Glu Val  
   65                                  70                                  75                                  80

Gly Lys Asp Ile Thr Val Glu Glu Leu Arg Glu Phe Tyr Asp Ala Ile  
                                   85                                  90                                  95

Val Phe Ser Thr Gly Ala Thr Gly Asp Gln Asp Leu Arg Val Pro Gly  
                                   100                                  105                                  110

Ser Asp Leu Glu Gly Ser Trp Gly Ala Gly Glu Phe Val Gly Phe Tyr  
                                   115                                  120                                  125

Asp Gly Asn Pro Asn Phe Glu Arg Asn Trp Asp Leu Ser Ala Glu Lys  
   130                                  135                                  140

Val Ala Val Val Gly Val Gly Asn Val Ala Leu Asp Val Ala Arg Ile  
 145                                  150                                  155                                  160

Leu Ala Lys Thr Gly Asp Glu Leu Leu Val Thr Glu Ile Pro Asp Asn  
                                   165                                  170                                  175

Val Tyr Glu Ser Leu Ala Lys Asn Gln Ala Lys Glu Val His Val Phe  
                                   180                                  185                                  190

Gly Arg Arg Gly Pro Ala Gln Ala Lys Phe Thr Pro Leu Glu Leu Lys  
                                   195                                  200                                  205

Glu Leu Asp His Ser Asp Thr Ile Glu Val Ile Val Asn Pro Glu Asp  
   210                                  215                                  220

Ile Asp Tyr Asp Ala Ala Ser Glu Gln Ala Arg Arg Asp Ser Lys Ser  
 225                                  230                                  235                                  240

Gln Asp Leu Val Cys Gln Thr Leu Glu Ser Tyr Ala Met Arg Asp Pro

245										250					255				
Lys	Gly	Ala	Pro	His	Lys	Leu	Phe	Ile	His	Phe	Phe	Glu	Ser	Pro	Val				
			260					265					270						
Glu	Ile	Leu	Gly	Glu	Asp	Gly	Lys	Val	Val	Gly	Leu	Lys	Thr	Glu	Arg				
		275					280					285							
Thr	Gln	Leu	Asp	Gly	Asn	Gly	Gly	Val	Thr	Gly	Thr	Gly	Glu	Phe	Lys				
	290					295					300								
Thr	Trp	Asp	Met	Gln	Ser	Val	Tyr	Arg	Ala	Val	Gly	Tyr	Arg	Ser	Asp				
305					310					315					320				
Ala	Ile	Glu	Gly	Val	Pro	Phe	Asp	Asp	Glu	Arg	Ala	Val	Val	Pro	Asn				
				325					330					335					
Asp	Gly	Gly	His	Ile	Ile	Asp	Pro	Glu	Val	Gly	Ser	Pro	Ile	Thr	Gly				
			340					345					350						
Leu	Tyr	Ala	Thr	Gly	Trp	Ile	Lys	Arg	Gly	Pro	Ile	Gly	Leu	Ile	Gly				
		355				360						365							
Asn	Thr	Lys	Ser	Asp	Ala	Lys	Glu	Thr	Thr	Glu	Met	Leu	Leu	Ala	Asp				
	370					375					380								
His	Ala	Ala	Gly	Ser	Leu	Pro	Ala	Pro	Ala	Lys	Pro	Glu	Leu	Glu	Ser				
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Ile	Ile	Glu	Phe	Leu	Asp	Glu	Arg	Lys	Val	Ala	Phe	Thr	Thr	Trp	Asp				
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